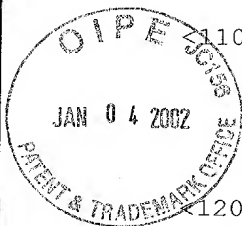


SEQUENCE LISTING



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<110> Pompejus, Markus
Kroger, Burkhard
Schroder, Hartwig
Zelder, Oskar
Haberhauer, Gregor

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INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
TRANSPORT

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Ser Gly Cys Gly Lys Ser Thr Val Leu Arg Ser Ile Asn Arg Met His
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Glu Val Thr Pro Gly Ala Tyr Val Lys Gly Glu Ile Leu Leu Asp Gly
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Glu Asn Ile Tyr Gly Ser Lys Ile Asp Pro Val Ala Val Arg Asn Thr
70 75 80 85

atc ggc atg gtc ttc cag aag gct aac cca ttc cca acc atg tcc atc 403
Ile Gly Met Val Phe Gln Lys Ala Asn Pro Phe Pro Thr Met Ser Ile
90 95 100

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Glu Asp Asn Val Val Ala Gly Leu Lys Leu Ser Gly Glu Lys Asn Lys
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aag aag ctc aag gaa gtt gct gag aag tct ctt cgt ggc gca aac ctg 499
Lys Lys Leu Lys Glu Val Ala Glu Lys Ser Leu Arg Gly Ala Asn Leu
120 125 130

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Trp	Glu	Glu	Val	Lys	Asp	Arg	Leu	Asp	Lys	Pro	Gly	Gly	Gly	Leu	Ser	
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Asp Gln Thr Ala Phe Tyr Ser Leu Glu Ala Thr Gly Arg Pro Gly Arg
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Ile Leu Leu Asp Gly Glu Asn Ile Tyr Gly Ser Lys Ile Asp Pro Val
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 85 90 95

Pro Thr Met Ser Ile Glu Asp Asn Val Val Ala Gly Leu Lys Leu Ser
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Gly Glu Lys Asn Lys Lys Lys Leu Lys Glu Val Ala Glu Lys Ser Leu
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Arg Gly Ala Asn Leu Trp Glu Glu Val Lys Asp Arg Leu Asp Lys Pro
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 165 170 175

Ala Leu Asp Pro Ile Ser Thr Leu Ala Val Glu Asp Leu Ile His Glu
 180 185 190

Leu Lys Glu Glu Phe Thr Ile Val Ile Val Thr His Asn Met Gln Gln
 195 200 205

Ala Ala Arg Val Ser Asp Gln Thr Ala Phe Tyr Ser Leu Glu Ala Thr
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 Met Thr Asn Asn Val
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gtt act ccg cgc atg gat gag cct tta aag aag agc tca gcc ttc acc 163
 Val Thr Pro Arg Met Asp Glu Pro Leu Lys Lys Ser Ser Ala Phe Thr
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gac atc tcc tcc agc cgt aag acc acc aac acc gca gca acc gtc atc 211
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 40 45 50

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 Trp Thr Val Ile Ser Arg Gly Ile Ala Pro Ile Leu Thr Ala Asp Trp
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 35 40 45

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 Leu Pro Gly Gly Gly Ala Ala His Ala Met Ile Gly Thr Phe Met Gln
 85 90 95
 Ala Val Val Thr Ser Val Ile Ser Ile Pro Ile Gly Ile Phe Thr Ala
 100 105 110
 Ile Tyr Leu Val Glu Tyr Ser Asn Gly Asn Arg Leu Gly Arg Leu Thr
 115 120 125
 Thr Phe Met Val Asp Ile Leu Thr Gly Val Pro Ser Ile Val Ala Ala
 130 135 140
 Leu Phe Val Tyr Ser Leu Trp Ile Val Leu Phe Gly Phe Asp Arg Ser
 145 150 155 160
 Gly Phe Ala Val Ser Leu Ser Leu Val Ile Leu Met Val Pro Val Ile
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 Glu Ala Ser Tyr Ala Leu Gly Val Pro Lys Trp Lys Thr Ile Ala Lys
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 Ile Val Leu Pro Thr Ala Leu Ser Gly Ile Val Thr Gly Val Met Leu
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 Ala Val Ala Arg Val Met Gly Glu Ser Ala Pro Val Leu Val Leu Val
 225 230 235 240
 Gly Ser Ser Gln Ala Ile Asn Trp Asn Pro Phe Gly Gly Pro Gln Ala
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 Ser Leu Pro Leu Met Met Leu Asp Met Tyr Lys Ala Gly Thr Ala Pro
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 Ala Thr Ala Arg Glu Val Phe Ile Gln Thr Pro Lys Gly His Ile Glu
 230 235 240 245
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 Pro Gly Asp Arg Ile Phe Glu Val Leu Ser Thr Ala Ser Ala Ala Ile
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Tyr Ser Gly Ala Trp Asn Thr Thr Asp Ile Asp Ala Met Tyr Phe Gly
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 Tyr Ser Pro Lys Arg Leu Val Lys Pro Leu Gly Tyr Met Val Asp Met
 145 150 155 160
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 165 170 175
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 Gly Ser Phe Phe Leu Phe Ala Thr Tyr Gln Asn Ser Pro Ser Phe Ala
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 Thr Gly Arg Asn Met Leu Thr Gly Gly Ile Val Leu Ala Val Met Ile
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 Leu Pro Val Ile Glu Ala Thr Ala Arg Glu Val Phe Ile Gln Thr Pro
 225 230 235 240
 Lys Gly His Ile Glu Ser Ala Leu Ala Leu Gly Ala Thr Arg Trp Glu
 245 250 255
 Val Val Arg Leu Thr Val Leu Pro Phe Gly Met Ser Gly Tyr Val Ser
 260 265 270
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 Asn Ala Glu Lys Leu Glu Glu Leu Arg Thr Gly Cys Glu Ser Gln Ala
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 Val Glu Leu Leu Ala Leu Glu Thr Pro Val Ala Arg Asp Leu Arg Gln
 40 45 50

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 Val Val Ser Ser Ile Tyr Ile Val Glu Glu Ile Thr Arg Met Gly Ala
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 Leu Ala Met His Val Ala Asn Ser Val Arg Arg Arg Tyr Pro Asp Pro
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 90 95 100

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 Ala Ala Asp Met Thr Asp His Ile Arg Gln Ile Leu Ile Asp Pro Glu
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 170 175 180

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 Ser Thr Gly Leu His Pro Glu Glu Tyr Met Glu Lys Arg Glu Gln Gln
 185 190 195

agg gcc gat gcc gac atg gag aag cgc tgg gcc gag ctg gag cgg cag 739
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777

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 Arg Asp Leu Arg Gln Val Val Ser Ser Ile Tyr Ile Val Glu Glu Ile
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 Thr Arg Met Gly Ala Leu Ala Met His Val Ala Asn Ser Val Arg Arg
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 Arg Tyr Pro Asp Pro Val Ile Pro Glu Asp Met Arg Gly Tyr Phe Lys
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 Glu Met Ala Arg Leu Ala Ala Asp Met Thr Asp His Ile Arg Gln Ile
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 Leu Ile Asp Pro Glu Pro Asp Leu Ala Leu Glu Met Ala Lys Ser Asp
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 Arg Pro Trp Pro His Asp Thr Lys Ser Ala Val Asp Leu Thr Leu Leu
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 Ser Arg Phe Tyr Glu Arg Tyr Ala Asp His Thr Val Asn Val Ala Ala
 165 170 175
 Arg Ile Ile Tyr Leu Ser Thr Gly Leu His Pro Glu Glu Tyr Met Glu
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Asp Val Arg Pro Gly Arg Val Leu Ala Leu Leu Gly Glu Asn Gly Ala
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Gly Lys Ser Thr Leu Ile Lys Met Met Ser Gly Val Tyr Gln Pro Asp
55 60 65

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Gly Gly Gln Ile Leu Val Asp Gly Lys Pro Thr Thr Leu Pro Asp Thr
70 75 80 85

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90 95 100

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Pro Arg Lys Trp Gly Leu Val Asn Phe Lys His Leu Arg Arg Gln Ala
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gcg ttg act ggt cgt gaa att gat cag tta ttc aaa gtg gtg gat cag 691
Ala Leu Thr Gly Arg Glu Ile Asp Gln Leu Phe Lys Val Val Asp Gln
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200 205 210

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cac att ccg gaa gat cga aaa gcc cag ggc ctg gtg ctg ggg tcg tct His Ile Pro Glu Asp Arg Lys Ala Gln Gly Leu Val Leu Gly Ser Ser 345 350 355	1171
gtg gag gac aac ctg gga ttg gcg act ttg gcg tcg aca gcc cgc gca Val Glu Asp Asn Leu Gly Leu Ala Thr Leu Ala Ser Thr Ala Arg Ala 360 365 370	1219
ggt ttg gtc gat cga tca gga cag cac aaa cga gcc gcc gag gtc gcg Gly Leu Val Asp Arg Ser Gly Gln His Lys Arg Ala Ala Glu Val Ala 375 380 385	1267
gaa aaa ctc cgc atc cgg atg gca agc ctc aaa caa ccg att agc gat Glu Lys Leu Arg Ile Arg Met Ala Ser Leu Lys Gln Pro Ile Ser Asp 390 395 400 405	1315
tta tcg ggc ggc aat cag caa aag gcc gtg ttc ggc cgc tgg gtg ctt Leu Ser Gly Gly Asn Gln Gln Lys Ala Val Phe Gly Arg Trp Val Leu 410 415 420	1363
gcc ggg tca aac gtg ctg ctt ctc gac gaa ccg acc cgt ggc gtt gac Ala Gly Ser Asn Val Leu Leu Leu Asp Glu Pro Thr Arg Gly Val Asp 425 430 435	1411
gtc ggc gcg aag gtg gaa att tac aac atc att aat gag atg acg gaa Val Gly Ala Lys Val Glu Ile Tyr Asn Ile Ile Asn Glu Met Thr Glu 440 445 450	1459

aaa ggt ggc gct gtg ctc atg gtg tca tgc gag ctt ccc gaa gtc ttg 1507
 Lys Gly Gly Ala Val Leu Met Val Ser Ser Glu Leu Pro Glu Val Leu
 455 460 465

ggc atg gct gat cgc att ttg gtc atg tct ggt gga cgc atc gca ggc 1555
 Gly Met Ala Asp Arg Ile Leu Val Met Ser Gly Gly Arg Ile Ala Gly
 470 475 480 485

gaa ctg cca gcg aag gga aca acc cag gac gat gtc atg gct cta gct 1603
 Glu Leu Pro Ala Lys Gly Thr Thr Gln Asp Asp Val Met Ala Leu Ala
 490 495 500

gtt tcc cag gtg gat gat tcc atc acc gag gaa gct gct gca gaa atc 1651
 Val Ser Gln Val Asp Asp Ser Ile Thr Glu Glu Ala Ala Ala Glu Ile
 505 510 515

gaa aac aca aag gag gac cgt tgagcaccgc cgtagttttca cag 1695
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<210> 10

<211> 524

<212> PRT

<213> Corynebacterium glutamicum

<400> 10

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Asn Gln Val Ser Ile Asp Val Arg Pro Gly Arg Val Leu Ala Leu Leu
 35 40 45

Gly Glu Asn Gly Ala Gly Lys Ser Thr Leu Ile Lys Met Met Ser Gly
 50 55 60

Val Tyr Gln Pro Asp Gly Gly Gln Ile Leu Val Asp Gly Lys Pro Thr
 65 70 75 80

Thr Leu Pro Asp Thr Lys Thr Ala Glu Ser Phe Gly Ile Ala Thr Ile
 85 90 95

His Gln Glu Leu Asn Leu Val Pro Thr Met Thr Val Ala Glu Asn Val
 100 105 110

Met Leu Gly Arg Thr Pro Arg Lys Trp Gly Leu Val Asn Phe Lys His
 115 120 125

Leu Arg Arg Gln Ala Gln Ala Ala Leu Asp Leu Ile Gly Val Asp Val
 130 135 140

Asp Leu Asn Ala Gln Val Gly Ser Leu Gly Ile Ala Arg Gln Gln Met
 145 150 155 160

Val Glu Ile Ala Lys Ala Leu Ser Met Asn Ala Arg Ile Leu Ile Leu
 165 170 175

Asp Glu Pro Thr Ala Ala Leu Thr Gly Arg Glu Ile Asp Gln Leu Phe

180					185					190					
Lys	Val	Val	Asp	Gln	Leu	Lys	Glu	Lys	Gly	Val	Ala	Met	Val	Phe	Ile
	195						200					205			
Ser	His	His	Leu	Asp	Glu	Ile	Ala	Arg	Ile	Gly	Asp	Thr	Val	Ser	Val
	210					215					220				
Leu	Arg	Asp	Gly	Gln	Phe	Ile	Ala	Glu	Leu	Pro	Ala	Asp	Thr	Asp	Glu
225					230					235					240
Asp	Glu	Leu	Val	Arg	Leu	Met	Val	Gly	Arg	Ser	Ile	Glu	Asn	Gln	Tyr
				245					250					255	
Pro	Arg	Ser	Ala	Pro	Glu	Ile	Gly	Gln	Pro	Leu	Leu	Glu	Val	Lys	Asn
			260					265					270		
Leu	Asn	Ala	Glu	Gly	Arg	Phe	Thr	Asp	Ile	Ser	Leu	Thr	Val	Arg	Ala
		275					280						285		
Gly	Glu	Val	Val	Gly	Leu	Ala	Gly	Leu	Val	Gly	Ala	Gly	Arg	Thr	Glu
	290					295					300				
Val	Val	Arg	Ser	Ile	Ala	Gly	Val	Asp	Lys	Val	Asp	Ser	Gly	Glu	Val
305					310					315					320
Ile	Val	Ala	Gly	Lys	Lys	Leu	Arg	Gly	Gly	Asp	Ile	Ser	Glu	Ala	Ile
				325					330					335	
Lys	Asn	Gly	Ile	Gly	His	Ile	Pro	Glu	Asp	Arg	Lys	Ala	Gln	Gly	Leu
		340						345					350		
Val	Leu	Gly	Ser	Ser	Val	Glu	Asp	Asn	Leu	Gly	Leu	Ala	Thr	Leu	Ala
		355					360					365			
Ser	Thr	Ala	Arg	Ala	Gly	Leu	Val	Asp	Arg	Ser	Gly	Gln	His	Lys	Arg
	370					375					380				
Ala	Ala	Glu	Val	Ala	Glu	Lys	Leu	Arg	Ile	Arg	Met	Ala	Ser	Leu	Lys
385					390					395					400
Gln	Pro	Ile	Ser	Asp	Leu	Ser	Gly	Gly	Asn	Gln	Gln	Lys	Ala	Val	Phe
				405					410					415	
Gly	Arg	Trp	Val	Leu	Ala	Gly	Ser	Asn	Val	Leu	Leu	Leu	Asp	Glu	Pro
			420					425					430		
Thr	Arg	Gly	Val	Asp	Val	Gly	Ala	Lys	Val	Glu	Ile	Tyr	Asn	Ile	Ile
		435					440					445			
Asn	Glu	Met	Thr	Glu	Lys	Gly	Gly	Ala	Val	Leu	Met	Val	Ser	Ser	Glu
	450					455					460				
Leu	Pro	Glu	Val	Leu	Gly	Met	Ala	Asp	Arg	Ile	Leu	Val	Met	Ser	Gly
465					470					475					480
Gly	Arg	Ile	Ala	Gly	Glu	Leu	Pro	Ala	Lys	Gly	Thr	Thr	Gln	Asp	Asp
				485					490					495	
Val	Met	Ala	Leu	Ala	Val	Ser	Gln	Val	Asp	Asp	Ser	Ile	Thr	Glu	Glu
			500					505					510		

Ala Ala Ala Glu Ile Glu Asn Thr Lys Glu Asp Arg
515 520

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<211> 882
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(859)
<223> RXA02438

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tgctcaatca ccgattcgag cgtttcaaca aggagcgatc atg aca gac ctc att 115
Met Thr Asp Leu Ile
1 5
caa ctc cgc gaa gta tcc aaa aaa tac ggt gct ttc cag gcc ctc aac 163
Gln Leu Arg Glu Val Ser Lys Lys Tyr Gly Ala Phe Gln Ala Leu Asn
10 15 20
gac atc aat ttg aac gtc cgc gca ggc gaa gtc acc tgt gtt ctg ggt 211
Asp Ile Asn Leu Asn Val Arg Ala Gly Glu Val Thr Cys Val Leu Gly
25 30 35
gac aac ggc gcc gga aaa tcc acc ctc atc aag att ctc tcc ggc ctg 259
Asp Asn Gly Ala Gly Lys Ser Thr Leu Ile Lys Ile Leu Ser Gly Leu
40 45 50
cat ccc gcc acc tcc ggc gaa gta atc gtg gcc ggc gat gta gtg aat 307
His Pro Ala Thr Ser Gly Glu Val Ile Val Ala Gly Asp Val Val Asn
55 60 65
ttt gga tcc ccc cgc gac gcc ctc gac gcc gga atc gcc acc gtc tac 355
Phe Gly Ser Pro Arg Asp Ala Leu Asp Ala Gly Ile Ala Thr Val Tyr
70 75 80 85
caa gac cta gca gtg gtc ggg cag atg agt gtg tgg cgc aac ttc ttc 403
Gln Asp Leu Ala Val Val Gly Gln Met Ser Val Trp Arg Asn Phe Phe
90 95 100
ctc ggc cag gaa ctc acc ggc cga ttt ggc gtt ctg aaa caa gaa gaa 451
Leu Gly Gln Glu Leu Thr Gly Arg Phe Gly Val Leu Lys Gln Glu Glu
105 110 115
atg cgc cgc atc acc gac gaa caa ctc cgc gaa atg ggc atc gaa ctc 499
Met Arg Arg Ile Thr Asp Glu Gln Leu Arg Glu Met Gly Ile Glu Leu
120 125 130
cgc gat gtc gac gtc cct gtg gcc tcc ctt tca ggt ggt caa cgc caa 547
Arg Asp Val Asp Val Pro Val Ala Ser Leu Ser Gly Gly Gln Arg Gln
135 140 145
gtt gtc gcc atc gcc cgc gcc atc tac ttc ggc gcg cgc gtc ctc att 595
Val Val Ala Ile Ala Arg Ala Ile Tyr Phe Gly Ala Arg Val Leu Ile
150 155 160 165

ttg gac gag ccc acc gca gcg ctg ggc gtg aaa caa tct ggc atg gtg 643
 Leu Asp Glu Pro Thr Ala Ala Leu Gly Val Lys Gln Ser Gly Met Val
 170 175 180

ctg cgc ttt att gcc gca gca cgc gac cgg ggg atc ggc gtc att ttc 691
 Leu Arg Phe Ile Ala Ala Ala Arg Asp Arg Gly Ile Gly Val Ile Phe
 185 190 195

atc acg cac aac ccc cac cac gcc tac ctt gtc ggt gat cac ttc atc 739
 Ile Thr His Asn Pro His His Ala Tyr Leu Val Gly Asp His Phe Ile
 200 205 210

ctg ctc aac tta ggc aag cag gtc atg gac aaa tcc cgc gca gaa gtc 787
 Leu Leu Asn Leu Gly Lys Gln Val Met Asp Lys Ser Arg Ala Glu Val
 215 220 225

gag ctg gaa gaa ctc acc ctc gcc atg tcc ggc ggc ggc gag ctc gac 835
 Glu Leu Glu Glu Leu Thr Leu Ala Met Ser Gly Gly Gly Glu Leu Asp
 230 235 240 245

tca ctc agc cac gaa ttg aag cgt taacctactt cttcttttcg ctc 882
 Ser Leu Ser His Glu Leu Lys Arg
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<210> 12

<211> 253

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 12

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Phe Gln Ala Leu Asn Asp Ile Asn Leu Asn Val Arg Ala Gly Glu Val
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Thr Cys Val Leu Gly Asp Asn Gly Ala Gly Lys Ser Thr Leu Ile Lys
 35 40 45

Ile Leu Ser Gly Leu His Pro Ala Thr Ser Gly Glu Val Ile Val Ala
 50 55 60

Gly Asp Val Val Asn Phe Gly Ser Pro Arg Asp Ala Leu Asp Ala Gly
 65 70 75 80

Ile Ala Thr Val Tyr Gln Asp Leu Ala Val Val Gly Gln Met Ser Val
 85 90 95

Trp Arg Asn Phe Phe Leu Gly Gln Glu Leu Thr Gly Arg Phe Gly Val
 100 105 110

Leu Lys Gln Glu Glu Met Arg Arg Ile Thr Asp Glu Gln Leu Arg Glu
 115 120 125

Met Gly Ile Glu Leu Arg Asp Val Asp Val Pro Val Ala Ser Leu Ser
 130 135 140

Gly Gly Gln Arg Gln Val Val Ala Ile Ala Arg Ala Ile Tyr Phe Gly
 145 150 155 160

Ala Arg Val Leu Ile Leu Asp Glu Pro Thr Ala Ala Leu Gly Val Lys
 165 170 175

Gln Ser Gly Met Val Leu Arg Phe Ile Ala Ala Ala Arg Asp Arg Gly
 180 185 190

Ile Gly Val Ile Phe Ile Thr His Asn Pro His His Ala Tyr Leu Val
 195 200 205

Gly Asp His Phe Ile Leu Leu Asn Leu Gly Lys Gln Val Met Asp Lys
 210 215 220

Ser Arg Ala Glu Val Glu Leu Glu Glu Leu Thr Leu Ala Met Ser Gly
 225 230 235 240

Gly Gly Glu Leu Asp Ser Leu Ser His Glu Leu Lys Arg
 245 250

<210> 13
 <211> 1035
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1012)
 <223> RXA00203

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acagaagaag tccacaacgg catccaaaat tggacattgg atg ctc aat aac ggt 115
 Met Leu Asn Asn Gly
 1 5

gcg ttg gtg ggg ctg att gca ctg tgt gtt gga ctt ttt att gca aca 163
 Ala Leu Val Gly Leu Ile Ala Leu Cys Val Gly Leu Phe Ile Ala Thr
 10 15 20

ccc cac ttt ctc acc att cct aac ctg atc aac atc ggt atc caa tcg 211
 Pro His Phe Leu Thr Ile Pro Asn Leu Ile Asn Ile Gly Ile Gln Ser
 25 30 35

gcg acg gtg gcg atc ctg gcg ttc ggc atg acc ttc gtc atc gtt acc 259
 Ala Thr Val Ala Ile Leu Ala Phe Gly Met Thr Phe Val Ile Val Thr
 40 45 50

gca ggc att gat ttg tct gtg gga tca gtg gct gcg ttg ggt gcg atg 307
 Ala Gly Ile Asp Leu Ser Val Gly Ser Val Ala Ala Leu Gly Ala Met
 55 60 65

acc tcg gcg tat ttc ttc gcg gaa gtt ggt ttg ccg ggc tgg atc acg 355
 Thr Ser Ala Tyr Phe Phe Ala Glu Val Gly Leu Pro Gly Trp Ile Thr
 70 75 80 85

ctg ctg att ggc ctg ttc atc gga ttg ttg gcg ggt gcg atc tct ggc 403
 Leu Leu Ile Gly Leu Phe Ile Gly Leu Leu Ala Gly Ala Ile Ser Gly
 90 95 100


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att tct att gct tat ggc aag ttg cct gcg ttt att gcc acc ttg gcc 451
Ile Ser Ile Ala Tyr Gly Lys Leu Pro Ala Phe Ile Ala Thr Leu Ala
105 110 115

atg atg tcg atc gcc agg gga atc acc ttg gtc att tcc caa ggc tca 499
Met Met Ser Ile Ala Arg Gly Ile Thr Leu Val Ile Ser Gln Gly Ser
120 125 130

cca att ccc agt gca cca gct gtg aac gct ttg ggg cgc acc tac ttt 547
Pro Ile Pro Ser Ala Pro Ala Val Asn Ala Leu Gly Arg Thr Tyr Phe
135 140 145

ggc atc ccg atg ccg att ctg atg atg gca ctg gct ggc att gtg tgt 595
Gly Ile Pro Met Pro Ile Leu Met Met Ala Leu Ala Gly Ile Val Cys
150 155 160 165

tgg ttt att ttg agc cgc acc gtg ctg gga cgg tcc atg tac gcc att 643
Trp Phe Ile Leu Ser Arg Thr Val Leu Gly Arg Ser Met Tyr Ala Ile
170 175 180

ggc gga aac atg gaa gca gcc cga cta tct ggt ctg cca gtg aag aaa 691
Gly Gly Asn Met Glu Ala Ala Arg Leu Ser Gly Leu Pro Val Lys Lys
185 190 195

atc ctg gtc atg gtc tat gca ctg gct ggt gtg tat gca gca ctt gcg 739
Ile Leu Val Met Val Tyr Ala Leu Ala Gly Val Tyr Ala Ala Leu Ala
200 205 210

ggt ctg gtc atg acg gga cgc ttg tcg tcc gcg cag ccg cag gca ggc 787
Gly Leu Val Met Thr Gly Arg Leu Ser Ser Ala Gln Pro Gln Ala Gly
215 220 225

gtg gga tac gaa ctc gat gcg att gcc gcc gtg gtc att ggt ggt gcg 835
Val Gly Tyr Glu Leu Asp Ala Ile Ala Ala Val Val Ile Gly Gly Ala
230 235 240 245

tca ctt gct ggc gga acc gga aaa gca acg ggc act ttg att ggt gcc 883
Ser Leu Ala Gly Gly Thr Gly Lys Ala Thr Gly Thr Leu Ile Gly Ala
250 255 260

atc ttg ttg gcc gtg atc cgc aat ggc ttg aac att ttg aac gtg tcc 931
Ile Leu Leu Ala Val Ile Arg Asn Gly Leu Asn Ile Leu Asn Val Ser
265 270 275

tcg ttc tgg cag cag att gtc atc ggt tgt gtc atc gcg ctt gcg gtg 979
Ser Phe Trp Gln Gln Ile Val Ile Gly Cys Val Ile Ala Leu Ala Val
280 285 290

ggc ttc gat gtc atc cga aac aaa acc tct aag taattcctga aaggaaattt 1032
Gly Phe Asp Val Ile Arg Asn Lys Thr Ser Lys
295 300

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tca 1035

<210> 14

<211> 304

<212> PRT

<213> Corynebacterium glutamicum

<400> 14

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 20 25 30
 Ile Gly Ile Gln Ser Ala Thr Val Ala Ile Leu Ala Phe Gly Met Thr
 35 40 45
 Phe Val Ile Val Thr Ala Gly Ile Asp Leu Ser Val Gly Ser Val Ala
 50 55 60
 Ala Leu Gly Ala Met Thr Ser Ala Tyr Phe Phe Ala Glu Val Gly Leu
 65 70 75 80
 Pro Gly Trp Ile Thr Leu Leu Ile Gly Leu Phe Ile Gly Leu Leu Ala
 85 90 95
 Gly Ala Ile Ser Gly Ile Ser Ile Ala Tyr Gly Lys Leu Pro Ala Phe
 100 105 110
 Ile Ala Thr Leu Ala Met Met Ser Ile Ala Arg Gly Ile Thr Leu Val
 115 120 125
 Ile Ser Gln Gly Ser Pro Ile Pro Ser Ala Pro Ala Val Asn Ala Leu
 130 135 140
 Gly Arg Thr Tyr Phe Gly Ile Pro Met Pro Ile Leu Met Met Ala Leu
 145 150 155 160
 Ala Gly Ile Val Cys Trp Phe Ile Leu Ser Arg Thr Val Leu Gly Arg
 165 170 175
 Ser Met Tyr Ala Ile Gly Gly Asn Met Glu Ala Ala Arg Leu Ser Gly
 180 185 190
 Leu Pro Val Lys Lys Ile Leu Val Met Val Tyr Ala Leu Ala Gly Val
 195 200 205
 Tyr Ala Ala Leu Ala Gly Leu Val Met Thr Gly Arg Leu Ser Ser Ala
 210 215 220
 Gln Pro Gln Ala Gly Val Gly Tyr Glu Leu Asp Ala Ile Ala Ala Val
 225 230 235 240
 Val Ile Gly Gly Ala Ser Leu Ala Gly Gly Thr Gly Lys Ala Thr Gly
 245 250 255
 Thr Leu Ile Gly Ala Ile Leu Leu Ala Val Ile Arg Asn Gly Leu Asn
 260 265 270
 Ile Leu Asn Val Ser Ser Phe Trp Gln Gln Ile Val Ile Gly Cys Val
 275 280 285
 Ile Ala Leu Ala Val Gly Phe Asp Val Ile Arg Asn Lys Thr Ser Lys
 290 295 300

<210> 15
 <211> 1011
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(988)

<223> RXA00270

<400> 15

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tggagatccc tcaagagatt ttggataagg ccgaacgcgt atg atc ggc gct ttt 115
Met Ile Gly Ala Phe
1 5

gag ttc gga ttg ttg tac gga gtt gtc gca ttg ggc gtc tat ttg acg 163
Glu Phe Gly Leu Leu Tyr Gly Val Val Ala Leu Gly Val Tyr Leu Thr
10 15 20

ttc cgt gtg ctc aac ttt ccc gac ctc acc gtt gac ggc agc ctg acc 211
Phe Arg Val Leu Asn Phe Pro Asp Leu Thr Val Asp Gly Ser Leu Thr
25 30 35

act ggc gcg gca aca gct gcg aca gct ctt atg tct ggc tgg cct ccc 259
Thr Gly Ala Ala Thr Ala Ala Thr Ala Leu Met Ser Gly Trp Pro Pro
40 45 50

ctt atg gct act gcc gct ggt ttc gtt act ggc ttt atc gct ggc atg 307
Leu Met Ala Thr Ala Ala Gly Phe Val Thr Gly Phe Ile Ala Gly Met
55 60 65

atc acc ggt ttg ctg cac acc aag ggc aag atc gat ggt ttg ctc gca 355
Ile Thr Gly Leu Leu His Thr Lys Gly Lys Ile Asp Gly Leu Leu Ala
70 75 80 85

ggt att ttg acc atg att gcg ttg tgg tcg gtt aac ttg cgc atc atg 403
Gly Ile Leu Thr Met Ile Ala Leu Trp Ser Val Asn Leu Arg Ile Met
90 95 100

ggt ggc gcg aac gtg cca ttg ttg cgc acc gat aac ctc ttc acc ccg 451
Gly Gly Ala Asn Val Pro Leu Leu Arg Thr Asp Asn Leu Phe Thr Pro
105 110 115

ctt cgc gac gcc ggc ctc ctc ggc aca tgg gca ggc ccg gcg atc ctc 499
Leu Arg Asp Ala Gly Leu Leu Gly Thr Trp Ala Gly Pro Ala Ile Leu
120 125 130

gcc gtt gca gtg gga att ttg gga ctc atc gtc atc tgg ttc ctc aac 547
Ala Val Ala Val Gly Ile Leu Gly Leu Ile Val Ile Trp Phe Leu Asn
135 140 145

act gat atc gga ctg tcg ctg cga tcc acc ggc gac aac ggg ccg atg 595
Thr Asp Ile Gly Leu Ser Leu Arg Ser Thr Gly Asp Asn Gly Pro Met
150 155 160 165

gtg cag tcc ttt ggt gtt tca acg gat ttc acc aaa atc ctc acc atc 643
Val Gln Ser Phe Gly Val Ser Thr Asp Phe Thr Lys Ile Leu Thr Ile
170 175 180

tcc ctg tcc aat ggt ttt gtt ggt ctt gcc ggt gca ctc atc gct cag 691
Ser Leu Ser Asn Gly Phe Val Gly Leu Ala Gly Ala Leu Ile Ala Gln
185 190 195

tac cag ggc ttc gca gat att tcg atg ggt att ggc ctc atc gtg atc 739
 Tyr Gln Gly Phe Ala Asp Ile Ser Met Gly Ile Gly Leu Ile Val Ile
 200 205 210
 ggt ctc gca tcg gtt att ttg ggc cag gcc atc ttc ggt cag cgt cgc 787
 Gly Leu Ala Ser Val Ile Leu Gly Gln Ala Ile Phe Gly Gln Arg Arg
 215 220 225
 gtg tgg ttg gct gtg ttg gct gtc atc gtc ggt gcc atc gcg tac cgc 835
 Val Trp Leu Ala Val Leu Ala Val Ile Val Gly Ala Ile Ala Tyr Arg
 230 235 240 245
 ctg atc att ttc gca gca ctg cgc gtt ggc ctt gac ccc aac gat atg 883
 Leu Ile Ile Phe Ala Ala Leu Arg Val Gly Leu Asp Pro Asn Asp Met
 250 255 260
 aag gca att tct gcg atc ttg gtg gtt gtc gcc atg ctg ctg ccg agg 931
 Lys Ala Ile Ser Ala Ile Leu Val Val Val Ala Met Leu Leu Pro Arg
 265 270 275
 tgg cgt gcg aag ttc tcc aag gca ccg aag cct aag caa cca gta gca 979
 Trp Arg Ala Lys Phe Ser Lys Ala Pro Lys Pro Lys Gln Pro Val Ala
 280 285 290
 gtg gag gct taagacatgt tatccatcaa cgg 1011
 Val Glu Ala
 295

<210> 16

<211> 296

<212> PRT

<213> Corynebacterium glutamicum

<400> 16

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 Asp Gly Ser Leu Thr Thr Gly Ala Ala Thr Ala Ala Thr Ala Leu Met
 35 40 45
 Ser Gly Trp Pro Pro Leu Met Ala Thr Ala Ala Gly Phe Val Thr Gly
 50 55 60
 Phe Ile Ala Gly Met Ile Thr Gly Leu Leu His Thr Lys Gly Lys Ile
 65 70 75 80
 Asp Gly Leu Leu Ala Gly Ile Leu Thr Met Ile Ala Leu Trp Ser Val
 85 90 95
 Asn Leu Arg Ile Met Gly Gly Ala Asn Val Pro Leu Leu Arg Thr Asp
 100 105 110
 Asn Leu Phe Thr Pro Leu Arg Asp Ala Gly Leu Leu Gly Thr Trp Ala
 115 120 125
 Gly Pro Ala Ile Leu Ala Val Ala Val Gly Ile Leu Gly Leu Ile Val

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<210> 17
<211> 1146
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1123)
<223> RXA02439
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Met Thr Lys Ile Lys
1 5
agt ggg gag gcg tcg aca agc att gtt gag cgc gcc tta aag cgc ccc 163
Ser Gly Glu Ala Ser Thr Ser Ile Val Glu Arg Ala Leu Lys Arg Pro
10 15 20
gaa ctg acc agc ctg ctt ggc gcc gtg ctt gtt ttt acg ctg ttt atg 211
Glu Leu Thr Ser Leu Leu Gly Ala Val Leu Val Phe Thr Leu Phe Met
25 30 35
gtg gtc gcg ccg gca ttt agg tca tgg gat tcg atg gcg acc gtg ctg 259
Val Val Ala Pro Ala Phe Arg Ser Trp Asp Ser Met Ala Thr Val Leu
40 45 50

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tat gcg agt tcc acg atc ggc atc atg gcg gtt gcc gtg ggc ctg ctg	307
Tyr Ala Ser Ser Thr Ile Gly Ile Met Ala Val Ala Val Gly Leu Leu	
55 60 65	
atg atc gct gat gaa ttc gac ctg tcc acc ggc gtt gcc gtg aca act	355
Met Ile Ala Asp Glu Phe Asp Leu Ser Thr Gly Val Ala Val Thr Thr	
70 75 80 85	
gca gcg ctg gcg gcc tcg atg ttt agc tat aac ctg tgg ctg aac acc	403
Ala Ala Leu Ala Ala Ser Met Phe Ser Tyr Asn Leu Trp Leu Asn Thr	
90 95 100	
tgg gtg ggc gcg ctg att gca ttg gtg att tcg ctg gcc atc ggc ttt	451
Trp Val Gly Ala Leu Ile Ala Leu Val Ile Ser Leu Ala Ile Gly Phe	
105 110 115	
ttc aac ggc ttt ttg gta gtg aaa acc aag att gca tcc ttc ctg atc	499
Phe Asn Gly Phe Leu Val Val Lys Thr Lys Ile Ala Ser Phe Leu Ile	
120 125 130	
acc ctt gcc act ttc ctt atg ctg cag ggt att aat ctg gcg gtc acc	547
Thr Leu Ala Thr Phe Leu Met Leu Gln Gly Ile Asn Leu Ala Val Thr	
135 140 145	
aag ctg att tcc ggc acc gtg gcc acg cca acc atc gcg gat atg gaa	595
Lys Leu Ile Ser Gly Thr Val Ala Thr Pro Thr Ile Ala Asp Met Glu	
150 155 160 165	
ggt ttt cct tca gcg cgt gcg gtg ttt gcc agc tcg att ccc atc ttt	643
Gly Phe Pro Ser Ala Arg Ala Val Phe Ala Ser Ser Ile Pro Ile Phe	
170 175 180	
ggt gtg aat att cgc atc act gtt ttt tgg tgg ctg ctg ttt gtt atc	691
Gly Val Asn Ile Arg Ile Thr Val Phe Trp Trp Leu Leu Phe Val Ile	
185 190 195	
gtc ggc act ttt gtg ttg ttt aag acg cgc atc ggc aac tgg att ttt	739
Val Gly Thr Phe Val Leu Phe Lys Thr Arg Ile Gly Asn Trp Ile Phe	
200 205 210	
gcg gtc ggt ggc gat gaa gag gca gct cgc gca gtc ggc gtt ccc gtg	787
Ala Val Gly Gly Asp Glu Glu Ala Ala Arg Ala Val Gly Val Pro Val	
215 220 225	
cgt ggc gtg aaa atc ggc ctg ttc atg ttc gtt ggt ttt gcc gcc tgg	835
Arg Gly Val Lys Ile Gly Leu Phe Met Phe Val Gly Phe Ala Ala Trp	
230 235 240 245	
ttt gtg ggc atg cac aac ctg ttc ctc ttt gat tcg att cag gct ggt	883
Phe Val Gly Met His Asn Leu Phe Leu Phe Asp Ser Ile Gln Ala Gly	
250 255 260	
caa ggc gtg ggt aat gag ttc ctc tac atc atc gct gcg gtg atc gga	931
Gln Gly Val Gly Asn Glu Phe Leu Tyr Ile Ile Ala Ala Val Ile Gly	
265 270 275	
ggc atc tcc atg act ggt ggc cgc gga aca gtg gtg ggc aca atg att	979
Gly Ile Ser Met Thr Gly Gly Arg Gly Thr Val Val Gly Thr Met Ile	
280 285 290	

ggt gca ctc atc ttt gga atg acc aac caa ggc att gtt tat gca ggt 1027
 Gly Ala Leu Ile Phe Gly Met Thr Asn Gln Gly Ile Val Tyr Ala Gly
 295 300 305

tgg aac cct gac tgg ttc atg ttc ttc ctc ggc ggc acc cta ctt ctg 1075
 Trp Asn Pro Asp Trp Phe Met Phe Phe Leu Gly Gly Thr Leu Leu Leu
 310 315 320 325

gct gtt ttg ctc aat cac cga ttc gag cgt ttc aac aag gag cga tca 1123
 Ala Val Leu Leu Asn His Arg Phe Glu Arg Phe Asn Lys Glu Arg Ser
 330 335 340

tgacagacct cattcaactc cgc 1146

<210> 18
 <211> 341
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 18
 Met Thr Lys Ile Lys Ser Gly Glu Ala Ser Thr Ser Ile Val Glu Arg
 1 5 10 15

Ala Leu Lys Arg Pro Glu Leu Thr Ser Leu Leu Gly Ala Val Leu Val
 20 25 30

Phe Thr Leu Phe Met Val Val Ala Pro Ala Phe Arg Ser Trp Asp Ser
 35 40 45

Met Ala Thr Val Leu Tyr Ala Ser Ser Thr Ile Gly Ile Met Ala Val
 50 55 60

Ala Val Gly Leu Leu Met Ile Ala Asp Glu Phe Asp Leu Ser Thr Gly
 65 70 75 80

Val Ala Val Thr Thr Ala Ala Leu Ala Ala Ser Met Phe Ser Tyr Asn
 85 90 95

Leu Trp Leu Asn Thr Trp Val Gly Ala Leu Ile Ala Leu Val Ile Ser
 100 105 110

Leu Ala Ile Gly Phe Phe Asn Gly Phe Leu Val Val Lys Thr Lys Ile
 115 120 125

Ala Ser Phe Leu Ile Thr Leu Ala Thr Phe Leu Met Leu Gln Gly Ile
 130 135 140

Asn Leu Ala Val Thr Lys Leu Ile Ser Gly Thr Val Ala Thr Pro Thr
 145 150 155 160

Ile Ala Asp Met Glu Gly Phe Pro Ser Ala Arg Ala Val Phe Ala Ser
 165 170 175

Ser Ile Pro Ile Phe Gly Val Asn Ile Arg Ile Thr Val Phe Trp Trp
 180 185 190

Leu Leu Phe Val Ile Val Gly Thr Phe Val Leu Phe Lys Thr Arg Ile
 195 200 205

Gly Asn Trp Ile Phe Ala Val Gly Gly Asp Glu Glu Ala Ala Arg Ala

210 215 220
 Val Gly Val Pro Val Arg Gly Val Lys Ile Gly Leu Phe Met Phe Val
 225 230 235 240
 Gly Phe Ala Ala Trp Phe Val Gly Met His Asn Leu Phe Leu Phe Asp
 245 250 255
 Ser Ile Gln Ala Gly Gln Gly Val Gly Asn Glu Phe Leu Tyr Ile Ile
 260 265 270
 Ala Ala Val Ile Gly Gly Ile Ser Met Thr Gly Gly Arg Gly Thr Val
 275 280 285
 Val Gly Thr Met Ile Gly Ala Leu Ile Phe Gly Met Thr Asn Gln Gly
 290 295 300
 Ile Val Tyr Ala Gly Trp Asn Pro Asp Trp Phe Met Phe Phe Leu Gly
 305 310 315 320
 Gly Thr Leu Leu Leu Ala Val Leu Leu Asn His Arg Phe Glu Arg Phe
 325 330 335
 Asn Lys Glu Arg Ser
 340

<210> 19
 <211> 746
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(723)
 <223> RXN02994

<400> 19
 atc aag atg acg gga gtg caa aaa tac ttc ggc gac ttt cat gcc ctt 48
 Ile Lys Met Thr Gly Val Gln Lys Tyr Phe Gly Asp Phe His Ala Leu
 1 5 10 15
 acg gat att gat ctt gaa att ccc aga gga caa gtt gtc gtc gta ctt 96
 Thr Asp Ile Asp Leu Glu Ile Pro Arg Gly Gln Val Val Val Val Leu
 20 25 30
 gga cca tcc gga tcc ggc aag tca acc ctt tgc cgc acg atc aac cgt 144
 Gly Pro Ser Gly Ser Gly Lys Ser Thr Leu Cys Arg Thr Ile Asn Arg
 35 40 45
 ctc gaa acc atc gag gaa ggc acc atc gaa atc gat gga aag gtt ctc 192
 Leu Glu Thr Ile Glu Glu Gly Thr Ile Glu Ile Asp Gly Lys Val Leu
 50 55 60
 cca gaa gaa ggt aaa ggc tta gcc aat ctc cgc gcc gat gtc gga atg 240
 Pro Glu Glu Gly Lys Gly Leu Ala Asn Leu Arg Ala Asp Val Gly Met
 65 70 75 80
 gta ttc cag tcc ttc aac ctc ttc ccc cac ctc acc atc aaa gac aac 288
 Val Phe Gln Ser Phe Asn Leu Phe Pro His Leu Thr Ile Lys Asp Asn
 85 90 95

gtc act ctt gca ccc atc aaa gtg cga aag atg aaa aag tct gaa gcc 336
 Val Thr Leu Ala Pro Ile Lys Val Arg Lys Met Lys Lys Ser Glu Ala
 100 105 110

gaa aag ctt gcg atg agc ctg ttg gaa cgc gtc ggc atc gca aac caa 384
 Glu Lys Leu Ala Met Ser Leu Leu Glu Arg Val Gly Ile Ala Asn Gln
 115 120 125

gct gat aaa tat ccg gcg caa ctg tcc ggc ggt cag caa cag cgt gtg 432
 Ala Asp Lys Tyr Pro Ala Gln Leu Ser Gly Gly Gln Gln Gln Arg Val
 130 135 140

gcc atc gcg cgc gca ctt gcg atg aac cca aag atc atg ctt ttc gac 480
 Ala Ile Ala Arg Ala Leu Ala Met Asn Pro Lys Ile Met Leu Phe Asp
 145 150 155 160

gag ccc acc tcc gcc ctt gac cct gaa atg gtc aac gaa gtg ttg gac 528
 Glu Pro Thr Ser Ala Leu Asp Pro Glu Met Val Asn Glu Val Leu Asp
 165 170 175

gtc atg gca agc ctt gcc aag gaa ggc atg acg atg gtg tgt gtt acc 576
 Val Met Ala Ser Leu Ala Lys Glu Gly Met Thr Met Val Cys Val Thr
 180 185 190

cac gag atg gga ttc gca cgc aaa gca gcc gat cgt gtg ttg ttc atg 624
 His Glu Met Gly Phe Ala Arg Lys Ala Ala Asp Arg Val Leu Phe Met
 195 200 205

gcg gat ggg ctc att gtg gaa gat acg gaa cca gat tcc ttc ttc acc 672
 Ala Asp Gly Leu Ile Val Glu Asp Thr Glu Pro Asp Ser Phe Phe Thr
 210 215 220

aac cct aag tct gat cgt gca aaa gac ttc ctc ggc aag atc ctt gcc 720
 Asn Pro Lys Ser Asp Arg Ala Lys Asp Phe Leu Gly Lys Ile Leu Ala
 225 230 235 240

cac tagtttttgg ctgcgcctct atc 746
 His

<210> 20

<211> 241

<212> PRT

<213> Corynebacterium glutamicum

<400> 20

Ile Lys Met Thr Gly Val Gln Lys Tyr Phe Gly Asp Phe His Ala Leu
 1 5 10 15

Thr Asp Ile Asp Leu Glu Ile Pro Arg Gly Gln Val Val Val Val Leu
 20 25 30

Gly Pro Ser Gly Ser Gly Lys Ser Thr Leu Cys Arg Thr Ile Asn Arg
 35 40 45

Leu Glu Thr Ile Glu Glu Gly Thr Ile Glu Ile Asp Gly Lys Val Leu
 50 55 60

Pro Glu Glu Gly Lys Gly Leu Ala Asn Leu Arg Ala Asp Val Gly Met

65	70	75	80
Val Phe Gln Ser Phe Asn Leu Phe Pro His Leu Thr Ile Lys Asp Asn	85	90	95
Val Thr Leu Ala Pro Ile Lys Val Arg Lys Met Lys Lys Ser Glu Ala	100	105	110
Glu Lys Leu Ala Met Ser Leu Leu Glu Arg Val Gly Ile Ala Asn Gln	115	120	125
Ala Asp Lys Tyr Pro Ala Gln Leu Ser Gly Gly Gln Gln Gln Arg Val	130	135	140
Ala Ile Ala Arg Ala Leu Ala Met Asn Pro Lys Ile Met Leu Phe Asp	145	150	155
Glu Pro Thr Ser Ala Leu Asp Pro Glu Met Val Asn Glu Val Leu Asp	165	170	175
Val Met Ala Ser Leu Ala Lys Glu Gly Met Thr Met Val Cys Val Thr	180	185	190
His Glu Met Gly Phe Ala Arg Lys Ala Ala Asp Arg Val Leu Phe Met	195	200	205
Ala Asp Gly Leu Ile Val Glu Asp Thr Glu Pro Asp Ser Phe Phe Thr	210	215	220
Asn Pro Lys Ser Asp Arg Ala Lys Asp Phe Leu Gly Lys Ile Leu Ala	225	230	235
His			240

<210> 21
 <211> 1790
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1767)
 <223> FRXA01245

<400> 21	
gcc tcc tgg gtc acc acc ctg ggg ctg ggc ggg ttc cac cta gat ttc	48
Ala Ser Trp Val Thr Thr Leu Gly Leu Gly Gly Phe His Leu Asp Phe	
1 5 10 15	
tgg tgg gaa ctg gcc ctg ctg gtg acc ata atg ctg ttg ggc cac tgg	96
Trp Trp Glu Leu Ala Leu Leu Val Thr Ile Met Leu Leu Gly His Trp	
20 25 30	
ctg gag atg cgc gct ctt ggt gca gcc tcc tcc gcg ctt gac gcg ctg	144
Leu Glu Met Arg Ala Leu Gly Ala Ala Ser Ser Ala Leu Asp Ala Leu	
35 40 45	
gca gcg ctc ctg ccc gat gag gcc gag aag gtc gtc gac ggg acc acc	192
Ala Ala Leu Leu Pro Asp Glu Ala Glu Lys Val Val Asp Gly Thr Thr	

50	55	60	
cgc acc gta gcg atc tca gag ctg gcc gtc gac gat gtc gtg ctg gtc			240
Arg Thr Val Ala Ile Ser Glu Leu Ala Val Asp Asp Val Val Leu Val			
65	70	75	80
cga gca ggt gcc cgc gtc ccg gcc gac ggg acc atc atg gac gga gcg			288
Arg Ala Gly Ala Arg Val Pro Ala Asp Gly Thr Ile Met Asp Gly Ala			
	85	90	95
gcc gaa ttc gat gag gcc atg atc acc ggc gaa tcc cga ccc gtc tac			336
Ala Glu Phe Asp Glu Ala Met Ile Thr Gly Glu Ser Arg Pro Val Tyr			
	100	105	110
cgg gat acc ggt gag acc gtg gtg gcc ggc acc gtg gcc acc gac aac			384
Arg Asp Thr Gly Glu Thr Val Val Ala Gly Thr Val Ala Thr Asp Asn			
	115	120	125
acc gtc cgt atc cgg gtg gag gcc acc ggt ggg gac acc gcc ctg gca			432
Thr Val Arg Ile Arg Val Glu Ala Thr Gly Gly Asp Thr Ala Leu Ala			
	130	135	140
ggc atc cag cgc atg gtc gcc gac gcc cag gcc tcc tcc tcc cgg gcc			480
Gly Ile Gln Arg Met Val Ala Asp Ala Gln Ala Ser Ser Ser Arg Ala			
	145	150	155
cag gcc ctg gcc gat cga gcc gca gcc tta ctg ttc tgg ttc gcc ctg			528
Gln Ala Leu Ala Asp Arg Ala Ala Ala Leu Leu Phe Trp Phe Ala Leu			
	165	170	175
atc acg gcc ctg atc acc gcc gtg gtc tgg acc atc atc ggc agc ccc			576
Ile Thr Ala Leu Ile Thr Ala Val Val Trp Thr Ile Ile Gly Ser Pro			
	180	185	190
gac gat gcc gtg gtc cgc gcg gtg acc gtg ctg atc atc gcc tgc ccg			624
Asp Asp Ala Val Val Arg Ala Val Thr Val Leu Ile Ile Ala Cys Pro			
	195	200	205
cac gcc ctg ggc ctg gcc atc ccg ctg gtc atc gcg atc tcc tcc gag			672
His Ala Leu Gly Leu Ala Ile Pro Leu Val Ile Ala Ile Ser Ser Glu			
	210	215	220
cgc gcc gcg aaa tcc ggg gtg ctc atc aag gac cgc atg gca ctc gag			720
Arg Ala Ala Lys Ser Gly Val Leu Ile Lys Asp Arg Met Ala Leu Glu			
	225	230	235
cac atg cgc acc atc gac gtc gtc ttg ttc gat aag acc ggc acc ctg			768
His Met Arg Thr Ile Asp Val Val Leu Phe Asp Lys Thr Gly Thr Leu			
	245	250	255
acc gaa ggc gca cac gcc gtc acc ggc gtg gct ccg gcc acg ggt atc			816
Thr Glu Gly Ala His Ala Val Thr Gly Val Ala Pro Ala Thr Gly Ile			
	260	265	270
gcc gag ggt gag ctg ctg gcc ctg gcc gcc gcc gct gag gcc gat agt			864
Ala Glu Gly Glu Leu Leu Ala Leu Ala Ala Ala Ala Glu Ala Asp Ser			
	275	280	285
gag cac ccc gtg gcc cgc gcg atc gtg act gcc gcg gcc gca cac ccg			912
Glu His Pro Val Ala Arg Ala Ile Val Thr Ala Ala Ala Ala His Pro			
	290	295	300

gag gcc tcg cag cgt cag ctg cgc gca acc ggt ttc acc gcc gcc tcc	960
Glu Ala Ser Gln Arg Gln Leu Arg Ala Thr Gly Phe Thr Ala Ala Ser	
305 310 315 320	
ggc cgc ggg atc cgg gcc acc gtc gac ggt gcc gaa atc ctc gtg ggc	1008
Gly Arg Gly Ile Arg Ala Thr Val Asp Gly Ala Glu Ile Leu Val Gly	
325 330 335	
ggg ccg aac atg cta cgc gag ttc aat ctg acc acc ccg ggt gag ctc	1056
Gly Pro Asn Met Leu Arg Glu Phe Asn Leu Thr Thr Pro Gly Glu Leu	
340 345 350	
gcc gac atc acc ggt tcc tgg gca cag cga ggt gcc gga gtg cta cat	1104
Ala Asp Ile Thr Gly Ser Trp Ala Gln Arg Gly Ala Gly Val Leu His	
355 360 365	
gtc gtc cgc gac ggt gag atc atc ggt gcg gtg gca gtg gag gac aaa	1152
Val Val Arg Asp Gly Glu Ile Ile Gly Ala Val Ala Val Glu Asp Lys	
370 375 380	
atc cgc ccc gaa tcc cgc gcg gcg gta cgc gcc ctg cag gcc cgc ggg	1200
Ile Arg Pro Glu Ser Arg Ala Ala Val Arg Ala Leu Gln Ala Arg Gly	
385 390 395 400	
gtg aag gtg gcg atg atc acc ggt gac gcc acc cag gtc gcc cag gca	1248
Val Lys Val Ala Met Ile Thr Gly Asp Ala Thr Gln Val Ala Gln Ala	
405 410 415	
gtg ggc aag gat ctg ggg atc gat gag gtc ttc gcc gag gtt ctg ccg	1296
Val Gly Lys Asp Leu Gly Ile Asp Glu Val Phe Ala Glu Val Leu Pro	
420 425 430	
cag gac aag gac acc aag gtc acc cag ctg cag gag cgc ggt ctg agc	1344
Gln Asp Lys Asp Thr Lys Val Thr Gln Leu Gln Glu Arg Gly Leu Ser	
435 440 445	
gtg gcc atg gtc ggc gac ggt gtc aat gac gcc ccg gcc ctg gcc cgg	1392
Val Ala Met Val Gly Asp Gly Val Asn Asp Ala Pro Ala Leu Ala Arg	
450 455 460	
gcc gag gtc ggt att gcg att ggc gcg ggt aca gat gtg gcg atg gag	1440
Ala Glu Val Gly Ile Ala Ile Gly Ala Gly Thr Asp Val Ala Met Glu	
465 470 475 480	
tcc gcc ggg gtg gtc ctg gcc agt gat gat ccc ccg gcc gtg ctg tcg	1488
Ser Ala Gly Val Val Leu Ala Ser Asp Asp Pro Arg Ala Val Leu Ser	
485 490 495	
atg atc gag ctc tcc cat gcc agc tac cgc aag atg gtc cag aac ctg	1536
Met Ile Glu Leu Ser His Ala Ser Tyr Arg Lys Met Val Gln Asn Leu	
500 505 510	
gtc tgg gcg acc ggg tac aac atc gtg gcc gtt ccg ctg gcc gcc ggt	1584
Val Trp Ala Thr Gly Tyr Asn Ile Val Ala Val Pro Leu Ala Ala Gly	
515 520 525	
gtg ctc gcc cct atc ggt gtg ctg ctt ccc ccg gcg gcg gcc gcc atc	1632
Val Leu Ala Pro Ile Gly Val Leu Leu Pro Pro Ala Ala Ala Ile	
530 535 540	

ttg atg tcc ctg tcc acg atc atc gtc gcc ctc aac gcc cag ctg cta 1680
 Leu Met Ser Leu Ser Thr Ile Ile Val Ala Leu Asn Ala Gln Leu Leu
 545 550 555 560

cgc cgg atc gac ctg gac ccg gct cac cta gct ccg acc gac ggg aag 1728
 Arg Arg Ile Asp Leu Asp Pro Ala His Leu Ala Pro Thr Asp Gly Lys
 565 570 575

gag gag aag gct gct gtg agc tct gca gcc ccc gtc cgc tgactttcaa 1777
 Glu Glu Lys Ala Ala Val Ser Ser Ala Ala Pro Val Arg
 580 585

tgcttcatgg act 1790

<210> 22

<211> 589

<212> PRT

<213> Corynebacterium glutamicum

<400> 22

Ala Ser Trp Val Thr Thr Leu Gly Leu Gly Gly Phe His Leu Asp Phe
 1 5 10 15

Trp Trp Glu Leu Ala Leu Leu Val Thr Ile Met Leu Leu Gly His Trp
 20 25 30

Leu Glu Met Arg Ala Leu Gly Ala Ala Ser Ser Ala Leu Asp Ala Leu
 35 40 45

Ala Ala Leu Leu Pro Asp Glu Ala Glu Lys Val Val Asp Gly Thr Thr
 50 55 60

Arg Thr Val Ala Ile Ser Glu Leu Ala Val Asp Asp Val Val Leu Val
 65 70 75 80

Arg Ala Gly Ala Arg Val Pro Ala Asp Gly Thr Ile Met Asp Gly Ala
 85 90 95

Ala Glu Phe Asp Glu Ala Met Ile Thr Gly Glu Ser Arg Pro Val Tyr
 100 105 110

Arg Asp Thr Gly Glu Thr Val Val Ala Gly Thr Val Ala Thr Asp Asn
 115 120 125

Thr Val Arg Ile Arg Val Glu Ala Thr Gly Gly Asp Thr Ala Leu Ala
 130 135 140

Gly Ile Gln Arg Met Val Ala Asp Ala Gln Ala Ser Ser Ser Arg Ala
 145 150 155 160

Gln Ala Leu Ala Asp Arg Ala Ala Ala Leu Leu Phe Trp Phe Ala Leu
 165 170 175

Ile Thr Ala Leu Ile Thr Ala Val Val Trp Thr Ile Ile Gly Ser Pro
 180 185 190

Asp Asp Ala Val Val Arg Ala Val Thr Val Leu Ile Ile Ala Cys Pro
 195 200 205

His Ala Leu Gly Leu Ala Ile Pro Leu Val Ile Ala Ile Ser Ser Glu

210	215	220
Arg Ala Ala Lys Ser Gly Val Leu Ile Lys Asp Arg Met Ala Leu Glu 225 230 235 240		
His Met Arg Thr Ile Asp Val Val Leu Phe Asp Lys Thr Gly Thr Leu 245 250 255		
Thr Glu Gly Ala His Ala Val Thr Gly Val Ala Pro Ala Thr Gly Ile 260 265 270		
Ala Glu Gly Glu Leu Leu Ala Leu Ala Ala Ala Glu Ala Asp Ser 275 280 285		
Glu His Pro Val Ala Arg Ala Ile Val Thr Ala Ala Ala Ala His Pro 290 295 300		
Glu Ala Ser Gln Arg Gln Leu Arg Ala Thr Gly Phe Thr Ala Ala Ser 305 310 315 320		
Gly Arg Gly Ile Arg Ala Thr Val Asp Gly Ala Glu Ile Leu Val Gly 325 330 335		
Gly Pro Asn Met Leu Arg Glu Phe Asn Leu Thr Thr Pro Gly Glu Leu 340 345 350		
Ala Asp Ile Thr Gly Ser Trp Ala Gln Arg Gly Ala Gly Val Leu His 355 360 365		
Val Val Arg Asp Gly Glu Ile Ile Gly Ala Val Ala Val Glu Asp Lys 370 375 380		
Ile Arg Pro Glu Ser Arg Ala Ala Val Arg Ala Leu Gln Ala Arg Gly 385 390 395 400		
Val Lys Val Ala Met Ile Thr Gly Asp Ala Thr Gln Val Ala Gln Ala 405 410 415		
Val Gly Lys Asp Leu Gly Ile Asp Glu Val Phe Ala Glu Val Leu Pro 420 425 430		
Gln Asp Lys Asp Thr Lys Val Thr Gln Leu Gln Glu Arg Gly Leu Ser 435 440 445		
Val Ala Met Val Gly Asp Gly Val Asn Asp Ala Pro Ala Leu Ala Arg 450 455 460		
Ala Glu Val Gly Ile Ala Ile Gly Ala Gly Thr Asp Val Ala Met Glu 465 470 475 480		
Ser Ala Gly Val Val Leu Ala Ser Asp Asp Pro Arg Ala Val Leu Ser 485 490 495		
Met Ile Glu Leu Ser His Ala Ser Tyr Arg Lys Met Val Gln Asn Leu 500 505 510		
Val Trp Ala Thr Gly Tyr Asn Ile Val Ala Val Pro Leu Ala Ala Gly 515 520 525		
Val Leu Ala Pro Ile Gly Val Leu Leu Pro Pro Ala Ala Ala Ala Ile 530 535 540		

Leu Met Ser Leu Ser Thr Ile Ile Val Ala Leu Asn Ala Gln Leu Leu
545 550 555 560

Arg Arg Ile Asp Leu Asp Pro Ala His Leu Ala Pro Thr Asp Gly Lys
565 570 575

Glu Glu Lys Ala Ala Val Ser Ser Ala Ala Pro Val Arg
580 585

<210> 23

<211> 807

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(784)

<223> RXA00002

<400> 23

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ggctgcagac aagctcgctg ctgaggattc tcacctgcac gtg ctg cac cgc gaa 115
Val Leu His Arg Glu
1 5

ggc aag ggt ggc ctt ctt ggc gct tat atc gcc ggc ttc gag tgg ggc 163
Gly Lys Gly Gly Leu Leu Gly Ala Tyr Ile Ala Gly Phe Glu Trp Gly
10 15 20

cta gag aag gat tac cat gtt ctg tgc gaa atg gat gcc gac ggc tcc 211
Leu Glu Lys Asp Tyr His Val Leu Cys Glu Met Asp Ala Asp Gly Ser
25 30 35

cac gca cca gaa cag ctc cac ctc ttg ctt gag gaa att gaa aag ggc 259
His Ala Pro Glu Gln Leu His Leu Leu Leu Glu Glu Ile Glu Lys Gly
40 45 50

gca gat ctg gtc att ggc tcc cgc tac gta ccg ggt gga gag aca gtg 307
Ala Asp Leu Val Ile Gly Ser Arg Tyr Val Pro Gly Gly Glu Thr Val
55 60 65

aac tgg cct gcc aac cgc gaa ctg ctg tcc cgc ttg ggc aac aag tac 355
Asn Trp Pro Ala Asn Arg Glu Leu Leu Ser Arg Leu Gly Asn Lys Tyr
70 75 80 85

att tct gtt gcc ctg ggt gcc ggc atc aat gac atg act gcc ggc tac 403
Ile Ser Val Ala Leu Gly Ala Gly Ile Asn Asp Met Thr Ala Gly Tyr
90 95 100

cgt gct ttc cgg cgt gag ctg ctt gag cac ctc gac ttt gag gag ctt 451
Arg Ala Phe Arg Arg Glu Leu Leu Glu His Leu Asp Phe Glu Glu Leu
105 110 115

tcc aac gcc gga tac atc ttc cag gtg gac gtt gcc ttc cgc gcc atc 499
Ser Asn Ala Gly Tyr Ile Phe Gln Val Asp Val Ala Phe Arg Ala Ile
120 125 130

aag gat ggc ttc gat gtc cgc gag gtt ccg atc acc ttc acc gag cgc 547

Lys Asp Gly Phe Asp Val Arg Glu Val Pro Ile Thr Phe Thr Glu Arg
 135 140 145
 gag ctt ggt gaa tcc aag ctg gac ggc tcc ttt gtc aag gat tcc ctg 595
 Glu Leu Gly Glu Ser Lys Leu Asp Gly Ser Phe Val Lys Asp Ser Leu
 150 155 160 165
 ctc gaa gta acc aag tgg gga gtg gct cac cgc tcc gag cag atc agc 643
 Leu Glu Val Thr Lys Trp Gly Val Ala His Arg Ser Glu Gln Ile Ser
 170 175 180
 gat ttc aca tcg gaa gta tcc aag atc gcc tcc cgc acg gtc aag gac 691
 Asp Phe Thr Ser Glu Val Ser Lys Ile Ala Ser Arg Thr Val Lys Asp
 185 190 195
 atg gag ctt ggc cct aag gcc acc acg gcc aag aac gct gta ccg gac 739
 Met Glu Leu Gly Pro Lys Ala Thr Thr Ala Lys Asn Ala Val Pro Asp
 200 205 210
 ttc gtt tcc gaa gtc tct aac cta gct aaa ggc acc ttc aag aag 784
 Phe Val Ser Glu Val Ser Asn Leu Ala Lys Gly Thr Phe Lys Lys
 215 220 225
 taactcgatg cccgcggcgt ctc 807

<210> 24
 <211> 228
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 24
 Val Leu His Arg Glu Gly Lys Gly Gly Leu Leu Gly Ala Tyr Ile Ala
 1 5 10 15
 Gly Phe Glu Trp Gly Leu Glu Lys Asp Tyr His Val Leu Cys Glu Met
 20 25 30
 Asp Ala Asp Gly Ser His Ala Pro Glu Gln Leu His Leu Leu Glu
 35 40 45
 Glu Ile Glu Lys Gly Ala Asp Leu Val Ile Gly Ser Arg Tyr Val Pro
 50 55 60
 Gly Gly Glu Thr Val Asn Trp Pro Ala Asn Arg Glu Leu Leu Ser Arg
 65 70 75 80
 Leu Gly Asn Lys Tyr Ile Ser Val Ala Leu Gly Ala Gly Ile Asn Asp
 85 90 95
 Met Thr Ala Gly Tyr Arg Ala Phe Arg Arg Glu Leu Leu Glu His Leu
 100 105 110
 Asp Phe Glu Glu Leu Ser Asn Ala Gly Tyr Ile Phe Gln Val Asp Val
 115 120 125
 Ala Phe Arg Ala Ile Lys Asp Gly Phe Asp Val Arg Glu Val Pro Ile
 130 135 140
 Thr Phe Thr Glu Arg Glu Leu Gly Glu Ser Lys Leu Asp Gly Ser Phe
 145 150 155 160

Val Lys Asp Ser Leu Leu Glu Val Thr Lys Trp Gly Val Ala His Arg
 165 170 175

Ser Glu Gln Ile Ser Asp Phe Thr Ser Glu Val Ser Lys Ile Ala Ser
 180 185 190

Arg Thr Val Lys Asp Met Glu Leu Gly Pro Lys Ala Thr Thr Ala Lys
 195 200 205

Asn Ala Val Pro Asp Phe Val Ser Glu Val Ser Asn Leu Ala Lys Gly
 210 215 220

Thr Phe Lys Lys
 225

<210> 25
 <211> 696
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(673)
 <223> RXA00160

<400> 25
 tacaggggtg gggttacccc ctaaggtggt cacaacttga taacggactg gttaataaat 60

ggccaatctg accatttttaa cctccataaa aaggattctc atg cta aac atc gca 115
 Met Leu Asn Ile Ala
 1 5

cgc aac cgc aac atg aag cgt cga cta gca att gct gct ttc gtc gcc 163
 Arg Asn Arg Asn Met Lys Arg Arg Leu Ala Ile Ala Ala Phe Val Ala
 10 15 20

acc gca acc gct acc gcc acc atg gca cca gca tcc gcg caa acc gac 211
 Thr Ala Thr Ala Thr Met Ala Pro Ala Ser Ala Gln Thr Asp
 25 30 35

tac gca ggc ctt tcc tcc ggc gtt gcc gac acc gtc gca gaa gct gca 259
 Tyr Ala Gly Leu Ser Ser Gly Val Ala Asp Thr Val Ala Glu Ala Ala
 40 45 50

gga gtc gca acc acc gcc gtc gca cca gcc gcc acc gta gcg cgc cca 307
 Gly Val Ala Thr Thr Ala Val Ala Pro Ala Ala Thr Val Ala Arg Pro
 55 60 65

gca aac ggc acc ttc acc tca gga ttc gga cca cgt tgg gga acc ttc 355
 Ala Asn Gly Thr Phe Thr Ser Gly Phe Gly Pro Arg Trp Gly Thr Phe
 70 75 80 85

cac aac ggc atc gac atc gca aac tca atc ggc acc cca atc tac gcc 403
 His Asn Gly Ile Asp Ile Ala Asn Ser Ile Gly Thr Pro Ile Tyr Ala
 90 95 100

gtc atg gcc ggc act gtc atc agc tct ggc cca gca tcc ggc tat gga 451
 Val Met Ala Gly Thr Val Ile Ser Ser Gly Pro Ala Ser Gly Tyr Gly
 105 110 115

cag tgg atc cgc atc cag cac gac gac gga tcc atc tcc atc tac gga 499
 Gln Trp Ile Arg Ile Gln His Asp Asp Gly Ser Ile Ser Ile Tyr Gly
 120 125 130

 cac atg gaa tac ctc tac gtc tcc gtc ggc gaa cgc gtc gca gca ggc 547
 His Met Glu Tyr Leu Tyr Val Ser Val Gly Glu Arg Val Ala Ala Gly
 135 140 145

 cag gaa atc gca gga atg ggc agc caa gga ttc tcc acc ggc tcc cac 595
 Gln Glu Ile Ala Gly Met Gly Ser Gln Gly Phe Ser Thr Gly Ser His
 150 155 160 165

 ctc cac ttc gag atc cac cca gac ggc gtc acc cca gtc gac cca cag 643
 Leu His Phe Glu Ile His Pro Asp Gly Val Thr Pro Val Asp Pro Gln
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 gca tgg ctc gca aac cac ggc atc tac gtt taagcgctag ccgttcgtgg gat 696
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 <213> Corynebacterium glutamicum

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 Ser Ala Gln Thr Asp Tyr Ala Gly Leu Ser Ser Gly Val Ala Asp Thr
 35 40 45

 Val Ala Glu Ala Ala Gly Val Ala Thr Thr Ala Val Ala Pro Ala Ala
 50 55 60

 Thr Val Ala Arg Pro Ala Asn Gly Thr Phe Thr Ser Gly Phe Gly Pro
 65 70 75 80

 Arg Trp Gly Thr Phe His Asn Gly Ile Asp Ile Ala Asn Ser Ile Gly
 85 90 95

 Thr Pro Ile Tyr Ala Val Met Ala Gly Thr Val Ile Ser Ser Gly Pro
 100 105 110

 Ala Ser Gly Tyr Gly Gln Trp Ile Arg Ile Gln His Asp Asp Gly Ser
 115 120 125

 Ile Ser Ile Tyr Gly His Met Glu Tyr Leu Tyr Val Ser Val Gly Glu
 130 135 140

 Arg Val Ala Ala Gly Gln Glu Ile Ala Gly Met Gly Ser Gln Gly Phe
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 Ser Thr Gly Ser His Leu His Phe Glu Ile His Pro Asp Gly Val Thr
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Pro Val Asp Pro Gln Ala Trp Leu Ala Asn His Gly Ile Tyr Val
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 <223> RXA00345

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 Met Ala Gly Met Lys Lys Leu Leu
 1 5
 tgg aca ctc ccc atc ctc cca ctg gta cta gct ggc tgc tca act gga 161
 Trp Thr Leu Pro Ile Leu Pro Leu Val Leu Ala Gly Cys Ser Thr Gly
 10 15 20
 tca gca gat tcc gcg gat tcc acc aac gct gcc gga tcc aat tcc ctt 209
 Ser Ala Asp Ser Ala Asp Ser Thr Asn Ala Ala Gly Ser Asn Ser Leu
 25 30 35 40
 aaa gtg gtc acc tcc acc cag gtg tgg gct gac gtc gcc gaa gct gtc 257
 Lys Val Val Thr Ser Thr Gln Val Trp Ala Asp Val Ala Glu Ala Val
 45 50 55
 gcc cca gat gta gac att gaa gca att att acc ggt ggc gac atc gac 305
 Ala Pro Asp Val Asp Ile Glu Ala Ile Ile Thr Gly Gly Asp Ile Asp
 60 65 70
 cct cat tcc ttc gag cct tcc gct acc gat atg gct aaa gtt tcc gaa 353
 Pro His Ser Phe Glu Pro Ser Ala Thr Asp Met Ala Lys Val Ser Glu
 75 80 85
 gct gac atc att atc gtc ggt ggc ggc ggc tat gat tcc tgg ctc tac 401
 Ala Asp Ile Ile Ile Val Gly Gly Gly Gly Tyr Asp Ser Trp Leu Tyr
 90 95 100
 ggc acc ttg gaa gac gat gat cgc atc atc cac gca ttg gat ctc tca 449
 Gly Thr Leu Glu Asp Asp Arg Ile Ile His Ala Leu Asp Leu Ser
 105 110 115 120
 gag cat gac cac agc gag cat gat gat cac gag cac gaa gcc gaa gaa 497
 Glu His Asp His Ser Glu His Asp Asp His Glu His Glu Ala Glu Glu
 125 130 135
 gcc cac gaa cac gac cac gat gaa gag ggc cac gat cat gac gtc gac 545
 Ala His Glu His Asp His Asp Glu Glu Gly His Asp His Asp Val Asp
 140 145 150
 aac gag cac gtc tgg tac tcc act gaa tac gtc tct gag gta gct gaa 593
 Asn Glu His Val Trp Tyr Ser Thr Glu Tyr Val Ser Glu Val Ala Glu
 155 160 165

gag ttc gca gaa aaa gtc acc gag ctt gat ccc gag gca cag gcc gat 641
 Glu Phe Ala Glu Lys Val Thr Glu Leu Asp Pro Glu Ala Gln Ala Asp
 170 175 180

gca acg gct gtg acc acc aag atg gac gag ctg cac aat cag att cac 689
 Ala Thr Ala Val Thr Thr Lys Met Asp Glu Leu His Asn Gln Ile His
 185 190 195 200

gat ctt cca gca gtt cgc att gct cag acc gag ccg atc gcc gat cac 737
 Asp Leu Pro Ala Val Arg Ile Ala Gln Thr Glu Pro Ile Ala Asp His
 205 210 215

att ttg tcc cac tcc gac atg gtg gaa tcc acc cct gag ggt tac cgc 785
 Ile Leu Ser His Ser Asp Met Val Glu Ser Thr Pro Glu Gly Tyr Arg
 220 225 230

gca acc acg ttg agc gag agc gag cca acc gca gca gat gtt gcg tcg 833
 Ala Thr Thr Leu Ser Glu Ser Glu Pro Thr Ala Ala Asp Val Ala Ser
 235 240 245

ttc cag gat gca att aac aac ggt gac ctc gat gtt ttg atc tac aac 881
 Phe Gln Asp Ala Ile Asn Asn Gly Asp Leu Asp Val Leu Ile Tyr Asn
 250 255 260

cca cag tcc gcg tcg act gtc gcg acc agc ttg aag gat ttg gca gaa 929
 Pro Gln Ser Ala Ser Thr Val Ala Thr Ser Leu Lys Asp Leu Ala Glu
 265 270 275 280

gaa aaa ggc atc cca gtt gtt gag atc tat gag acc cct caa aac acc 977
 Glu Lys Gly Ile Pro Val Val Glu Ile Tyr Glu Thr Pro Gln Asn Thr
 285 290 295

gag aat ttc ctc gat gca ttc acc aag gca gtt gat gat ctc acc gct 1025
 Glu Asn Phe Leu Asp Ala Phe Thr Lys Ala Val Asp Asp Leu Thr Ala
 300 305 310

gcc act aac cag gtt tagaattatt taaatgctgt tga 1063
 Ala Thr Asn Gln Val
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 <211> 317
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 28
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Val Leu Ala Gly Cys Ser Thr Gly Ser Ala Asp Ser Ala Asp Ser Thr
 20 25 30

Asn Ala Ala Gly Ser Asn Ser Leu Lys Val Val Thr Ser Thr Gln Val
 35 40 45

Trp Ala Asp Val Ala Glu Ala Val Ala Pro Asp Val Asp Ile Glu Ala
 50 55 60

Ile Ile Thr Gly Gly Asp Ile Asp Pro His Ser Phe Glu Pro Ser Ala
 65 70 75 80

Thr Asp Met Ala Lys Val Ser Glu Ala Asp Ile Ile Ile Val Gly Gly
 85 90 95
 Gly Gly Tyr Asp Ser Trp Leu Tyr Gly Thr Leu Glu Asp Asp Asp Arg
 100 105 110
 Ile Ile His Ala Leu Asp Leu Ser Glu His Asp His Ser Glu His Asp
 115 120 125
 Asp His Glu His Glu Ala Glu Glu Ala His Glu His Asp His Asp Glu
 130 135 140
 Glu Gly His Asp His Asp Val Asp Asn Glu His Val Trp Tyr Ser Thr
 145 150 155 160
 Glu Tyr Val Ser Glu Val Ala Glu Glu Phe Ala Glu Lys Val Thr Glu
 165 170 175
 Leu Asp Pro Glu Ala Gln Ala Asp Ala Thr Ala Val Thr Thr Lys Met
 180 185 190
 Asp Glu Leu His Asn Gln Ile His Asp Leu Pro Ala Val Arg Ile Ala
 195 200 205
 Gln Thr Glu Pro Ile Ala Asp His Ile Leu Ser His Ser Asp Met Val
 210 215 220
 Glu Ser Thr Pro Glu Gly Tyr Arg Ala Thr Thr Leu Ser Glu Ser Glu
 225 230 235 240
 Pro Thr Ala Ala Asp Val Ala Ser Phe Gln Asp Ala Ile Asn Asn Gly
 245 250 255
 Asp Leu Asp Val Leu Ile Tyr Asn Pro Gln Ser Ala Ser Thr Val Ala
 260 265 270
 Thr Ser Leu Lys Asp Leu Ala Glu Glu Lys Gly Ile Pro Val Val Glu
 275 280 285
 Ile Tyr Glu Thr Pro Gln Asn Thr Glu Asn Phe Leu Asp Ala Phe Thr
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	Met	Lys	Leu	Arg	Arg	
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atc aca acc acc gcc atc gct ggc ctc ttc gcc gca acc gca ctt gtt						163
Ile Thr Thr Thr Ala Ile Ala Gly Leu Phe Ala Ala Thr Ala Leu Val						
	10				20	
gcc tgt ggc tcc gat tcc gat gga agc agc acc act gtt gct gaa ggc						211
Ala Cys Gly Ser Asp Ser Asp Gly Ser Ser Thr Thr Val Ala Glu Gly						
	25				35	
acc gaa ggc gtg acc atc cgc atc ggc acc acc gac gct gcg aag gaa						259
Thr Glu Gly Val Thr Ile Arg Ile Gly Thr Thr Asp Ala Ala Lys Glu						
	40				50	
gca tgg acc gta ttc gaa gac aag gca gct gaa gag ggc atc acc ctc						307
Ala Trp Thr Val Phe Glu Asp Lys Ala Ala Glu Glu Gly Ile Thr Leu						
	55				65	
gac atc gtt cct ttc tct gac tac tcc acc cca aat gag gct ctt gcc						355
Asp Ile Val Pro Phe Ser Asp Tyr Ser Thr Pro Asn Glu Ala Leu Ala						
	70				80	85
cag gat cag ctg gac gtt aac ctc ttc cag cac ctg aag ttc ctg gct						403
Gln Asp Gln Leu Asp Val Asn Leu Phe Gln His Leu Lys Phe Leu Ala						
	90				95	100
gag tac aac gtc ggc tcc ggc gca gac ctc acc cca gtt ggc tcc agc						451
Glu Tyr Asn Val Gly Ser Gly Ala Asp Leu Thr Pro Val Gly Ser Ser						
	105				110	115
gaa atc gtg cca ctg gca cta ttc tgg aag gac cac gac tcc atc gac						499
Glu Ile Val Pro Leu Ala Leu Phe Trp Lys Asp His Asp Ser Ile Asp						
	120				125	130
ggc att gac ggc gag tcc gtt gcc atc cct aac gat cct tcc aac cag						547
Gly Ile Asp Gly Glu Ser Val Ala Ile Pro Asn Asp Pro Ser Asn Gln						
	135				140	145
ggc cgc gcc atc aac gtt ctc gtt cag gca ggt ctg gtc acc ctg aag						595
Gly Arg Ala Ile Asn Val Leu Val Gln Ala Gly Leu Val Thr Leu Lys						
	150				155	160
acc cca ggt ctg gtc acc cca gct cca gtc gat atc gac gag gca gct						643
Thr Pro Gly Leu Val Thr Pro Ala Pro Val Asp Ile Asp Glu Ala Ala						
	170				175	180
tcc aag gtt tcc gtc atc cca gtc gac gca gct cag gca cca acc gct						691
Ser Lys Val Ser Val Ile Pro Val Asp Ala Ala Gln Ala Pro Thr Ala						
	185				190	195
tac cag gag ggt cgc cca gcg atc atc aac aac tcc ttc ctt gac cgc						739
Tyr Gln Glu Gly Arg Pro Ala Ile Ile Asn Asn Ser Phe Leu Asp Arg						
	200				205	210
gca ggc atc gat cca aac ctc gcg gtc ttc gaa gat gat cct gag tct						787
Ala Gly Ile Asp Pro Asn Leu Ala Val Phe Glu Asp Asp Pro Glu Ser						
	215				220	225
gaa gaa gca gag cca tac atc aac gtc ttc gtc acc aag gct gag gac						835
Glu Glu Ala Glu Pro Tyr Ile Asn Val Phe Val Thr Lys Ala Glu Asp						

230	235	240	245	
aag gac gat gcc aac atc gcc cgc ctc gtt gag ctg tgg cac gac cca				883
Lys Asp Asp Ala Asn Ile Ala Arg Leu Val Glu Leu Trp His Asp Pro	250	255	260	
gag gtt ctg gct gca gta gac cgc gac tct gag ggc acc tcc gtc cca				931
Glu Val Leu Ala Ala Val Asp Arg Asp Ser Glu Gly Thr Ser Val Pro	265	270	275	
gtt gat cgt cca gga gct gac ctt cag gaa atc ctt gat cgc ctt gag				979
Val Asp Arg Pro Gly Ala Asp Leu Gln Glu Ile Leu Asp Arg Leu Glu	280	285	290	
gct gat cag gaa aac gca taatctcttt tgagttcttt gca				1020
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Thr Val Ala Glu Gly Thr Glu Gly Val Thr Ile Arg Ile Gly Thr Thr				
	35	40	45	
Asp Ala Ala Lys Glu Ala Trp Thr Val Phe Glu Asp Lys Ala Ala Glu				
	50	55	60	
Glu Gly Ile Thr Leu Asp Ile Val Pro Phe Ser Asp Tyr Ser Thr Pro				
	65	70	75	80
Asn Glu Ala Leu Ala Gln Asp Gln Leu Asp Val Asn Leu Phe Gln His				
	85	90	95	
Leu Lys Phe Leu Ala Glu Tyr Asn Val Gly Ser Gly Ala Asp Leu Thr				
	100	105	110	
Pro Val Gly Ser Ser Glu Ile Val Pro Leu Ala Leu Phe Trp Lys Asp				
	115	120	125	
His Asp Ser Ile Asp Gly Ile Asp Gly Glu Ser Val Ala Ile Pro Asn				
	130	135	140	
Asp Pro Ser Asn Gln Gly Arg Ala Ile Asn Val Leu Val Gln Ala Gly				
	145	150	155	160
Leu Val Thr Leu Lys Thr Pro Gly Leu Val Thr Pro Ala Pro Val Asp				
	165	170	175	
Ile Asp Glu Ala Ala Ser Lys Val Ser Val Ile Pro Val Asp Ala Ala				
	180	185	190	

Gln Ala Pro Thr Ala Tyr Gln Glu Gly Arg Pro Ala Ile Ile Asn Asn
 195 200 205

Ser Phe Leu Asp Arg Ala Gly Ile Asp Pro Asn Leu Ala Val Phe Glu
 210 215 220

Asp Asp Pro Glu Ser Glu Glu Ala Glu Pro Tyr Ile Asn Val Phe Val
 225 230 235 240

Thr Lys Ala Glu Asp Lys Asp Asp Ala Asn Ile Ala Arg Leu Val Glu
 245 250 255

Leu Trp His Asp Pro Glu Val Leu Ala Ala Val Asp Arg Asp Ser Glu
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Gly Thr Ser Val Pro Val Asp Arg Pro Gly Ala Asp Leu Gln Glu Ile
 275 280 285

Leu Asp Arg Leu Glu Ala Asp Gln Glu Asn Ala
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 <223> RXA00482

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actattgagt taatataaac atgaagaaag gatttgcttt atg cgc att tca agc 115
 Met Arg Ile Ser Ser
 1 5

aaa ctt gtc acc aca gca cta ctc gca gcc att tca ctt ttc ggg ata 163
 Lys Leu Val Thr Thr Ala Leu Leu Ala Ala Ile Ser Leu Phe Gly Ile
 10 15 20

tcc acg gca caa gcc caa gac att ttt gac ggc gga cga ctt gca ggt 211
 Ser Thr Ala Gln Ala Gln Asp Ile Phe Asp Gly Gly Arg Leu Ala Gly
 25 30 35

ggc tcc tcg cag gta tct aac cta agt tcg gtt cct gaa aac cta gcg 259
 Gly Ser Ser Gln Val Ser Asn Leu Ser Ser Val Pro Glu Asn Leu Ala
 40 45 50

ctg ccc gaa att gaa aat agc att gac cta gaa cgc tac aaa ggc aag 307
 Leu Pro Glu Ile Glu Asn Ser Ile Asp Leu Glu Arg Tyr Lys Gly Lys
 55 60 65

tgg tat caa gtc gca gca att ccc caa cca ttc tct tta cag tgc tca 355
 Trp Tyr Gln Val Ala Ala Ile Pro Gln Pro Phe Ser Leu Gln Cys Ser
 70 75 80 85

cat gac gtt acc gct gat tac ggc gtg atc gac tcg gac aca atc tct 403
 His Asp Val Thr Ala Asp Tyr Gly Val Ile Asp Ser Asp Thr Ile Ser

90	95	100	
gta aca aat aag tgt ggc act ttc ttt ggg cct tca gtt att gaa ggc			451
Val Thr Asn Lys Cys Gly Thr Phe Phe Gly Pro Ser Val Ile Glu Gly			
105	110	115	
agc gct aaa gta gtt tcc aat gct tca tta aag gtt agc ttc cca ggt			499
Ser Ala Lys Val Val Ser Asn Ala Ser Leu Lys Val Ser Phe Pro Gly			
120	125	130	
att cca ttt cag agt gaa gac aat caa gca aac tac cgc gtg acc tat			547
Ile Pro Phe Gln Ser Glu Asp Asn Gln Ala Asn Tyr Arg Val Thr Tyr			
135	140	145	
atc gaa gat gat tat tca cta gca atc gtc ggc agc cca agc cgg tcc			595
Ile Glu Asp Asp Tyr Ser Leu Ala Ile Val Gly Ser Pro Ser Arg Ser			
150	155	160	165
tca gga ttt ata cta tcc cgc acg cca cag ctc agt agt gac caa tgg			643
Ser Gly Phe Ile Leu Ser Arg Thr Pro Gln Leu Ser Ser Asp Gln Trp			
170	175	180	
tct cac gtt cgg aac att aca gag gac agt ggg tgg tgg cca tgc gca			691
Ser His Val Arg Asn Ile Thr Glu Asp Ser Gly Trp Trp Pro Cys Ala			
185	190	195	
ttc att aca gtc cca gcg aca ggt ggc tta aac acc gcc act ccg ctc			739
Phe Ile Thr Val Pro Ala Thr Gly Gly Leu Asn Thr Ala Thr Pro Leu			
200	205	210	
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Cys Thr Leu			
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Ser Leu Phe Gly Ile Ser Thr Ala Gln Ala Gln Asp Ile Phe Asp Gly			
20	25	30	
Gly Arg Leu Ala Gly Gly Ser Ser Gln Val Ser Asn Leu Ser Ser Val			
35	40	45	
Pro Glu Asn Leu Ala Leu Pro Glu Ile Glu Asn Ser Ile Asp Leu Glu			
50	55	60	
Arg Tyr Lys Gly Lys Trp Tyr Gln Val Ala Ala Ile Pro Gln Pro Phe			
65	70	75	80
Ser Leu Gln Cys Ser His Asp Val Thr Ala Asp Tyr Gly Val Ile Asp			
85	90	95	
Ser Asp Thr Ile Ser Val Thr Asn Lys Cys Gly Thr Phe Phe Gly Pro			
100	105	110	

Ser Val Ile Glu Gly Ser Ala Lys Val Val Ser Asn Ala Ser Leu Lys
 115 120 125

Val Ser Phe Pro Gly Ile Pro Phe Gln Ser Glu Asp Asn Gln Ala Asn
 130 135 140

Tyr Arg Val Thr Tyr Ile Glu Asp Asp Tyr Ser Leu Ala Ile Val Gly
 145 150 155 160

Ser Pro Ser Arg Ser Ser Gly Phe Ile Leu Ser Arg Thr Pro Gln Leu
 165 170 175

Ser Ser Asp Gln Trp Ser His Val Arg Asn Ile Thr Glu Asp Ser Gly
 180 185 190

Trp Trp Pro Cys Ala Phe Ile Thr Val Pro Ala Thr Gly Gly Leu Asn
 195 200 205

Thr Ala Thr Pro Leu Cys Thr Leu
 210 215

<210> 33
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1735)
 <223> RXN01164

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 Val Thr Leu Phe Val
 1 5

cgg ctc gcc ctt gct gct gtg ggc ggg ctt ttt gtc ttt gct tcc aat 163
 Arg Leu Ala Leu Ala Ala Val Gly Gly Leu Phe Val Phe Ala Ser Asn
 10 15 20

gaa ccg atc ggc tgg ttt gtc gcg gga att gtt ggc act gca tta ttt 211
 Glu Pro Ile Gly Trp Phe Val Ala Gly Ile Val Gly Thr Ala Leu Phe
 25 30 35

ttt atc tcc ctt gcg ccg tgg gat ctg gga gtt ccc caa aag cgg cgg 259
 Phe Ile Ser Leu Ala Pro Trp Asp Leu Gly Val Pro Gln Lys Arg Arg
 40 45 50

aag aag aat gag cca gtc cca ttt ttg caa cag atg tcc acg ggc cca 307
 Lys Lys Asn Glu Pro Val Pro Phe Leu Gln Gln Met Ser Thr Gly Pro
 55 60 65

act gtt gta cag ggc atg ctt tta ggt ttt gtc cat ggc ctg gtg aca 355
 Thr Val Val Gln Gly Met Leu Leu Gly Phe Val His Gly Leu Val Thr
 70 75 80 85

tat ttg cag ctg ttg ccg tgg atc ggt gag ttt gtt ggc tca ctg cct 403

Tyr	Leu	Gln	Leu	Leu	Pro	Trp	Ile	Gly	Glu	Phe	Val	Gly	Ser	Leu	Pro	
				90					95					100		
tat	gtc	gcg	ttg	tca	gtt	gtc	gag	gcg	ctt	tat	tcc	att	gct	ctt	ggt	451
Tyr	Val	Ala	Leu	Ser	Val	Val	Glu	Ala	Leu	Tyr	Ser	Ile	Ala	Leu	Gly	
			105					110					115			
gct	ttc	ggc	gtg	ctc	att	gcg	cgt	tgg	agg	gac	tgg	aag	gtt	ctc	ctg	499
Ala	Phe	Gly	Val	Leu	Ile	Ala	Arg	Trp	Arg	Asp	Trp	Lys	Val	Leu	Leu	
		120					125					130				
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Phe	Pro	Ala	Met	Tyr	Val	Ala	Val	Glu	Tyr	Leu	Arg	Ser	Ser	Trp	Pro	
	135						140				145					
ttt	gat	gga	ttc	gcg	tgg	gtt	cgc	ctg	gca	tgg	ggg	caa	att	aac	ggt	595
Phe	Asp	Gly	Phe	Ala	Trp	Val	Arg	Leu	Ala	Trp	Gly	Gln	Ile	Asn	Gly	
150					155				160						165	
cgc	ttg	gct	aat	ctc	gca	gcg	ctt	ggt	ggg	gta	gcg	ttt	gtc	act	ttt	643
Pro	Leu	Ala	Asn	Leu	Ala	Ala	Leu	Gly	Gly	Val	Ala	Phe	Val	Thr	Phe	
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tcc	acg	gtg	ctg	gct	gcc	gtg	ggt	gtg	gcc	atg	gtg	att	att	tcc	aag	691
Ser	Thr	Val	Leu	Ala	Ala	Val	Gly	Val	Ala	Met	Val	Ile	Ile	Ser	Lys	
			185					190					195			
aag	cga	ctg	gcc	ggc	gca	atc	atc	acc	gcg	agt	gtg	att	gct	atc	ggc	739
Lys	Arg	Leu	Ala	Gly	Ala	Ile	Ile	Thr	Ala	Ser	Val	Ile	Ala	Ile	Gly	
		200					205					210				
gcg	gtg	tca	tcc	ctg	tac	gtt	gac	cgc	aat	ggc	acg	agc	gat	gaa	agc	787
Ala	Val	Ser	Ser	Leu	Tyr	Val	Asp	Arg	Asn	Gly	Thr	Ser	Asp	Glu	Ser	
	215					220					225					
atc	gaa	gta	gcc	gca	att	cag	ggc	aat	gtg	cct	cgg	atg	gga	ttg	gac	835
Ile	Glu	Val	Ala	Ala	Ile	Gln	Gly	Asn	Val	Pro	Arg	Met	Gly	Leu	Asp	
230					235					240					245	
ttc	aat	gca	cag	cgc	cgc	gcg	gtg	ctg	gcg	aat	cac	gca	cgg	gaa	acc	883
Phe	Asn	Ala	Gln	Arg	Arg	Ala	Val	Leu	Ala	Asn	His	Ala	Arg	Glu	Thr	
				250					255					260		
ctc	aag	ctg	gat	gaa	caa	gtg	gat	ttg	gtg	atc	tgg	cgc	gag	aat	tcc	931
Leu	Lys	Leu	Asp	Glu	Gln	Val	Asp	Leu	Val	Ile	Trp	Pro	Glu	Asn	Ser	
			265					270					275			
tca	gac	gtc	aac	cca	ttt	tcc	gat	gca	caa	gca	aga	gcc	att	atc	gat	979
Ser	Asp	Val	Asn	Pro	Phe	Ser	Asp	Ala	Gln	Ala	Arg	Ala	Ile	Ile	Asp	
		280					285					290				
gga	gca	gtg	gaa	cat	gtt	cag	gca	cct	att	ttg	gtg	ggc	acg	atc	acc	1027
Gly	Ala	Val	Glu	His	Val	Gln	Ala	Pro	Ile	Leu	Val	Gly	Thr	Ile	Thr	
	295					300					305					
gtc	gat	gag	gtt	ggt	cca	cgc	aac	acc	atg	cag	gta	ttt	gat	cct	gtt	1075
Val	Asp	Glu	Val	Gly	Pro	Arg	Asn	Thr	Met	Gln	Val	Phe	Asp	Pro	Val	
310					315					320					325	
gaa	ggt	gcc	gcg	gag	tac	cac	aat	aag	aag	ttc	ttg	cag	cgc	ttt	ggt	1123
Glu	Gly	Ala	Ala	Glu	Tyr	His	Asn	Lys	Lys	Phe	Leu	Gln	Pro	Phe	Gly	

330	335	340	
gaa tac atg ccg ttt cgc gaa ttc ctg aga att ttc tcg ccc tac gtt Glu Tyr Met Pro Phe Arg Glu Phe Leu Arg Ile Phe Ser Pro Tyr Val 345 350 355			1171
gat tcc gct gga aac ttc cag ccc ggt gat ggc acc ggc gta gtg gag Asp Ser Ala Gly Asn Phe Gln Pro Gly Asp Gly Thr Gly Val Val Glu 360 365 370			1219
atg aat gct gcg aac tta ggc cgc gct gtg aca gtg ggc gtg atg acg Met Asn Ala Ala Asn Leu Gly Arg Ala Val Thr Val Gly Val Met Thr 375 380 385			1267
tgt tac gag gtc atc ttc gac cgt gct ggc cgc gac gcc atc gcc aat Cys Tyr Glu Val Ile Phe Asp Arg Ala Gly Arg Asp Ala Ile Ala Asn 390 395 400 405			1315
ggg gct gaa ttt ttg acc acg ccc acc aac aac gcc acc ttc gga ttc Gly Ala Glu Phe Leu Thr Thr Pro Thr Asn Asn Ala Thr Phe Gly Phe 410 415 420			1363
acg gac atg acg tat cag caa tta gca atg agc agg atg cgt gcc atc Thr Asp Met Thr Tyr Gln Gln Leu Ala Met Ser Arg Met Arg Ala Ile 425 430 435			1411
gaa ttt gat agg gcg gtg gtt gtt gca gct aca tcg ggt gtt tcg gct Glu Phe Asp Arg Ala Val Val Val Ala Ala Thr Ser Gly Val Ser Ala 440 445 450			1459
atc gtc aac cct gat gga agc att tcc caa aac acc cga att ttt gag Ile Val Asn Pro Asp Gly Ser Ile Ser Gln Asn Thr Arg Ile Phe Glu 455 460 465			1507
gcc gcc acc ttg acg gaa tcc att cca ctc aag gac act gtc acc atc Ala Ala Thr Leu Thr Glu Ser Ile Pro Leu Lys Asp Thr Val Thr Ile 470 475 480 485			1555
gca gcg cgg gtt ggt ttc tat gtt gaa tta ctg ttg gtt atc att ggt Ala Ala Arg Val Gly Phe Tyr Val Glu Leu Leu Leu Val Ile Ile Gly 490 495 500			1603
gta tta gct gga cta ttc gcc att cga atg aat agc cgt tca aag tct Val Leu Ala Gly Leu Phe Ala Ile Arg Met Asn Ser Arg Ser Lys Ser 505 510 515			1651
gcg aaa ggt tcc gct cgg ccc gca caa gtt cgg gtt aag aag gtg cct Ala Lys Gly Ser Ala Arg Pro Ala Gln Val Arg Val Lys Lys Val Pro 520 525 530			1699
gcg aaa aag gca gca act aat cgt cga aaa gta aaa taaaaacgtc Ala Lys Lys Ala Ala Thr Asn Arg Arg Lys Val Lys 535 540 545			1745
ccgaaggac gag			1758

<210> 34

<211> 545

<212> PRT

<213> Corynebacterium glutamicum

<400> 34

Val	Thr	Leu	Phe	Val	Arg	Leu	Ala	Leu	Ala	Ala	Val	Gly	Gly	Leu	Phe	1	5	10	15
Val	Phe	Ala	Ser	Asn	Glu	Pro	Ile	Gly	Trp	Phe	Val	Ala	Gly	Ile	Val	20	25	30	
Gly	Thr	Ala	Leu	Phe	Phe	Ile	Ser	Leu	Ala	Pro	Trp	Asp	Leu	Gly	Val	35	40	45	
Pro	Gln	Lys	Arg	Arg	Lys	Lys	Asn	Glu	Pro	Val	Pro	Phe	Leu	Gln	Gln	50	55	60	
Met	Ser	Thr	Gly	Pro	Thr	Val	Val	Gln	Gly	Met	Leu	Leu	Gly	Phe	Val	65	70	75	80
His	Gly	Leu	Val	Thr	Tyr	Leu	Gln	Leu	Leu	Pro	Trp	Ile	Gly	Glu	Phe	85	90	95	
Val	Gly	Ser	Leu	Pro	Tyr	Val	Ala	Leu	Ser	Val	Val	Glu	Ala	Leu	Tyr	100	105	110	
Ser	Ile	Ala	Leu	Gly	Ala	Phe	Gly	Val	Leu	Ile	Ala	Arg	Trp	Arg	Asp	115	120	125	
Trp	Lys	Val	Leu	Leu	Phe	Pro	Ala	Met	Tyr	Val	Ala	Val	Glu	Tyr	Leu	130	135	140	
Arg	Ser	Ser	Trp	Pro	Phe	Asp	Gly	Phe	Ala	Trp	Val	Arg	Leu	Ala	Trp	145	150	155	160
Gly	Gln	Ile	Asn	Gly	Pro	Leu	Ala	Asn	Leu	Ala	Ala	Leu	Gly	Gly	Val	165	170	175	
Ala	Phe	Val	Thr	Phe	Ser	Thr	Val	Leu	Ala	Ala	Val	Gly	Val	Ala	Met	180	185	190	
Val	Ile	Ile	Ser	Lys	Lys	Arg	Leu	Ala	Gly	Ala	Ile	Ile	Thr	Ala	Ser	195	200	205	
Val	Ile	Ala	Ile	Gly	Ala	Val	Ser	Ser	Leu	Tyr	Val	Asp	Arg	Asn	Gly	210	215	220	
Thr	Ser	Asp	Glu	Ser	Ile	Glu	Val	Ala	Ala	Ile	Gln	Gly	Asn	Val	Pro	225	230	235	240
Arg	Met	Gly	Leu	Asp	Phe	Asn	Ala	Gln	Arg	Arg	Ala	Val	Leu	Ala	Asn	245	250	255	
His	Ala	Arg	Glu	Thr	Leu	Lys	Leu	Asp	Glu	Gln	Val	Asp	Leu	Val	Ile	260	265	270	
Trp	Pro	Glu	Asn	Ser	Ser	Asp	Val	Asn	Pro	Phe	Ser	Asp	Ala	Gln	Ala	275	280	285	
Arg	Ala	Ile	Ile	Asp	Gly	Ala	Val	Glu	His	Val	Gln	Ala	Pro	Ile	Leu	290	295	300	
Val	Gly	Thr	Ile	Thr	Val	Asp	Glu	Val	Gly	Pro	Arg	Asn	Thr	Met	Gln	305	310	315	320

Val Phe Asp Pro Val Glu Gly Ala Ala Glu Tyr His Asn Lys Lys Phe
 325 330 335
 Leu Gln Pro Phe Gly Glu Tyr Met Pro Phe Arg Glu Phe Leu Arg Ile
 340 345 350
 Phe Ser Pro Tyr Val Asp Ser Ala Gly Asn Phe Gln Pro Gly Asp Gly
 355 360 365
 Thr Gly Val Val Glu Met Asn Ala Ala Asn Leu Gly Arg Ala Val Thr
 370 375 380
 Val Gly Val Met Thr Cys Tyr Glu Val Ile Phe Asp Arg Ala Gly Arg
 385 390 395 400
 Asp Ala Ile Ala Asn Gly Ala Glu Phe Leu Thr Thr Pro Thr Asn Asn
 405 410 415
 Ala Thr Phe Gly Phe Thr Asp Met Thr Tyr Gln Gln Leu Ala Met Ser
 420 425 430
 Arg Met Arg Ala Ile Glu Phe Asp Arg Ala Val Val Val Ala Ala Thr
 435 440 445
 Ser Gly Val Ser Ala Ile Val Asn Pro Asp Gly Ser Ile Ser Gln Asn
 450 455 460
 Thr Arg Ile Phe Glu Ala Ala Thr Leu Thr Glu Ser Ile Pro Leu Lys
 465 470 475 480
 Asp Thr Val Thr Ile Ala Ala Arg Val Gly Phe Tyr Val Glu Leu Leu
 485 490 495
 Leu Val Ile Ile Gly Val Leu Ala Gly Leu Phe Ala Ile Arg Met Asn
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 515 520 525
 Val Lys Lys Val Pro Ala Lys Lys Ala Ala Thr Asn Arg Arg Lys Val
 530 535 540

Lys
 545

<210> 35
 <211> 1675
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1675)
 <223> FRXA01164

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 tttcaccaaa ggtaaagatg aatccgacgg tgagaaataa gtg aca ctg ttt gtt 115

	Val	Thr	Leu	Phe	Val	
	1				5	
egg ctc gcc ctt gct gct gtg ggc ggg ctt ttt gtc ttt gct tcc aat						163
Arg Leu Ala Leu Ala Ala Val Gly Gly Leu Phe Val Phe Ala Ser Asn						
	10				20	
gaa ccg atc ggc tgg ttt gtc gcg gga att gtt ggc act gca tta ttt						211
Glu Pro Ile Gly Trp Phe Val Ala Gly Ile Val Gly Thr Ala Leu Phe						
	25				35	
ttt atc tcc ctt gcg ccg tgg gat ctg gga gtt ccc caa aag cgg cgg						259
Phe Ile Ser Leu Ala Pro Trp Asp Leu Gly Val Pro Gln Lys Arg Arg						
	40				50	
aag aag aat gag cca gtc cca ttt ttg caa cag atg tcc acg ggc cca						307
Lys Lys Asn Glu Pro Val Pro Phe Leu Gln Gln Met Ser Thr Gly Pro						
	55				65	
act gtt gta cag ggc atg ctt tta ggt ttt gtc cat ggc ctg gtg aca						355
Thr Val Val Gln Gly Met Leu Leu Gly Phe Val His Gly Leu Val Thr						
	70				80	85
tat ttg cag ctg ttg ccg tgg atc ggt gag ttt gtt ggc tca ctg cct						403
Tyr Leu Gln Leu Leu Pro Trp Ile Gly Glu Phe Val Gly Ser Leu Pro						
	90				95	100
tat gtc gcg ttg tca gtt gtc gag gcg ctt tat tcc att gct ctt ggt						451
Tyr Val Ala Leu Ser Val Val Glu Ala Leu Tyr Ser Ile Ala Leu Gly						
	105				110	115
gct ttc ggc gtg ctc att gcg cgt tgg agg gac tgg aag gtt ctc ctg						499
Ala Phe Gly Val Leu Ile Ala Arg Trp Arg Asp Trp Lys Val Leu Leu						
	120				125	130
ttt ccg gcg atg tat gtg gct gtg gag tat cta aga agc tgc tgg cca						547
Phe Pro Ala Met Tyr Val Ala Val Glu Tyr Leu Arg Ser Ser Trp Pro						
	135				140	145
ttt gat gga ttc gcg tgg gtt cgc ctg gca tgg ggt caa att aac ggt						595
Phe Asp Gly Phe Ala Trp Val Arg Leu Ala Trp Gly Gln Ile Asn Gly						
	150				155	160
ccg ttg gct aat ctc gca gcg ctt ggt ggg gta gcg ttt gtc act ttt						643
Pro Leu Ala Asn Leu Ala Ala Leu Gly Gly Val Ala Phe Val Thr Phe						
	170				175	180
tcc acg gtg ctg gct gcc gtg ggt gtg gcc atg gtg att att tcc aag						691
Ser Thr Val Leu Ala Ala Val Gly Val Ala Met Val Ile Ile Ser Lys						
	185				190	195
aag cga ctg gcc ggc gca atc atc acc gcg agt gtg att gct atc ggc						739
Lys Arg Leu Ala Gly Ala Ile Ile Thr Ala Ser Val Ile Ala Ile Gly						
	200				205	210
gcg gtg tca tcc ctg tac gtt gac cgc aat ggc acg agc gat gaa agc						787
Ala Val Ser Ser Leu Tyr Val Asp Arg Asn Gly Thr Ser Asp Glu Ser						
	215				220	225
atc gaa gta gcc gca att cag ggc aat gtg cct cgg atg gga ttg gac						835
Ile Glu Val Ala Ala Ile Gln Gly Asn Val Pro Arg Met Gly Leu Asp						

230	235	240	245	
ttc aat gca cag cgc cgc gcg gtg ctg gcg aat cac gca cgg gaa acc				883
Phe Asn Ala Gln Arg Arg Ala Val Leu Ala Asn His Ala Arg Glu Thr	250	255	260	
ctc aag ctg gat gaa caa gtg gat ttg gtg atc tgg ccg gag aat tcc				931
Leu Lys Leu Asp Glu Gln Val Asp Leu Val Ile Trp Pro Glu Asn Ser	265	270	275	
tca gac gtc aac cca ttt tcc gat gca caa gca aga gcc att atc gat				979
Ser Asp Val Asn Pro Phe Ser Asp Ala Gln Ala Arg Ala Ile Ile Asp	280	285	290	
gga gca gtg gaa cat gtt cag gca cct att ttg gtg ggc acg atc acc				1027
Gly Ala Val Glu His Val Gln Ala Pro Ile Leu Val Gly Thr Ile Thr	295	300	305	
gtc gat gag gtt ggt cca cgc aac acc atg cag gta ttt gat cct gtt				1075
Val Asp Glu Val Gly Pro Arg Asn Thr Met Gln Val Phe Asp Pro Val	310	315	320	325
gaa ggt gcc gcg gag tac cac aat aag aag ttc ttg cag ccg ttt ggt				1123
Glu Gly Ala Ala Glu Tyr His Asn Lys Lys Phe Leu Gln Pro Phe Gly	330	335	340	
gaa tac atg ccg ttt cgc gaa ttc ctg aga att ttc tcg ccc tac gtt				1171
Glu Tyr Met Pro Phe Arg Glu Phe Leu Arg Ile Phe Ser Pro Tyr Val	345	350	355	
gat tcc gct gga aac ttc cag ccc ggt gat ggc acc ggc gta gtg gag				1219
Asp Ser Ala Gly Asn Phe Gln Pro Gly Asp Gly Thr Gly Val Val Glu	360	365	370	
atg aat gct gcg aac tta ggc cgc gct gtg aca gtg ggc gtg atg acg				1267
Met Asn Ala Ala Asn Leu Gly Arg Ala Val Thr Val Gly Val Met Thr	375	380	385	
tgt tac gag gtc atc ttc gac cgt gct ggc cgc gac gcc atc gcc aat				1315
Cys Tyr Glu Val Ile Phe Asp Arg Ala Gly Arg Asp Ala Ile Ala Asn	395	400	405	
ggg gct gaa ttt ttg acc acg ccc acc aac aac gcc acc ttc gga ttc				1363
Gly Ala Glu Phe Leu Thr Thr Pro Thr Asn Asn Ala Thr Phe Gly Phe	410	415	420	
acg gac atg acg tat cag caa tta gca atg agc agg atg cgt gcc atc				1411
Thr Asp Met Thr Tyr Gln Gln Leu Ala Met Ser Arg Met Arg Ala Ile	425	430	435	
gaa ttt gat agg gcg gtg gtt gtt gca gct aca tcg ggt gtt tcg gct				1459
Glu Phe Asp Arg Ala Val Val Val Ala Ala Thr Ser Gly Val Ser Ala	440	445	450	
atc gtc aac cct gat gga agc att tcc caa aac acc cga att ttt gag				1507
Ile Val Asn Pro Asp Gly Ser Ile Ser Gln Asn Thr Arg Ile Phe Glu	455	460	465	
gcc gcc acc ttg acg gaa tcc att cca ctc aag gac act gtc acc atc				1555
Ala Ala Thr Leu Thr Glu Ser Ile Pro Leu Lys Asp Thr Val Thr Ile	470	475	480	485

gca gcg cgg gtt ggt ttc tat gtt gaa tta ctg ttg gtt atc att ggt 1603
 Ala Ala Arg Val Gly Phe Tyr Val Glu Leu Leu Val Ile Ile Gly
 490 495 500

gta tta gct gga cta ttc gcc att cga atg aat agc cgt tca aag tct 1651
 Val Leu Ala Gly Leu Phe Ala Ile Arg Met Asn Ser Arg Ser Lys Ser
 505 510 515

gcg aaa ggt tcc gct cgg ccc gca 1675
 Ala Lys Gly Ser Ala Arg Pro Ala
 520 525

<210> 36

<211> 525

<212> PRT

<213> Corynebacterium glutamicum

<400> 36

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 20 25 30

Gly Thr Ala Leu Phe Phe Ile Ser Leu Ala Pro Trp Asp Leu Gly Val
 35 40 45

Pro Gln Lys Arg Arg Lys Lys Asn Glu Pro Val Pro Phe Leu Gln Gln
 50 55 60

Met Ser Thr Gly Pro Thr Val Val Gln Gly Met Leu Leu Gly Phe Val
 65 70 75 80

His Gly Leu Val Thr Tyr Leu Gln Leu Leu Pro Trp Ile Gly Glu Phe
 85 90 95

Val Gly Ser Leu Pro Tyr Val Ala Leu Ser Val Val Glu Ala Leu Tyr
 100 105 110

Ser Ile Ala Leu Gly Ala Phe Gly Val Leu Ile Ala Arg Trp Arg Asp
 115 120 125

Trp Lys Val Leu Leu Phe Pro Ala Met Tyr Val Ala Val Glu Tyr Leu
 130 135 140

Arg Ser Ser Trp Pro Phe Asp Gly Phe Ala Trp Val Arg Leu Ala Trp
 145 150 155 160

Gly Gln Ile Asn Gly Pro Leu Ala Asn Leu Ala Ala Leu Gly Gly Val
 165 170 175

Ala Phe Val Thr Phe Ser Thr Val Leu Ala Ala Val Gly Val Ala Met
 180 185 190

Val Ile Ile Ser Lys Lys Arg Leu Ala Gly Ala Ile Ile Thr Ala Ser
 195 200 205

Val Ile Ala Ile Gly Ala Val Ser Ser Leu Tyr Val Asp Arg Asn Gly
 210 215 220

Thr Ser Asp Glu Ser Ile Glu Val Ala Ala Ile Gln Gly Asn Val Pro
 225 230 235 240
 Arg Met Gly Leu Asp Phe Asn Ala Gln Arg Arg Ala Val Leu Ala Asn
 245 250 255
 His Ala Arg Glu Thr Leu Lys Leu Asp Glu Gln Val Asp Leu Val Ile
 260 265 270
 Trp Pro Glu Asn Ser Ser Asp Val Asn Pro Phe Ser Asp Ala Gln Ala
 275 280 285
 Arg Ala Ile Ile Asp Gly Ala Val Glu His Val Gln Ala Pro Ile Leu
 290 295 300
 Val Gly Thr Ile Thr Val Asp Glu Val Gly Pro Arg Asn Thr Met Gln
 305 310 315 320
 Val Phe Asp Pro Val Glu Gly Ala Ala Glu Tyr His Asn Lys Lys Phe
 325 330 335
 Leu Gln Pro Phe Gly Glu Tyr Met Pro Phe Arg Glu Phe Leu Arg Ile
 340 345 350
 Phe Ser Pro Tyr Val Asp Ser Ala Gly Asn Phe Gln Pro Gly Asp Gly
 355 360 365
 Thr Gly Val Val Glu Met Asn Ala Ala Asn Leu Gly Arg Ala Val Thr
 370 375 380
 Val Gly Val Met Thr Cys Tyr Glu Val Ile Phe Asp Arg Ala Gly Arg
 385 390 395 400
 Asp Ala Ile Ala Asn Gly Ala Glu Phe Leu Thr Thr Pro Thr Asn Asn
 405 410 415
 Ala Thr Phe Gly Phe Thr Asp Met Thr Tyr Gln Gln Leu Ala Met Ser
 420 425 430
 Arg Met Arg Ala Ile Glu Phe Asp Arg Ala Val Val Val Ala Ala Thr
 435 440 445
 Ser Gly Val Ser Ala Ile Val Asn Pro Asp Gly Ser Ile Ser Gln Asn
 450 455 460
 Thr Arg Ile Phe Glu Ala Ala Thr Leu Thr Glu Ser Ile Pro Leu Lys
 465 470 475 480
 Asp Thr Val Thr Ile Ala Ala Arg Val Gly Phe Tyr Val Glu Leu Leu
 485 490 495
 Leu Val Ile Ile Gly Val Leu Ala Gly Leu Phe Ala Ile Arg Met Asn
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 Ser Arg Ser Lys Ser Ala Lys Gly Ser Ala Arg Pro Ala
 515 520 525

<210> 37

<211> 933

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(910)

<223> RXN01168

<400> 37

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                                         Met Ser Ser Glu Ala
                                         1 5
gta gat gct acg acg ctg gtg att att cca acg tac aac gag ctg gaa 163
Val Asp Ala Thr Thr Leu Val Ile Ile Pro Thr Tyr Asn Glu Leu Glu
                        10 15 20
aac ctt cca ctc atc gtg gat cgc gtg cgc acc gca acc cct gac gtt 211
Asn Leu Pro Leu Ile Val Asp Arg Val Arg Thr Ala Thr Pro Asp Val
                        25 30 35
cac gta ctc atc gtg gac gac aac agc cca gac ggc acc ggc gag cgc 259
His Val Leu Ile Val Asp Asp Asn Ser Pro Asp Gly Thr Gly Glu Arg
                        40 45 50
gca gac aag ctt gct gct gac gac gac cac att ttt gtc ctc cac cgc 307
Ala Asp Lys Leu Ala Ala Asp Asp Asp His Ile Phe Val Leu His Arg
                        55 60 65
gaa ggc aaa ggc ggc ctg tgc gca gag tac atg gct ggc ttc cag tgg 355
Glu Gly Lys Gly Gly Leu Cys Ala Glu Tyr Met Ala Gly Phe Gln Trp
                        70 75 80 85
ggc ctg gag cgc gac tac cag gtc ctg tgc gaa atg gac gcc gac ggc 403
Gly Leu Glu Arg Asp Tyr Gln Val Leu Cys Glu Met Asp Ala Asp Gly
                        90 95 100
tcc cac gca cca gaa cag ctg cac ctg ctg ctc gct gag atc acc aat 451
Ser His Ala Pro Glu Gln Leu His Leu Leu Leu Ala Glu Ile Thr Asn
                        105 110 115
ggc gct gac ctg gtc atc ggc tcg cgc tac gtg cca ggc ggc cgc gta 499
Gly Ala Asp Leu Val Ile Gly Ser Arg Tyr Val Pro Gly Gly Arg Val
                        120 125 130
gtc aac tgg ccc aag aac cgt tgg ctc ttg tcc aag ggc ggc aac gtc 547
Val Asn Trp Pro Lys Asn Arg Trp Leu Leu Ser Lys Gly Gly Asn Val
                        135 140 145
tac atc agc gtc gcg ctc ggc gcc ggc ttg acc gat atg acc gca ggg 595
Tyr Ile Ser Val Ala Leu Gly Ala Gly Leu Thr Asp Met Thr Ala Gly
                        150 155 160 165
tac cgc gct ttt cga cgt gaa gtg cta gaa gca ctg ccg ctt gat gag 643
Tyr Arg Ala Phe Arg Arg Glu Val Leu Glu Ala Leu Pro Leu Asp Glu
                        170 175 180
ctc tcc aac gct ggg tac att ttc caa gtt gag att gcc tac cgt gca 691
Leu Ser Asn Ala Gly Tyr Ile Phe Gln Val Glu Ile Ala Tyr Arg Ala

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185	190	195	
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Val Glu Ala Gly Phe Asp Val Arg Glu Val Pro Ile Thr Phe Thr Glu			
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cgt gag atc ggc gaa tcc aag ctg gac ggc agc ttt gtc aag gat tcc			787
Arg Glu Ile Gly Glu Ser Lys Leu Asp Gly Ser Phe Val Lys Asp Ser			
215	220	225	
ctg ctc gag gta acc aag tgg ggc ctc aag cac cgc ggt ggc cag gcc			835
Leu Leu Glu Val Thr Lys Trp Gly Leu Lys His Arg Gly Gly Gln Ala			
230	235	240	245
aag gaa ctg tcc aag gaa atg gtc ggc ctg ctg aac tat gag tgg aag			883
Lys Glu Leu Ser Lys Glu Met Val Gly Leu Leu Asn Tyr Glu Trp Lys			
250	255	260	
cac ttc aaa aag cgc aac acc tgg ctc taaactgctt gccgggttagt gaa			933
His Phe Lys Lys Arg Asn Thr Trp Leu			
265	270		
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Tyr Asn Glu Leu Glu Asn Leu Pro Leu Ile Val Asp Arg Val Arg Thr			
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Ala Thr Pro Asp Val His Val Leu Ile Val Asp Asp Asn Ser Pro Asp			
35	40	45	
Gly Thr Gly Glu Arg Ala Asp Lys Leu Ala Ala Asp Asp Asp His Ile			
50	55	60	
Phe Val Leu His Arg Glu Gly Lys Gly Gly Leu Cys Ala Glu Tyr Met			
65	70	75	80
Ala Gly Phe Gln Trp Gly Leu Glu Arg Asp Tyr Gln Val Leu Cys Glu			
85	90	95	
Met Asp Ala Asp Gly Ser His Ala Pro Glu Gln Leu His Leu Leu Leu			
100	105	110	
Ala Glu Ile Thr Asn Gly Ala Asp Leu Val Ile Gly Ser Arg Tyr Val			
115	120	125	
Pro Gly Gly Arg Val Val Asn Trp Pro Lys Asn Arg Trp Leu Leu Ser			
130	135	140	
Lys Gly Gly Asn Val Tyr Ile Ser Val Ala Leu Gly Ala Gly Leu Thr			
145	150	155	160
Asp Met Thr Ala Gly Tyr Arg Ala Phe Arg Arg Glu Val Leu Glu Ala			
165	170	175	

Leu Pro Leu Asp Glu Leu Ser Asn Ala Gly Tyr Ile Phe Gln Val Glu
 180 185 190
 Ile Ala Tyr Arg Ala Val Glu Ala Gly Phe Asp Val Arg Glu Val Pro
 195 200 205
 Ile Thr Phe Thr Glu Arg Glu Ile Gly Glu Ser Lys Leu Asp Gly Ser
 210 215 220
 Phe Val Lys Asp Ser Leu Leu Glu Val Thr Lys Trp Gly Leu Lys His
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 Arg Gly Gly Gln Ala Lys Glu Leu Ser Lys Glu Met Val Gly Leu Leu
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 Asn Tyr Glu Trp Lys His Phe Lys Lys Arg Asn Thr Trp Leu
 260 265 270

<210> 39
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(720)
 <223> FRXA01168

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 cca gac ggc acc ggc gag cgc gca gac aag ctt gct gct gac gac gac 96
 Pro Asp Gly Thr Gly Glu Arg Ala Asp Lys Leu Ala Ala Asp Asp Asp
 20 25 30

 cac att ttt gtc ctc cac cgc gaa ggc aaa ggc ggc ctg tgc gca gag 144
 His Ile Phe Val Leu His Arg Glu Gly Lys Gly Gly Leu Cys Ala Glu
 35 40 45

 tac atg gct ggc ttc cag tgg ggc ctg gag cgc gac tac cag gtc ctg 192
 Tyr Met Ala Gly Phe Gln Trp Gly Leu Glu Arg Asp Tyr Gln Val Leu
 50 55 60

 tgc gaa atg gac gcc gac ggc tcc cac gca cca gaa cag ctg cac ctg 240
 Cys Glu Met Asp Ala Asp Gly Ser His Ala Pro Glu Gln Leu His Leu
 65 70 75 80

 ctg ctc gct gag atc acc aat ggc gct gac ctg gtc atc ggc tgc cgc 288
 Leu Leu Ala Glu Ile Thr Asn Gly Ala Asp Leu Val Ile Gly Ser Arg
 85 90 95

 tac gtg cca ggc ggc cgc gta gtc aac tgg ccc aag aac cgt tgg ctc 336
 Tyr Val Pro Gly Gly Arg Val Val Asn Trp Pro Lys Asn Arg Trp Leu
 100 105 110

 ttg tcc aag ggc ggc aac gtc tac atc agc gtc gcg ctc ggc gcc ggc 384
 Leu Ser Lys Gly Gly Asn Val Tyr Ile Ser Val Ala Leu Gly Ala Gly

115	120	125	
ttg acc gat atg acc gca ggg tac cgc gct ttt cga cgt gaa gtg cta			432
Leu Thr Asp Met Thr Ala Gly Tyr Arg Ala Phe Arg Arg Glu Val Leu			
130	135	140	
gaa gca ctg ccg ctt gat gag ctc tcc aac gct ggg tac att ttc caa			480
Glu Ala Leu Pro Leu Asp Glu Leu Ser Asn Ala Gly Tyr Ile Phe Gln			
145	150	155	160
gtt gag att gcc tac cgt gca gtt gaa gcc gga ttc gat gtt cgt gaa			528
Val Glu Ile Ala Tyr Arg Ala Val Glu Ala Gly Phe Asp Val Arg Glu			
	165	170	175
gtt ccc atc act ttc acc gag cgt gag atc ggc gaa tcc aag ctg gac			576
Val Pro Ile Thr Phe Thr Glu Arg Glu Ile Gly Glu Ser Lys Leu Asp			
	180	185	190
ggc agc ttt gtc aag gat tcc ctg ctc gag gta acc aag tgg ggc ctc			624
Gly Ser Phe Val Lys Asp Ser Leu Leu Glu Val Thr Lys Trp Gly Leu			
	195	200	205
aag cac cgc ggt ggc cag gcc aag gaa ctg tcc aag gaa atg gtc ggc			672
Lys His Arg Gly Gly Gln Ala Lys Glu Leu Ser Lys Glu Met Val Gly			
	210	215	220
ctg ctg aac tat gag tgg aag cac ttc aaa aag cgc aac acc tgg ctc			720
Leu Leu Asn Tyr Glu Trp Lys His Phe Lys Lys Arg Asn Thr Trp Leu			
225	230	235	240
taaactgctt gccggtagt gaa			743

<210> 40
 <211> 240
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 40
 Arg Thr Ala Thr Pro Asp Val His Val Leu Ile Val Asp Asp Asn Ser
 1 5 10 15
 Pro Asp Gly Thr Gly Glu Arg Ala Asp Lys Leu Ala Ala Asp Asp Asp
 20 25 30
 His Ile Phe Val Leu His Arg Glu Gly Lys Gly Gly Leu Cys Ala Glu
 35 40 45
 Tyr Met Ala Gly Phe Gln Trp Gly Leu Glu Arg Asp Tyr Gln Val Leu
 50 55 60
 Cys Glu Met Asp Ala Asp Gly Ser His Ala Pro Glu Gln Leu His Leu
 65 70 75 80
 Leu Leu Ala Glu Ile Thr Asn Gly Ala Asp Leu Val Ile Gly Ser Arg
 85 90 95
 Tyr Val Pro Gly Gly Arg Val Val Asn Trp Pro Lys Asn Arg Trp Leu
 100 105 110
 Leu Ser Lys Gly Gly Asn Val Tyr Ile Ser Val Ala Leu Gly Ala Gly

115	120	125
Leu Thr Asp Met Thr Ala Gly Tyr Arg Ala Phe Arg Arg Glu Val Leu		
130	135	140
Glu Ala Leu Pro Leu Asp Glu Leu Ser Asn Ala Gly Tyr Ile Phe Gln		
145	150	155
Val Glu Ile Ala Tyr Arg Ala Val Glu Ala Gly Phe Asp Val Arg Glu		
	165	170
Val Pro Ile Thr Phe Thr Glu Arg Glu Ile Gly Glu Ser Lys Leu Asp		
	180	185
Gly Ser Phe Val Lys Asp Ser Leu Leu Glu Val Thr Lys Trp Gly Leu		
	195	200
Lys His Arg Gly Gly Gln Ala Lys Glu Leu Ser Lys Glu Met Val Gly		
	210	215
Leu Leu Asn Tyr Glu Trp Lys His Phe Lys Lys Arg Asn Thr Trp Leu		
	225	230
		235
		240

<210> 41
 <211> 1293
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1270)
 <223> RXN02062

<400> 41
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 Met Arg Val Gly Met
 1 5
 atg aca aga gag tat cca cca gag gtt tac ggc ggc gct ggc gtg cac 163
 Met Thr Arg Glu Tyr Pro Pro Glu Val Tyr Gly Gly Ala Gly Val His
 10 15 20
 gtc acc gaa ttg acc cga ttc atg cgt gag atc gct gaa gtt gat gtt 211
 Val Thr Glu Leu Thr Arg Phe Met Arg Glu Ile Ala Glu Val Asp Val
 25 30 35
 cac tgc atg ggt gca cct cgc gat atg gag gga gtt ttc gtc cac ggc 259
 His Cys Met Gly Ala Pro Arg Asp Met Glu Gly Val Phe Val His Gly
 40 45 50
 gtc gat cct gcc ttg gaa agc gcg aac cct gcg att aag aca ctg tcc 307
 Val Asp Pro Ala Leu Glu Ser Ala Asn Pro Ala Ile Lys Thr Leu Ser
 55 60 65
 acc ggt tta cgc atg gca gaa gct gca aac aac gtg gat gtc gtg cac 355
 Thr Gly Leu Arg Met Ala Glu Ala Ala Asn Asn Val Asp Val Val His
 70 75 80 85

tca cac act tgg tat gca ggt ctt ggc ggc cac ctt gca gct cgt etc	403
Ser His Thr Trp Tyr Ala Gly Leu Gly Gly His Leu Ala Ala Arg Leu	
90 95 100	
cac ggc att cct cac gtg gct acc gcg cac tct ttg gag cca gat cgc	451
His Gly Ile Pro His Val Ala Thr Ala His Ser Leu Glu Pro Asp Arg	
105 110 115	
cca tgg aag cgt gag cag ctt ggc ggt gga tac gac gtg tcc tcc tgg	499
Pro Trp Lys Arg Glu Gln Leu Gly Gly Gly Tyr Asp Val Ser Ser Trp	
120 125 130	
tct gaa aaa aat gcc atg gaa tac gct gac gcg gtc atc gct gtg tcg	547
Ser Glu Lys Asn Ala Met Glu Tyr Ala Asp Ala Val Ile Ala Val Ser	
135 140 145	
gct cgc atg aaa gat tcc atc ctc gct gcg tac cct cgc atc gag ccg	595
Ala Arg Met Lys Asp Ser Ile Leu Ala Ala Tyr Pro Arg Ile Glu Pro	
150 155 160 165	
gac aac gtg cgt gtt gtc ctc aac ggc atc gac act gag ttg tgg cag	643
Asp Asn Val Arg Val Val Leu Asn Gly Ile Asp Thr Glu Leu Trp Gln	
170 175 180	
cct cgc ccg act ttc gat gac gcg gaa gat tcc gta ctc cgc tcc cta	691
Pro Arg Pro Thr Phe Asp Asp Ala Glu Asp Ser Val Leu Arg Ser Leu	
185 190 195	
ggc gtt gac cca cag cgg ccc atc gtc gca ttt gtc ggc cgc atc acc	739
Gly Val Asp Pro Gln Arg Pro Ile Val Ala Phe Val Gly Arg Ile Thr	
200 205 210	
cgc caa aaa ggc gtc gag cac ctc atc aag gca gca gcg ctt ttc gac	787
Arg Gln Lys Gly Val Glu His Leu Ile Lys Ala Ala Ala Leu Phe Asp	
215 220 225	
gag tcc gtg cag ctt gtg ctc tgt gcc ggc gcg cca gac acc ccc gaa	835
Glu Ser Val Gln Leu Val Leu Cys Ala Gly Ala Pro Asp Thr Pro Glu	
230 235 240 245	
atc gca gct cgc acc acc gcc ctg gtg gaa gaa ctc cag gca aag cgc	883
Ile Ala Ala Arg Thr Thr Ala Leu Val Glu Glu Leu Gln Ala Lys Arg	
250 255 260	
gaa ggc att ttc tgg gtt cag gac atg ctg ggc aag gac aaa atc caa	931
Glu Gly Ile Phe Trp Val Gln Asp Met Leu Gly Lys Asp Lys Ile Gln	
265 270 275	
gag att ctc acc gct gct gac acc ttc gtg tgc cca tcc att tac gag	979
Glu Ile Leu Thr Ala Ala Asp Thr Phe Val Cys Pro Ser Ile Tyr Glu	
280 285 290	
cca ctg ggc atc gtg aac ttg gaa gca atg gcc tgc aac acc gca gtt	1027
Pro Leu Gly Ile Val Asn Leu Glu Ala Met Ala Cys Asn Thr Ala Val	
295 300 305	
gtc gca tcc gac gtt gga ggc atc cct gag gtt gtt gtc gac ggc acc	1075
Val Ala Ser Asp Val Gly Gly Ile Pro Glu Val Val Val Asp Gly Thr	
310 315 320 325	
acc ggc gcc ctc gtt cac tac gac gaa aat gat gtc gaa acc ttc gag	1123

Thr Gly Ala Leu Val His Tyr Asp Glu Asn Asp Val Glu Thr Phe Glu
 330 335 340

cgc gat atc gcc gaa gcg gtg aat aaa atg gtc gct gat cga gag acc 1171
 Arg Asp Ile Ala Glu Ala Val Asn Lys Met Val Ala Asp Arg Glu Thr
 345 350 355

gca gcc aaa ttt ggt ctc gca ggg cgc gaa cgt gct atc aat gat ttc 1219
 Ala Ala Lys Phe Gly Leu Ala Gly Arg Glu Arg Ala Ile Asn Asp Phe
 360 365 370

tcc tgg gca acg att gct cag cag acc att gat gtg tac aaa tcc ttg 1267
 Ser Trp Ala Thr Ile Ala Gln Gln Thr Ile Asp Val Tyr Lys Ser Leu
 375 380 385

atg taaaaccgaa agccgggggaa cct 1293
 Met
 390

<210> 42
 <211> 390
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 42
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Ala Glu Val Asp Val His Cys Met Gly Ala Pro Arg Asp Met Glu Gly
 35 40 45

Val Phe Val His Gly Val Asp Pro Ala Leu Glu Ser Ala Asn Pro Ala
 50 55 60

Ile Lys Thr Leu Ser Thr Gly Leu Arg Met Ala Glu Ala Ala Asn Asn
 65 70 75 80

Val Asp Val Val His Ser His Thr Trp Tyr Ala Gly Leu Gly Gly His
 85 90 95

Leu Ala Ala Arg Leu His Gly Ile Pro His Val Ala Thr Ala His Ser
 100 105 110

Leu Glu Pro Asp Arg Pro Trp Lys Arg Glu Gln Leu Gly Gly Gly Tyr
 115 120 125

Asp Val Ser Ser Trp Ser Glu Lys Asn Ala Met Glu Tyr Ala Asp Ala
 130 135 140

Val Ile Ala Val Ser Ala Arg Met Lys Asp Ser Ile Leu Ala Ala Tyr
 145 150 155 160

Pro Arg Ile Glu Pro Asp Asn Val Arg Val Val Leu Asn Gly Ile Asp
 165 170 175

Thr Glu Leu Trp Gln Pro Arg Pro Thr Phe Asp Asp Ala Glu Asp Ser
 180 185 190

Val Leu Arg Ser Leu Gly Val Asp Pro Gln Arg Pro Ile Val Ala Phe
 195 200 205
 Val Gly Arg Ile Thr Arg Gln Lys Gly Val Glu His Leu Ile Lys Ala
 210 215 220
 Ala Ala Leu Phe Asp Glu Ser Val Gln Leu Val Leu Cys Ala Gly Ala
 225 230 235 240
 Pro Asp Thr Pro Glu Ile Ala Ala Arg Thr Thr Ala Leu Val Glu Glu
 245 250 255
 Leu Gln Ala Lys Arg Glu Gly Ile Phe Trp Val Gln Asp Met Leu Gly
 260 265 270
 Lys Asp Lys Ile Gln Glu Ile Leu Thr Ala Ala Asp Thr Phe Val Cys
 275 280 285
 Pro Ser Ile Tyr Glu Pro Leu Gly Ile Val Asn Leu Glu Ala Met Ala
 290 295 300
 Cys Asn Thr Ala Val Val Ala Ser Asp Val Gly Gly Ile Pro Glu Val
 305 310 315 320
 Val Val Asp Gly Thr Thr Gly Ala Leu Val His Tyr Asp Glu Asn Asp
 325 330 335
 Val Glu Thr Phe Glu Arg Asp Ile Ala Glu Ala Val Asn Lys Met Val
 340 345 350
 Ala Asp Arg Glu Thr Ala Ala Lys Phe Gly Leu Ala Gly Arg Glu Arg
 355 360 365
 Ala Ile Asn Asp Phe Ser Trp Ala Thr Ile Ala Gln Gln Thr Ile Asp
 370 375 380
 Val Tyr Lys Ser Leu Met
 385 390

<210> 43
 <211> 1293
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1270)
 <223> FRXA02062

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 Met Arg Val Gly Met
 1 5
 atg aca aga gag tat cca cca gag gtt tac ggc ggc gct ggc gtg cac 163
 Met Thr Arg Glu Tyr Pro Pro Glu Val Tyr Gly Gly Ala Gly Val His
 10 15 20

gtc acc gaa ttg acc cga ttc atg cgt gag atc gct gaa gtt gat gtt	211
Val Thr Glu Leu Thr Arg Phe Met Arg Glu Ile Ala Glu Val Asp Val	
25 30 35	
cac tgc atg ggt gca cct cgc gat atg gag gga gtt ttc gtc cac ggc	259
His Cys Met Gly Ala Pro Arg Asp Met Glu Gly Val Phe Val His Gly	
40 45 50	
gtc gat cct gcc ttg gaa agc gcg aac cct gcg att aag aca ctg tcc	307
Val Asp Pro Ala Leu Glu Ser Ala Asn Pro Ala Ile Lys Thr Leu Ser	
55 60 65	
acc ggt tta cgc atg gca gaa gct gca aac aac gtg gat gtc gtg cac	355
Thr Gly Leu Arg Met Ala Glu Ala Ala Asn Asn Val Asp Val Val His	
70 75 80 85	
tca cac act tgg tat gca ggt ctt ggc ggc cac ctt gca gct cgt ctc	403
Ser His Thr Trp Tyr Ala Gly Leu Gly Gly His Leu Ala Ala Arg Leu	
90 95 100	
cac ggc att cct cac gtg gct acc gcg cac tct ttg gag cca gat cgc	451
His Gly Ile Pro His Val Ala Thr Ala His Ser Leu Glu Pro Asp Arg	
105 110 115	
cca tgg aag cgt gag cag ctt ggc ggt gga tac gac gtg tcc tcc tgg	499
Pro Trp Lys Arg Glu Gln Leu Gly Gly Gly Tyr Asp Val Ser Ser Trp	
120 125 130	
tct gaa aaa aat gcc atg gaa tac gct gac gcg gtc atc gct gtg tcg	547
Ser Glu Lys Asn Ala Met Glu Tyr Ala Asp Ala Val Ile Ala Val Ser	
135 140 145	
gct cgc atg aaa gat tcc atc ctc gct gcg tac cct cgc atc gag ccg	595
Ala Arg Met Lys Asp Ser Ile Leu Ala Ala Tyr Pro Arg Ile Glu Pro	
150 155 160 165	
gac aac gtg cgt gtt gtc ctc aac ggc atc gac act gag ttg tgg cag	643
Asp Asn Val Arg Val Val Leu Asn Gly Ile Asp Thr Glu Leu Trp Gln	
170 175 180	
cct cgc ccg act ttc gat gac gcg gaa gat tcc gta ctc cgc tcc cta	691
Pro Arg Pro Thr Phe Asp Asp Ala Glu Asp Ser Val Leu Arg Ser Leu	
185 190 195	
ggc gtt gac cca cag cgg ccc atc gtc gca ttt gtc ggc cgc atc acc	739
Gly Val Asp Pro Gln Arg Pro Ile Val Ala Phe Val Gly Arg Ile Thr	
200 205 210	
cgc caa aaa ggc gtc gag cac ctc atc aag gca gca gcg ctt ttc gac	787
Arg Gln Lys Gly Val Glu His Leu Ile Lys Ala Ala Ala Leu Phe Asp	
215 220 225	
gag tcc gtg cag ctt gtg ctc tgt gcc ggc gcg cca gac acc ccc gaa	835
Glu Ser Val Gln Leu Val Leu Cys Ala Gly Ala Pro Asp Thr Pro Glu	
230 235 240 245	
atc gca gct cgc acc acc gcc ctg gtg gaa gaa ctc cag gca aag cgc	883
Ile Ala Ala Arg Thr Thr Ala Leu Val Glu Glu Leu Gln Ala Lys Arg	
250 255 260	

gaa ggc att ttc tgg gtt cag gac atg ctg ggc aag gac aaa atc caa 931
 Glu Gly Ile Phe Trp Val Gln Asp Met Leu Gly Lys Asp Lys Ile Gln
 265 270 275

 gag att ctc acc gct gct gac acc ttc gtg tgc cca tcc att tac gag 979
 Glu Ile Leu Thr Ala Ala Asp Thr Phe Val Cys Pro Ser Ile Tyr Glu
 280 285 290

 cca ctg ggc atc gtg aac ttg gaa gca atg gcc tgc aac acc gca gtt 1027
 Pro Leu Gly Ile Val Asn Leu Glu Ala Met Ala Cys Asn Thr Ala Val
 295 300 305

 gtc gca tcc gac gtt gga ggc atc cct gag gtt gtt gtc gac ggc acc 1075
 Val Ala Ser Asp Val Gly Gly Ile Pro Glu Val Val Val Asp Gly Thr
 310 315 320 325

 acc ggc gcc ctc gtt cac tac gac gaa aat gat gtc gaa acc ttc gag 1123
 Thr Gly Ala Leu Val His Tyr Asp Glu Asn Asp Val Glu Thr Phe Glu
 330 335 340

 cgc gat atc gcc gaa gcg gtg aat aaa atg gtc gct gat cga gag acc 1171
 Arg Asp Ile Ala Glu Ala Val Asn Lys Met Val Ala Asp Arg Glu Thr
 345 350 355

 gca gcc aaa ttt ggt ctc gca ggg cgc gaa cgt gct atc aat gat ttc 1219
 Ala Ala Lys Phe Gly Leu Ala Gly Arg Glu Arg Ala Ile Asn Asp Phe
 360 365 370

 tcc tgg gca acg att gct cag cag acc att gat gtg tac aaa tcc ttg 1267
 Ser Trp Ala Thr Ile Ala Gln Gln Thr Ile Asp Val Tyr Lys Ser Leu
 375 380 385

 atg taaaaccgaa agccggggaa cct 1293
 Met
 390

<210> 44

<211> 390

<212> PRT

<213> Corynebacterium glutamicum

<400> 44

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 Ala Glu Val Asp Val His Cys Met Gly Ala Pro Arg Asp Met Glu Gly
 35 40 45

 Val Phe Val His Gly Val Asp Pro Ala Leu Glu Ser Ala Asn Pro Ala
 50 55 60

 Ile Lys Thr Leu Ser Thr Gly Leu Arg Met Ala Glu Ala Ala Asn Asn
 65 70 75 80

 Val Asp Val Val His Ser His Thr Trp Tyr Ala Gly Leu Gly Gly His
 85 90 95

Leu Ala Ala Arg Leu His Gly Ile Pro His Val Ala Thr Ala His Ser
 100 105 110
 Leu Glu Pro Asp Arg Pro Trp Lys Arg Glu Gln Leu Gly Gly Gly Tyr
 115 120 125
 Asp Val Ser Ser Trp Ser Glu Lys Asn Ala Met Glu Tyr Ala Asp Ala
 130 135 140
 Val Ile Ala Val Ser Ala Arg Met Lys Asp Ser Ile Leu Ala Ala Tyr
 145 150 155 160
 Pro Arg Ile Glu Pro Asp Asn Val Arg Val Val Leu Asn Gly Ile Asp
 165 170 175
 Thr Glu Leu Trp Gln Pro Arg Pro Thr Phe Asp Asp Ala Glu Asp Ser
 180 185 190
 Val Leu Arg Ser Leu Gly Val Asp Pro Gln Arg Pro Ile Val Ala Phe
 195 200 205
 Val Gly Arg Ile Thr Arg Gln Lys Gly Val Glu His Leu Ile Lys Ala
 210 215 220
 Ala Ala Leu Phe Asp Glu Ser Val Gln Leu Val Leu Cys Ala Gly Ala
 225 230 235 240
 Pro Asp Thr Pro Glu Ile Ala Ala Arg Thr Thr Ala Leu Val Glu Glu
 245 250 255
 Leu Gln Ala Lys Arg Glu Gly Ile Phe Trp Val Gln Asp Met Leu Gly
 260 265 270
 Lys Asp Lys Ile Gln Glu Ile Leu Thr Ala Ala Asp Thr Phe Val Cys
 275 280 285
 Pro Ser Ile Tyr Glu Pro Leu Gly Ile Val Asn Leu Glu Ala Met Ala
 290 295 300
 Cys Asn Thr Ala Val Val Ala Ser Asp Val Gly Gly Ile Pro Glu Val
 305 310 315 320
 Val Val Asp Gly Thr Thr Gly Ala Leu Val His Tyr Asp Glu Asn Asp
 325 330 335
 Val Glu Thr Phe Glu Arg Asp Ile Ala Glu Ala Val Asn Lys Met Val
 340 345 350
 Ala Asp Arg Glu Thr Ala Ala Lys Phe Gly Leu Ala Gly Arg Glu Arg
 355 360 365
 Ala Ile Asn Asp Phe Ser Trp Ala Thr Ile Ala Gln Gln Thr Ile Asp
 370 375 380
 Val Tyr Lys Ser Leu Met
 385 390

<210> 45
 <211> 498
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(475)

<223> RXA02222

<400> 45

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aagattgcaa aaaccttgaa aaagtgtatg gcagcgatgg ttg ggt cga cct ccc 115
                               Leu Gly Arg Pro Pro
                               1           5

cca gga gac gtt cat act ctc cta gac gat atc gga gca gag gaa tct 163
Pro Gly Asp Val His Thr Leu Leu Asp Asp Ile Gly Ala Glu Glu Ser
                10                15                20

gaa gca gat aaa gtt cca att gaa tgg caa aac gcc ctg act aag gca 211
Glu Ala Asp Lys Val Pro Ile Glu Trp Gln Asn Ala Leu Thr Lys Ala
                25                30                35

gac agg tat gca aac cgg caa cac atg tct cag gca cga ctc tat cgc 259
Asp Arg Tyr Ala Asn Arg Gln His Met Ser Gln Ala Arg Leu Tyr Arg
                40                45                50

caa tta acc agt gat gtt gga gag ggc ttc act gaa gaa gct gcc caa 307
Gln Leu Thr Ser Asp Val Gly Glu Gly Phe Thr Glu Glu Ala Ala Gln
                55                60                65

tac gca atc gaa aat gtg aac gca gac tgg aac gct aac gcc cta gta 355
Tyr Ala Ile Glu Asn Val Asn Ala Asp Trp Asn Ala Asn Ala Leu Val
                70                75                80                85

aaa gca aga aat tac cag gag cgc caa gca atg tca gta gac cgc att 403
Lys Ala Arg Asn Tyr Gln Glu Arg Gln Ala Met Ser Val Asp Arg Ile
                90                95                100

tac agg caa ott act agt gaa cac ggt gaa ggg ttt acc cca gag cag 451
Tyr Arg Gln Leu Thr Ser Glu His Gly Glu Gly Phe Thr Pro Glu Gln
                105                110                115

gca caa tac gcg atc gac aac cta taaggcataa agatcctagt att 498
Ala Gln Tyr Ala Ile Asp Asn Leu
                120                125
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<210> 46

<211> 125

<212> PRT

<213> Corynebacterium glutamicum

<400> 46

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Leu Gly Arg Pro Pro Pro Gly Asp Val His Thr Leu Leu Asp Asp Ile
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Gly Ala Glu Glu Ser Glu Ala Asp Lys Val Pro Ile Glu Trp Gln Asn
  20           25           30

Ala Leu Thr Lys Ala Asp Arg Tyr Ala Asn Arg Gln His Met Ser Gln
  35           40           45
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Ala Arg Leu Tyr Arg Gln Leu Thr Ser Asp Val Gly Glu Gly Phe Thr
 50 55 60

Glu Glu Ala Ala Gln Tyr Ala Ile Glu Asn Val Asn Ala Asp Trp Asn
 65 70 75 80

Ala Asn Ala Leu Val Lys Ala Arg Asn Tyr Gln Glu Arg Gln Ala Met
 85 90 95

Ser Val Asp Arg Ile Tyr Arg Gln Leu Thr Ser Glu His Gly Glu Gly
 100 105 110

Phe Thr Pro Glu Gln Ala Gln Tyr Ala Ile Asp Asn Leu
 115 120 125

<210> 47
 <211> 1344
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1321)
 <223> RXA02313

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 Met Arg Val Ala Ile
 1 5

gtt gca gag tcg ttc ctt cca aat gtc aac gga gtc acc aac tcg gtg 163
 Val Ala Glu Ser Phe Leu Pro Asn Val Asn Gly Val Thr Asn Ser Val
 10 15 20

ctc cgg gtg ttg gag cat ttg aaa gcc aac gga cac gac gcg ctc gtc 211
 Leu Arg Val Leu Glu His Leu Lys Ala Asn Gly His Asp Ala Leu Val
 25 30 35

atc gcg ccg ggt gcc cgg gat ttt gaa gaa gaa atc ggc cac tac ctg 259
 Ile Ala Pro Gly Ala Arg Asp Phe Glu Glu Glu Ile Gly His Tyr Leu
 40 45 50

ggc ttt gaa att gtg cgc gtc ccc acc gtt cgg gtc cca ctg att gat 307
 Gly Phe Glu Ile Val Arg Val Pro Thr Val Arg Val Pro Leu Ile Asp
 55 60 65

tca ctg ccc atc ggt gtt cct ctg ccc tca gtt acc tct gtg ctg cgc 355
 Ser Leu Pro Ile Gly Val Pro Leu Pro Ser Val Thr Ser Val Leu Arg
 70 75 80 85

gag tac aac cca gac atc att cac ctg gca tcc cca ttt gtg ctc ggt 403
 Glu Tyr Asn Pro Asp Ile Ile His Leu Ala Ser Pro Phe Val Leu Gly
 90 95 100

gga gcg gca gca ttc gca gca agg cag ctg cgc atc cca gca att gct 451
 Gly Ala Ala Ala Phe Ala Ala Arg Gln Leu Arg Ile Pro Ala Ile Ala
 105 110 115

atc tat caa act gat gtc gca ggg ttc tcc cag cgc tac cac ctg gca	499
Ile Tyr Gln Thr Asp Val Ala Gly Phe Ser Gln Arg Tyr His Leu Ala	
120 125 130	
ccg ttg gcc act gca agc tgg gaa tgg atc aag acg gtc cac aac atg	547
Pro Leu Ala Thr Ala Ser Trp Glu Trp Ile Lys Thr Val His Asn Met	
135 140 145	
tgc cag cgc acc ctt gct ccc tca tcc atg agc att gac gag ctg cgt	595
Cys Gln Arg Thr Leu Ala Pro Ser Ser Met Ser Ile Asp Glu Leu Arg	
150 155 160 165	
gac cac gga att aat gat att ttc cac tgg gct cgg ggc gtg gac tcc	643
Asp His Gly Ile Asn Asp Ile Phe His Trp Ala Arg Gly Val Asp Ser	
170 175 180	
aag cgt ttc cac cct gga aag cgt tcc gta gcg cta cgt aag tct tgg	691
Lys Arg Phe His Pro Gly Lys Arg Ser Val Ala Leu Arg Lys Ser Trp	
185 190 195	
gat cca agt gga gca aag aag atc gtt ggt ttc gtt ggg cgc ctt gca	739
Asp Pro Ser Gly Ala Lys Lys Ile Val Gly Phe Val Gly Arg Leu Ala	
200 205 210	
tcc gaa aag ggc gtg gag cgc ctt gct gga tta tcc gga cgc tca gac	787
Ser Glu Lys Gly Val Glu Arg Leu Ala Gly Leu Ser Gly Arg Ser Asp	
215 220 225	
atc caa ttg gtc atc gtc ggt gat ggc cca gag gcc aag tac ctg cag	835
Ile Gln Leu Val Ile Val Gly Asp Gly Pro Glu Ala Lys Tyr Leu Gln	
230 235 240 245	
gaa atg atg ccg gat gcg atc ttc aca gga gct ctc ggc ggc gag gaa	883
Glu Met Met Pro Asp Ala Ile Phe Thr Gly Ala Leu Gly Gly Glu Glu	
250 255 260	
cta gcc acc acc tac gca tca ctc gat ctg ttt gtg cac cca ggt gag	931
Leu Ala Thr Thr Tyr Ala Ser Leu Asp Leu Phe Val His Pro Gly Glu	
265 270 275	
ttt gaa acc ttc tgc cag gcg atc cag gaa gcc caa gca tca ggt gtg	979
Phe Glu Thr Phe Cys Gln Ala Ile Gln Glu Ala Gln Ala Ser Gly Val	
280 285 290	
ccc acc att ggc cca cgc gca ggt ggt ccc att gat ttg atc aac gaa	1027
Pro Thr Ile Gly Pro Arg Ala Gly Gly Pro Ile Asp Leu Ile Asn Glu	
295 300 305	
ggc gtc aac ggc ctg ctt ctt gat gtt gta gat ttc aag gaa acc ctc	1075
Gly Val Asn Gly Leu Leu Leu Asp Val Val Asp Phe Lys Glu Thr Leu	
310 315 320 325	
ccc gct gca gcc gaa tgg att ttg gac gat tcc cgc cac tcc gaa atg	1123
Pro Ala Ala Ala Glu Trp Ile Leu Asp Asp Ser Arg His Ser Glu Met	
330 335 340	
tgc gca gct gct tgg gaa ggt gtg aaa gac aag acc tgg gaa gct ttg	1171
Cys Ala Ala Ala Trp Glu Gly Val Lys Asp Lys Thr Trp Glu Ala Leu	
345 350 355	

tgc acc cag ctt ctc cag cac tac gcg gat gta atc gca ttg tca cag 1219
 Cys Thr Gln Leu Leu Gln His Tyr Ala Asp Val Ile Ala Leu Ser Gln
 360 365 370

cgc atc cca ctg aca ttc ttt ggc cct agc gct gaa gta gca aag ctt 1267
 Arg Ile Pro Leu Thr Phe Phe Gly Pro Ser Ala Glu Val Ala Lys Leu
 375 380 385

cca ctg tgg gtt gct cgc gcg ctg ggt gtt cgc acc cgc atc agc atc 1315
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<210> 48
 <211> 407
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 48
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 20 25 30

His Asp Ala Leu Val Ile Ala Pro Gly Ala Arg Asp Phe Glu Glu Glu
 35 40 45

Ile Gly His Tyr Leu Gly Phe Glu Ile Val Arg Val Pro Thr Val Arg
 50 55 60

Val Pro Leu Ile Asp Ser Leu Pro Ile Gly Val Pro Leu Pro Ser Val
 65 70 75 80

Thr Ser Val Leu Arg Glu Tyr Asn Pro Asp Ile Ile His Leu Ala Ser
 85 90 95

Pro Phe Val Leu Gly Gly Ala Ala Ala Phe Ala Ala Arg Gln Leu Arg
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Ile Pro Ala Ile Ala Ile Tyr Gln Thr Asp Val Ala Gly Phe Ser Gln
 115 120 125

Arg Tyr His Leu Ala Pro Leu Ala Thr Ala Ser Trp Glu Trp Ile Lys
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Thr Val His Asn Met Cys Gln Arg Thr Leu Ala Pro Ser Ser Met Ser
 145 150 155 160

Ile Asp Glu Leu Arg Asp His Gly Ile Asn Asp Ile Phe His Trp Ala
 165 170 175

Arg Gly Val Asp Ser Lys Arg Phe His Pro Gly Lys Arg Ser Val Ala
 180 185 190

Leu Arg Lys Ser Trp Asp Pro Ser Gly Ala Lys Lys Ile Val Gly Phe
 195 200 205

Val Gly Arg Leu Ala Ser Glu Lys Gly Val Glu Arg Leu Ala Gly Leu
210 215 220

Ser Gly Arg Ser Asp Ile Gln Leu Val Ile Val Gly Asp Gly Pro Glu
225 230 235 240

Ala Lys Tyr Leu Gln Glu Met Met Pro Asp Ala Ile Phe Thr Gly Ala
245 250 255

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Val His Pro Gly Glu Phe Glu Thr Phe Cys Gln Ala Ile Gln Glu Ala
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Gln Ala Ser Gly Val Pro Thr Ile Gly Pro Arg Ala Gly Gly Pro Ile
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Phe Lys Glu Thr Leu Pro Ala Ala Ala Glu Trp Ile Leu Asp Asp Ser
325 330 335

Arg His Ser Glu Met Cys Ala Ala Ala Trp Glu Gly Val Lys Asp Lys
340 345 350

Thr Trp Glu Ala Leu Cys Thr Gln Leu Leu Gln His Tyr Ala Asp Val
355 360 365

Ile Ala Leu Ser Gln Arg Ile Pro Leu Thr Phe Phe Gly Pro Ser Ala
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<223> RXA02491

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Gly Gly Met Asn Val Tyr Ile Leu Ser Thr Ala Thr Glu Leu Ala Lys	
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Gln Gly Ile Glu Val Asp Ile Tyr Thr Arg Ala Thr Arg Pro Ser Gln	
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Gly Glu Ile Val Arg Val Ala Glu Asn Leu Arg Val Ile Asn Ile Ala	
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Ala Gly Pro Tyr Glu Gly Leu Ser Lys Glu Glu Leu Pro Thr Gln Leu	
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Ala Ala Phe Thr Gly Gly Met Leu Ser Phe Thr Arg Arg Glu Lys Val	
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Thr Tyr Asp Leu Ile His Ser His Tyr Trp Leu Ser Gly Gln Val Gly	
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Trp Leu Leu Arg Asp Leu Trp Arg Ile Pro Leu Ile His Thr Ala His	
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Thr Leu Ala Ala Val Lys Asn Ser Tyr Arg Asp Asp Ser Asp Thr Pro	
135 140 145	
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Glu Ser Glu Ala Arg Arg Ile Cys Glu Gln Gln Leu Val Asp Asn Ala	
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Asp Val Leu Ala Val Asn Thr Gln Glu Glu Met Gln Asp Leu Met His	
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cac tac gat gcg gat ccg gat cgg att tct gtg gtg tca ccg ggt gcg	691
His Tyr Asp Ala Asp Pro Asp Arg Ile Ser Val Val Ser Pro Gly Ala	
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Asp Val Glu Leu Tyr Ser Pro Gly Asn Asp Arg Ala Thr Glu Arg Ser	
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Arg Arg Glu Leu Gly Ile Pro Leu His Thr Lys Val Val Ala Phe Val	
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Gly Arg Leu Gln Pro Phe Lys Gly Pro Gln Val Leu Ile Lys Ala Val	
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Ala Ala Leu Phe Asp Arg Asp Pro Asp Arg Asn Leu Arg Val Ile Ile	
250 255 260	

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 Cys Gly Gly Pro Ser Gly Pro Asn Ala Thr Pro Asp Thr Tyr Arg His
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atg gca gag gaa ctg ggc gtc gaa aag cga att cgc ttt ttg gac ccg 979
 Met Ala Glu Glu Leu Gly Val Glu Lys Arg Ile Arg Phe Leu Asp Pro
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 Arg Pro Pro Ser Glu Leu Val Ala Val Tyr Arg Ala Ala Asp Ile Val
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gcc gtg cca agt ttt aat gag tcc ttc gga ctc gtc gcc atg gag gcg 1075
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 Ile Ala Val Ala Glu Gly Glu Thr Gly Leu Leu Val Asp Gly His Ser
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 Thr Arg Ile Arg Met Gly Glu Asp Ala Val Glu His Ala Arg Thr Phe
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 390 395 400 405

att gcc aac gaa aat gtc gac ggt gaa acg cat cac gcc taagtaaacg 1364
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<212> PRT

<213> Corynebacterium glutamicum

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35 40 45

Thr Arg Pro Ser Gln Gly Glu Ile Val Arg Val Ala Glu Asn Leu Arg
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Val Ile Asn Ile Ala Ala Gly Pro Tyr Glu Gly Leu Ser Lys Glu Glu
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 Arg Arg Glu Lys Val Thr Tyr Asp Leu Ile His Ser His Tyr Trp Leu
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 Ile His Thr Ala His Thr Leu Ala Ala Val Lys Asn Ser Tyr Arg Asp
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 Asp Ser Asp Thr Pro Glu Ser Glu Ala Arg Arg Ile Cys Glu Gln Gln
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 165 170 175
 Gln Asp Leu Met His His Tyr Asp Ala Asp Pro Asp Arg Ile Ser Val
 180 185 190
 Val Ser Pro Gly Ala Asp Val Glu Leu Tyr Ser Pro Gly Asn Asp Arg
 195 200 205
 Ala Thr Glu Arg Ser Arg Arg Glu Leu Gly Ile Pro Leu His Thr Lys
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 Val Val Ala Phe Val Gly Arg Leu Gln Pro Phe Lys Gly Pro Gln Val
 225 230 235 240
 Leu Ile Lys Ala Val Ala Ala Leu Phe Asp Arg Asp Pro Asp Arg Asn
 245 250 255
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 260 265 270
 Asp Thr Tyr Arg His Met Ala Glu Glu Leu Gly Val Glu Lys Arg Ile
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 325 330 335
 Val Gly Gly Leu Pro Ile Ala Val Ala Glu Gly Glu Thr Gly Leu Leu
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 Val Asp Gly His Ser Pro His Ala Trp Ala Asp Ala Leu Ala Thr Leu
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 Leu Asp Asp Asp Glu Thr Arg Ile Arg Met Gly Glu Asp Ala Val Glu
 370 375 380
 His Ala Arg Thr Phe Ser Trp Ala Ala Thr Ala Ala Gln Leu Ser Ser

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Met Ala Ser Ile Met Ala Cys Leu Lys Ala Ala Arg Leu Asn Asn Pro			
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Met Lys Ile Leu Leu Cys Trp Arg Asp Thr Thr His Pro Gln Gly			
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Gly Gly Ser Glu Arg Tyr Leu Glu Arg Val Gly Glu Phe Leu Ala Asp			
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Phe Ser Val Tyr Pro Lys Ala Trp Val Ala Met Met Leu Gly Arg Val			
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Leu Thr His His Cys His Lys Glu Gln Trp Pro Val Val Gly Arg Val			
135 140 145			

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Tyr Lys Thr Ala Pro Tyr Val Thr Val Ser Glu Pro Ser Ala Glu Glu	
170 175 180	
ctc att gcg ttg ggt gtg gat cag cag cgg att cat atc gtg cgc aat	691
Leu Ile Ala Leu Gly Val Asp Gln Gln Arg Ile His Ile Val Arg Asn	
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ggc gtg gat ccc gtg ccg ctg cac acg ccg aag ctg gat cgc gat ggc	739
Gly Val Asp Pro Val Pro Leu His Thr Pro Lys Leu Asp Arg Asp Gly	
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cag cat gcg gtg acg ttg tgg cgc ctg gtt ccg cac aag cag att gag	787
Gln His Ala Val Thr Leu Ser Arg Leu Val Pro His Lys Gln Ile Glu	
215 220 225	
cat gcg atg gat gtc gtc gcg gcg ctc gac ggc gtg gtg ctg gat gta	835
His Ala Met Asp Val Val Ala Ala Leu Asp Gly Val Val Leu Asp Val	
230 235 240 245	
gtc gaa agc ggt tgg tgg cag aag gaa ctg gtc gat tat gcc cgc acg	883
Val Glu Ser Gly Trp Trp Gln Lys Glu Leu Val Asp Tyr Ala Arg Thr	
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Leu Gly Val Ser Asp Arg Val Val Phe His Gly Gln Val Ala Glu Asp	
265 270 275	
cac aag cac gcc ctg ttg gag cgc gcc acg att cat ctc atg oct tgg	979
His Lys His Ala Leu Leu Glu Arg Ala Thr Ile His Leu Met Pro Ser	
280 285 290	
cgc aag gaa ggc tgg ggc ctg gcg gtc acg gag gcg gcg cag cac ggc	1027
Arg Lys Glu Gly Trp Gly Leu Ala Val Thr Glu Ala Ala Gln His Gly	
295 300 305	
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Val Pro Thr Ile Gly Tyr Arg Ser Ser Gly Gly Leu Arg Asp Ser Val	
310 315 320 325	
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Val Asp Gly Glu Thr Gly Leu Leu Val Asp Ser Lys Ala Glu Leu Ile	
330 335 340	
tca gcc acc aaa acc ctg ctt atc gac gcc tcc ctc cgc tcc aag ctc	1171
Ser Ala Thr Lys Thr Leu Leu Ile Asp Ala Ser Leu Arg Ser Lys Leu	
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Gly Ala Ser Ala Lys Gln Arg Ala Glu Asn Tyr Lys Trp Asp Thr Ala	
360 365 370	
gga gcg cag ttc gag gaa cta ctt ctt ggt ctt gcg tgg aaa aag	1264
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1287

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<400> 52

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Thr	His	Pro	Gln	Gly	Gly	Gly	Ser	Glu	Arg	Tyr	Leu	Glu	Arg	Val	Gly
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Glu	Phe	Leu	Ala	Asp	Gln	Gly	His	Glu	Val	Val	Phe	Arg	Thr	Ala	Gly
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His	Thr	Asp	Ala	Pro	Arg	Arg	Ser	Phe	Arg	Asp	Gly	Val	Arg	Tyr	Ser
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Arg	Ser	Gly	Gly	Lys	Phe	Ser	Val	Tyr	Pro	Lys	Ala	Trp	Val	Ala	Met
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Val	Asp	Thr	Gln	Asn	Gly	Ile	Pro	Phe	Phe	Gly	Lys	Phe	Phe	Ser	Gly
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Lys	Pro	Thr	Val	Leu	Leu	Thr	His	His	Cys	His	Lys	Glu	Gln	Trp	Pro
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Val	Val	Gly	Arg	Val	Leu	Ala	Lys	Val	Gly	Trp	Leu	Ile	Glu	Ser	Gln
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Ile	Ala	Pro	Arg	Ala	Tyr	Lys	Thr	Ala	Pro	Tyr	Val	Thr	Val	Ser	Glu
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Pro	Ser	Ala	Glu	Glu	Leu	Ile	Ala	Leu	Gly	Val	Asp	Gln	Gln	Arg	Ile
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His	Ile	Val	Arg	Asn	Gly	Val	Asp	Pro	Val	Pro	Leu	His	Thr	Pro	Lys
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Leu	Asp	Arg	Asp	Gly	Gln	His	Ala	Val	Thr	Leu	Ser	Arg	Leu	Val	Pro
210						215					220				

His	Lys	Gln	Ile	Glu	His	Ala	Met	Asp	Val	Val	Ala	Ala	Leu	Asp	Gly
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Val	Val	Leu	Asp	Val	Val	Glu	Ser	Gly	Trp	Trp	Gln	Lys	Glu	Leu	Val
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Asp	Tyr	Ala	Arg	Thr	Leu	Gly	Val	Ser	Asp	Arg	Val	Val	Phe	His	Gly
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Gln	Val	Ala	Glu	Asp	His	Lys	His	Ala	Leu	Leu	Glu	Arg	Ala	Thr	Ile
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									Val	Ile	Val	Val	Ala	5				
									1									
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Met	Ala	Ser	Ile	Met	Ala	Cys	Leu	Lys	Ala	Ala	Arg	Leu	Asn	Asn	Pro			
				10					15					20				
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Gly	Gly	Ser	Glu	Arg	Tyr	Leu	Glu	Arg	Val	Gly	Glu	Phe	Leu	Ala	Asp			
			40					45					50					
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Gln	Gly	His	Glu	Val	Val	Phe	Arg	Thr	Ala	Gly	His	Thr	Asp	Ala	Pro			
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cgg	cgt	tct	ttc	cgc	gat	ggg	gtg	agg	tat	tcc	agg	agc	ggg	ggg	aag	355		
Arg	Arg	Ser	Phe	Arg	Asp	Gly	Val	Arg	Tyr	Ser	Arg	Ser	Gly	Gly	Lys			
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Gly Ile Gly Thr Phe Ser Lys Val Asp Val Val Val Asp Thr Gln Asn
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ggc att ccg ttt ttt gga aag ttt ttc tcc ggt aag ccg act gtg ttg 499
Gly Ile Pro Phe Phe Gly Lys Phe Phe Ser Gly Lys Pro Thr Val Leu
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Leu Thr His His Cys His Lys Glu Gln Trp Pro Val Val Gly Arg Val
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Leu Ala Lys Val Gly Trp Leu Ile Glu Ser Gln Ile Ala Pro Arg Ala
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Tyr Lys Thr Ala Pro Tyr Val Thr Val Ser Glu Pro Ser Ala Glu Glu
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Leu Ile Ala Leu Gly Val Asp Gln Gln Arg Ile His Ile Val Arg Asn
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Thr His Pro Gln Gly Gly Gly Ser Glu Arg Tyr Leu Glu Arg Val Gly
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Glu Phe Leu Ala Asp Gln Gly His Glu Val Val Phe Arg Thr Ala Gly
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His Thr Asp Ala Pro Arg Arg Ser Phe Arg Asp Gly Val Arg Tyr Ser
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Arg Ser Gly Gly Lys Phe Ser Val Tyr Pro Lys Ala Trp Val Ala Met
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Val Asp Thr Gln Asn Gly Ile Pro Phe Phe Gly Lys Phe Phe Ser Gly
 115 120 125

Lys Pro Thr Val Leu Leu Thr His His Cys His Lys Glu Gln Trp Pro
 130 135 140

Val Val Gly Arg Val Leu Ala Lys Val Gly Trp Leu Ile Glu Ser Gln
 145 150 155 160

Ile Ala Pro Arg Ala Tyr Lys Thr Ala Pro Tyr Val Thr Val Ser Glu
 165 170 175

Pro Ser Ala Glu Glu Leu Ile Ala Leu Gly Val Asp Gln Gln Arg Ile
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Leu Asp Arg Asp Gly Gln His Ala Val
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 Leu Gln Lys His Thr
 1 5

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 Gly Ser Tyr Thr Ser Gly Phe Gly Ala Arg Trp Gly Thr Asn His Asn
 120 125 130

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 Gly Val Asp Ile Ala Asn Ala Ile Gly Thr Pro Ile Leu Ala Ala Met
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gaa acc gtt gag gtg acc gtt ggt cag act gtt aag gct ggc gag cgc 691
 Glu Thr Val Glu Val Thr Val Gly Gln Thr Val Lys Ala Gly Glu Arg
 185 190 195

atc gca ggc atg ggt agc cga gga ttc tcc acc ggc tcc cac ctc cac 739
 Ile Ala Gly Met Gly Ser Arg Gly Phe Ser Thr Gly Ser His Leu His
 200 205 210

ttc gag gtt tac cct gca ggc ggt ggc gct gtt gat cca gct cct tgg 787
 Phe Glu Val Tyr Pro Ala Gly Gly Gly Ala Val Asp Pro Ala Pro Trp
 215 220 225

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 230 235

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<212> PRT

<213> *Corynebacterium glutamicum*

<400> 56

Leu Gln Lys His Thr Arg Gly Gly Lys His Arg Lys Gln Thr Thr Ser
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Pro Val Thr Lys Gly Gly Val Ala Phe Val Ala Val Ala Thr Gly Ala
 20 25 30

Val Ser Thr Ala Gly Ala Gly Gly Ala Val Ala Ala Gln Ala Ser Asn
 35 40 45

Gln Pro Val Glu Val Asn Phe Glu Leu Thr Ala Asn Asp Thr Thr Asp
 50 55 60

Leu Val Ala Gly Ser Ser Ala Pro Gln Ile Leu Ser Ile Ala Glu Phe

65	70	75	80
Lys Pro Val Val Asn Leu Gly Asp Gln Ile Val Lys Thr Ile Gln Tyr	85	90	95
Asn Ala Asp Arg Ile Gln Ala Asp Leu Asp Ala Arg Gly Pro Ser Val	100	105	110
Val Arg Pro Ala Glu Gly Ser Tyr Thr Ser Gly Phe Gly Ala Arg Trp	115	120	125
Gly Thr Asn His Asn Gly Val Asp Ile Ala Asn Ala Ile Gly Thr Pro	130	135	140
Ile Leu Ala Ala Met Asp Gly Thr Val Ile Asp Ala Gly Pro Ala Ser	145	150	155
Gly Phe Gly Asn Trp Val Arg Leu Gln His Glu Asp Gly Thr Ile Thr	165	170	175
Val Tyr Gly His Met Glu Thr Val Glu Val Thr Val Gly Gln Thr Val	180	185	190
Lys Ala Gly Glu Arg Ile Ala Gly Met Gly Ser Arg Gly Phe Ser Thr	195	200	205
Gly Ser His Leu His Phe Glu Val Tyr Pro Ala Gly Gly Gly Ala Val	210	215	220
Asp Pro Ala Pro Trp Leu Ala Glu Arg Gly Ile Thr Leu	225	230	235

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Gly Asp Ala Glu Ala Ala Leu Glu Phe Gly Val Gln Pro Val Gly Ala	
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tca gat tgg ctc gca ttc ggt ggt gaa ggc gtg gga ccg tgg att gag	144
Ser Asp Trp Leu Ala Phe Gly Gly Glu Gly Val Gly Pro Trp Ile Glu	
35 40 45	
gat tct gcc tac gat gaa gcg cca gaa ata atc gga acc atg gaa ccg	192
Asp Ser Ala Tyr Asp Glu Ala Pro Glu Ile Ile Gly Thr Met Glu Pro	
50 55 60	
gag tat gaa aag att gca gcg ctt gaa ccg gat ctg att ttg gac gtg	240

Glu	Tyr	Glu	Lys	Ile	Ala	Ala	Leu	Glu	Pro	Asp	Leu	Ile	Leu	Asp	Val	
65					70					75					80	
cgc	agc	tct	ggc	gac	cag	gaa	cgc	tat	gac	aag	ttg	tct	tca	atc	gca	288
Arg	Ser	Ser	Gly	Asp	Gln	Glu	Arg	Tyr	Asp	Lys	Leu	Ser	Ser	Ile	Ala	
			85						90					95		
ctg	acc	atc	ggc	gtt	cca	gaa	ggt	ggc	gat	agc	tac	ctc	acc	cca	cgc	336
Leu	Thr	Ile	Gly	Val	Pro	Glu	Gly	Gly	Asp	Ser	Tyr	Leu	Thr	Pro	Arg	
			100					105					110			
gct	gag	cag	gta	acc	atg	atc	gcc	act	gct	ctg	ggg	cag	gct	gaa	cgt	384
Ala	Glu	Gln	Val	Thr	Met	Ile	Ala	Thr	Ala	Leu	Gly	Gln	Ala	Glu	Arg	
		115					120					125				
ggt	gaa	gaa	gtg	aac	gct	gaa	tac	gag	cag	ctc	act	gct	gat	att	cgt	432
Gly	Glu	Glu	Val	Asn	Ala	Glu	Tyr	Glu	Gln	Leu	Thr	Ala	Asp	Ile	Arg	
	130					135					140					
gca	gct	cac	ccg	ggc	tgg	cct	gag	aag	acc	gcg	gct	gct	gta	tct	gca	480
Ala	Ala	His	Pro	Gly	Trp	Pro	Glu	Lys	Thr	Ala	Ala	Ala	Val	Ser	Ala	
145					150				155						160	
acg	gca	acc	agc	tgg	ggt	gca	tac	atc	aag	ggc	tcc	aac	cgt	gta	gat	528
Thr	Ala	Thr	Ser	Trp	Gly	Ala	Tyr	Ile	Lys	Gly	Ser	Asn	Arg	Val	Asp	
			165						170					175		
act	ttg	ctg	gac	ctg	ggc	ttc	cag	gaa	aac	cct	gag	ctg	gct	aaa	cag	576
Thr	Leu	Leu	Asp	Leu	Gly	Phe	Gln	Glu	Asn	Pro	Glu	Leu	Ala	Lys	Gln	
			180					185					190			
caa	cct	ggc	gat	acg	ggt	ttc	tcc	atc	aaa	ttc	agt	gaa	gag	act	ttc	624
Gln	Pro	Gly	Asp	Thr	Gly	Phe	Ser	Ile	Lys	Phe	Ser	Glu	Glu	Thr	Phe	
		195					200					205				
ggc	gtt	gtg	gat	tcc	gac	ctg	gtt	gtc	ggc	ttt	gcc	atc	ggt	atg	act	672
Gly	Val	Val	Asp	Ser	Asp	Leu	Val	Val	Gly	Phe	Ala	Ile	Gly	Met	Thr	
	210					215					220					
cct	gag	gaa	atg	gca	gag	cag	gtt	cca	tgg	cag	atg	ttg	acc	gcc	act	720
Pro	Glu	Glu	Met	Ala	Glu	Gln	Val	Pro	Trp	Gln	Met	Leu	Thr	Ala	Thr	
225					230					235					240	
cgt	gac	ggc	cgt	tcc	ttt	gtg	atg	ccc	cgt	gag	att	tcc	aat	gcg	ttt	768
Arg	Asp	Gly	Arg	Ser	Phe	Val	Met	Pro	Arg	Glu	Ile	Ser	Asn	Ala	Phe	
			245					250						255		
tct	ttg	ggt	tcc	ccg	cag	tcc	act	cgg	ttc	gcg	tta	gac	gcc	ttg	gtg	816
Ser	Leu	Gly	Ser	Pro	Gln	Ser	Thr	Arg	Phe	Ala	Leu	Asp	Ala	Leu	Val	
			260					265				270				
cca	ott	ctg	gag	gag	cat	gca	ggg	gag	tagtggtccg	gtggtgcggg	cag					866
Pro	Leu	Leu	Glu	Glu	His	Ala	Gly	Glu								
		275					280									

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<211> 281

<212> PRT

<213> Corynebacterium glutamicum

<400> 58

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 20 25 30

Ser Asp Trp Leu Ala Phe Gly Gly Glu Gly Val Gly Pro Trp Ile Glu
 35 40 45

Asp Ser Ala Tyr Asp Glu Ala Pro Glu Ile Ile Gly Thr Met Glu Pro
 50 55 60

Glu Tyr Glu Lys Ile Ala Ala Leu Glu Pro Asp Leu Ile Leu Asp Val
 65 70 75 80

Arg Ser Ser Gly Asp Gln Glu Arg Tyr Asp Lys Leu Ser Ser Ile Ala
 85 90 95

Leu Thr Ile Gly Val Pro Glu Gly Gly Asp Ser Tyr Leu Thr Pro Arg
 100 105 110

Ala Glu Gln Val Thr Met Ile Ala Thr Ala Leu Gly Gln Ala Glu Arg
 115 120 125

Gly Glu Glu Val Asn Ala Glu Tyr Glu Gln Leu Thr Ala Asp Ile Arg
 130 135 140

Ala Ala His Pro Gly Trp Pro Glu Lys Thr Ala Ala Ala Val Ser Ala
 145 150 155 160

Thr Ala Thr Ser Trp Gly Ala Tyr Ile Lys Gly Ser Asn Arg Val Asp
 165 170 175

Thr Leu Leu Asp Leu Gly Phe Gln Glu Asn Pro Glu Leu Ala Lys Gln
 180 185 190

Gln Pro Gly Asp Thr Gly Phe Ser Ile Lys Phe Ser Glu Glu Thr Phe
 195 200 205

Gly Val Val Asp Ser Asp Leu Val Val Gly Phe Ala Ile Gly Met Thr
 210 215 220

Pro Glu Glu Met Ala Glu Gln Val Pro Trp Gln Met Leu Thr Ala Thr
 225 230 235 240

Arg Asp Gly Arg Ser Phe Val Met Pro Arg Glu Ile Ser Asn Ala Phe
 245 250 255

Ser Leu Gly Ser Pro Gln Ser Thr Arg Phe Ala Leu Asp Ala Leu Val
 260 265 270

Pro Leu Leu Glu Glu His Ala Gly Glu
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<210> 59

<211> 702

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(679)

<223> RXA02650

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                                   Met Val Asn Val Thr
                                   1 5

tca aag gat gca ggg gca aac gtg acc ccc atg agt aag aaa gaa aag 163
Ser Lys Asp Ala Gly Ala Asn Val Thr Pro Met Ser Lys Lys Glu Lys
              10 15 20

agg aca acc gtt aaa cag gtg gtt gcc ttg atg gcc gcc atc gtt gtg 211
Arg Thr Thr Val Lys Gln Val Val Ala Leu Met Ala Ala Ile Val Val
              25 30 35

gtg att gcg tcc cta gac caa ata gtc aag cag att atg ctt agt tgg 259
Val Ile Ala Ser Leu Asp Gln Ile Val Lys Gln Ile Met Leu Ser Trp
              40 45 50

ttg gaa cct ggc gtt ccc gtt ccc atc att ggg gat tgg ttc cgc ttc 307
Leu Glu Pro Gly Val Pro Val Pro Ile Ile Gly Asp Trp Phe Arg Phe
              55 60 65

tac ctc ctg ttt aac ccc gga gcc gca ttt tcg atg ggt ggg gaa aac 355
Tyr Leu Leu Phe Asn Pro Gly Ala Ala Phe Ser Met Gly Gly Glu Asn
              70 75 80 85

agc acc tgg atc ttt aca acc atc cag ttg agc ttc gtc atc ggt atc 403
Ser Thr Trp Ile Phe Thr Thr Ile Gln Leu Ser Phe Val Ile Gly Ile
              90 95 100

gca att tat gcc cca cgc atc aaa cac aag tgg atc gcg gca gga ctt 451
Ala Ile Tyr Ala Pro Arg Ile Lys His Lys Trp Ile Ala Ala Gly Leu
              105 110 115

gcc ctt gtt gcc ggt gga gcc ttg gga aac gtg ttg gac cgg ttg ttc 499
Ala Leu Val Ala Gly Gly Ala Leu Gly Asn Val Leu Asp Arg Leu Phe
              120 125 130

aga gat cct tcc ttc ttc ttc gga cat gtt gtt gat tac atc tcc gta 547
Arg Asp Pro Ser Phe Phe Phe Gly His Val Val Asp Tyr Ile Ser Val
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gga aac ttt gca gta ttt aat atc gcc gat gcc tcg att tct tgc ggc 595
Gly Asn Phe Ala Val Phe Asn Ile Ala Asp Ala Ser Ile Ser Cys Gly
              150 155 160 165

gtc gtg gtg ttc ctg atc gga atg ttc ctt gag gac cgt gaa aac gcc 643
Val Val Val Phe Leu Ile Gly Met Phe Leu Glu Asp Arg Glu Asn Ala
              170 175 180

cag cat gcc aaa gca act gac gag aag gat gag gcc tgatgaacaa 689
Gln His Ala Lys Ala Thr Asp Glu Lys Asp Glu Ala
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ccgacaaagc aga 702

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 <213> Corynebacterium glutamicum

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 Ala Ala Ile Val Val Val Ile Ala Ser Leu Asp Gln Ile Val Lys Gln
 35 40 45
 Ile Met Leu Ser Trp Leu Glu Pro Gly Val Pro Val Pro Ile Ile Gly
 50 55 60
 Asp Trp Phe Arg Phe Tyr Leu Leu Phe Asn Pro Gly Ala Ala Phe Ser
 65 70 75 80
 Met Gly Gly Glu Asn Ser Thr Trp Ile Phe Thr Thr Ile Gln Leu Ser
 85 90 95
 Phe Val Ile Gly Ile Ala Ile Tyr Ala Pro Arg Ile Lys His Lys Trp
 100 105 110
 Ile Ala Ala Gly Leu Ala Leu Val Ala Gly Gly Ala Leu Gly Asn Val
 115 120 125
 Leu Asp Arg Leu Phe Arg Asp Pro Ser Phe Phe Phe Gly His Val Val
 130 135 140
 Asp Tyr Ile Ser Val Gly Asn Phe Ala Val Phe Asn Ile Ala Asp Ala
 145 150 155 160
 Ser Ile Ser Cys Gly Val Val Val Phe Leu Ile Gly Met Phe Leu Glu
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 Asp Arg Glu Asn Ala Gln His Ala Lys Ala Thr Asp Glu Lys Asp Glu
 180 185 190

Ala

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <223> RXA01094

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	Met Thr Leu Ala Thr	
	1 5	
att ccc tca cca ccg cag ggt gtg tgg tac ttg ggt ccc att ccg att		163
Ile Pro Ser Pro Pro Gln Gly Val Trp Tyr Leu Gly Pro Ile Pro Ile		
	10 15 20	
agg gcc tat gcg atg tgc atc atc gct ggc att att gtt gcc att tgg		211
Arg Ala Tyr Ala Met Cys Ile Ile Ala Gly Ile Ile Val Ala Ile Trp		
	25 30 35	
ctg acg aga aag cgc tac gcc gcc cgc ggt gga aac cct gaa atc gtc		259
Leu Thr Arg Lys Arg Tyr Ala Ala Arg Gly Gly Asn Pro Glu Ile Val		
	40 45 50	
ctt gat gca gcg atc gtg gca gtt cct gcc gga atc atc ggt gga cgc		307
Leu Asp Ala Ala Ile Val Ala Val Pro Ala Gly Ile Ile Gly Gly Arg		
	55 60 65	
att tat cac gtc att acc gac aac caa aag tac ttc tgc gat acc tgt		355
Ile Tyr His Val Ile Thr Asp Asn Gln Lys Tyr Phe Cys Asp Thr Cys		
	70 75 80 85	
aac ccc gtc gac gcc ttc aaa atc acc aac ggt ggt ctg ggc atc tgg		403
Asn Pro Val Asp Ala Phe Lys Ile Thr Asn Gly Gly Leu Gly Ile Trp		
	90 95 100	
ggt gca gtg atc ctc ggt ggc ctg gca gtg gcc gta ttc ttc cgg tac		451
Gly Ala Val Ile Leu Gly Gly Leu Ala Val Ala Val Phe Phe Arg Tyr		
	105 110 115	
aaa aag ctt cct ctt gca cct ttc gca gat gcc gtg gca cct gca gtt		499
Lys Lys Leu Pro Leu Ala Pro Phe Ala Asp Ala Val Ala Pro Ala Val		
	120 125 130	
atc ctg gcg cag gga att ggt cgt ctg ggc aac tgg ttt aac cag gag		547
Ile Leu Ala Gln Gly Ile Gly Arg Leu Gly Asn Trp Phe Asn Gln Glu		
	135 140 145	
ctc tac ggt gca gaa act acc gtt cca tgg gct ttg gaa atc tac tat		595
Leu Tyr Gly Ala Glu Thr Thr Val Pro Trp Ala Leu Glu Ile Tyr Tyr		
	150 155 160 165	
cgg gta gat gaa aat gga aaa ttc gca ccg gtg aca gga aca tcc acc		643
Arg Val Asp Glu Asn Gly Lys Phe Ala Pro Val Thr Gly Thr Ser Thr		
	170 175 180	
ggt gaa gta atg gct act gtt cat cca aca ttc ctc tat gaa ctg ttg		691
Gly Glu Val Met Ala Thr Val His Pro Thr Phe Leu Tyr Glu Leu Leu		
	185 190 195	
tgg aac cta ctg atc ttc gct ttg ttg atg tgg gct gac aag cga ttc		739
Trp Asn Leu Leu Ile Phe Ala Leu Leu Met Trp Ala Asp Lys Arg Phe		
	200 205 210	
aag ctg gaa cat ggc cga gta ttt gct ctc tac gta gct ggt tac acc		787
Lys Leu Glu His Gly Arg Val Phe Ala Leu Tyr Val Ala Gly Tyr Thr		
	215 220 225	
ttg ggc cgt ttc tgg att gaa caa atg cgc gtt gat gaa gcc acg ctt		835

Leu Gly Arg Phe Trp Ile Glu Gln Met Arg Val Asp Glu Ala Thr Leu
 230 235 240 245
 att ggc ggc atc cga atc aac acc atc gtc tcc gca gta gtg ttt gcc 883
 Ile Gly Gly Ile Arg Ile Asn Thr Ile Val Ser Ala Val Val Phe Ala
 250 255 260
 ggc gcg atc atc gtg ttc ttc ctg ttg aag aag ggt agg gaa act ccc 931
 Gly Ala Ile Ile Val Phe Phe Leu Leu Lys Lys Gly Arg Glu Thr Pro
 265 270 275
 gaa gag gta gat ccg act ttc gca gcg tct gtt gca gca gat gct gta 979
 Glu Glu Val Asp Pro Thr Phe Ala Ala Ser Val Ala Ala Asp Ala Val
 280 285 290
 gct tcg cca gat aga aaa ccc ttg ccg aaa gca ggg gag ggc att gat 1027
 Ala Ser Pro Asp Arg Lys Pro Leu Pro Lys Ala Gly Glu Gly Ile Asp
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 gga gaa acg ccc tca acg cga taggtttcaa ccataggaact gac 1071
 Gly Glu Thr Pro Ser Thr Arg
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 <213> Corynebacterium glutamicum

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 35 40 45
 Asn Pro Glu Ile Val Leu Asp Ala Ala Ile Val Ala Val Pro Ala Gly
 50 55 60
 Ile Ile Gly Gly Arg Ile Tyr His Val Ile Thr Asp Asn Gln Lys Tyr
 65 70 75 80
 Phe Cys Asp Thr Cys Asn Pro Val Asp Ala Phe Lys Ile Thr Asn Gly
 85 90 95
 Gly Leu Gly Ile Trp Gly Ala Val Ile Leu Gly Gly Leu Ala Val Ala
 100 105 110
 Val Phe Phe Arg Tyr Lys Lys Leu Pro Leu Ala Pro Phe Ala Asp Ala
 115 120 125
 Val Ala Pro Ala Val Ile Leu Ala Gln Gly Ile Gly Arg Leu Gly Asn
 130 135 140
 Trp Phe Asn Gln Glu Leu Tyr Gly Ala Glu Thr Thr Val Pro Trp Ala
 145 150 155 160
 Leu Glu Ile Tyr Tyr Arg Val Asp Glu Asn Gly Lys Phe Ala Pro Val

165										170					175				
Thr	Gly	Thr	Ser	Thr	Gly	Glu	Val	Met	Ala	Thr	Val	His	Pro	Thr	Phe				
			180					185					190						
Leu	Tyr	Glu	Leu	Leu	Trp	Asn	Leu	Leu	Ile	Phe	Ala	Leu	Leu	Met	Trp				
		195					200					205							
Ala	Asp	Lys	Arg	Phe	Lys	Leu	Glu	His	Gly	Arg	Val	Phe	Ala	Leu	Tyr				
	210					215					220								
Val	Ala	Gly	Tyr	Thr	Leu	Gly	Arg	Phe	Trp	Ile	Glu	Gln	Met	Arg	Val				
225					230					235					240				
Asp	Glu	Ala	Thr	Leu	Ile	Gly	Gly	Ile	Arg	Ile	Asn	Thr	Ile	Val	Ser				
				245					250					255					
Ala	Val	Val	Phe	Ala	Gly	Ala	Ile	Ile	Val	Phe	Phe	Leu	Leu	Lys	Lys				
			260					265					270						
Gly	Arg	Glu	Thr	Pro	Glu	Glu	Val	Asp	Pro	Thr	Phe	Ala	Ala	Ser	Val				
		275					280					285							
Ala	Ala	Asp	Ala	Val	Ala	Ser	Pro	Asp	Arg	Lys	Pro	Leu	Pro	Lys	Ala				
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<211> 1206

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1183)

<223> RXN00934

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				Val	Arg	Ile	Gly	Met	

1

5

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Val	Cys	Pro	Tyr	Ser	Phe	Asp	Glu	Pro	Gly	Gly	Val	Gln	Ala	His	Ile	
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ctt	gac	tta	gcg	cga	acc	ttc	att	gcc	caa	ggc	cat	gag	gtt	cag	gtg	211
Leu	Asp	Leu	Ala	Arg	Thr	Phe	Ile	Ala	Gln	Gly	His	Glu	Val	Gln	Val	
			25					30						35		

ctt	ggt	ccg	tgt	agt	gcg	gat	acg	cag	gtg	ccc	gat	ttc	gtg	gtg	cgc	259
Leu	Gly	Pro	Cys	Ser	Ala	Asp	Thr	Gln	Val	Pro	Asp	Phe	Val	Val	Arg	
		40					45					50				

ggt	ggt	ggc	agc	atc	ccg	att	ccg	tac	aat	ggc	tcg	gtt	gcc	cgc	ttg	307
Gly	Gly	Gly	Ser	Ile	Pro	Ile	Pro	Tyr	Asn	Gly	Ser	Val	Ala	Arg	Leu	

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Ser Phe Gly Pro Lys Met Phe Lys Ala Val Arg Thr Phe Leu Arg Glu			
70	75	80	85
ggc aac ttc gat gtg ctg cat atc cat gaa ccg aat tca cca agt ttt			403
Gly Asn Phe Asp Val Leu His Ile His Glu Pro Asn Ser Pro Ser Phe			
	90	95	100
tcc atg gcg gcg cta cgc ttt gcg gaa ggc ccc atc gtt gct act tac			451
Ser Met Ala Ala Leu Arg Phe Ala Glu Gly Pro Ile Val Ala Thr Tyr			
	105	110	115
cac gcc tcc agt agc gga tcg aag ctg ctc aag gct ttc tta cca gtg			499
His Ala Ser Ser Ser Gly Ser Lys Leu Leu Lys Ala Phe Leu Pro Val			
	120	125	130
ctt tcg ccc atg ctg gag aaa gtg cgc gca ggc atc gcc gtg tct gaa			547
Leu Ser Pro Met Leu Glu Lys Val Arg Ala Gly Ile Ala Val Ser Glu			
	135	140	145
atg gct cgg cgc tgg cag gtg gag caa gtc ggc ggc gat ccc gtg ctg			595
Met Ala Arg Arg Trp Gln Val Glu Gln Val Gly Gly Asp Pro Val Leu			
	150	155	160
atc ccc aac ggg gta gag acc tcc atg ttc aaa gcc gcg cgc caa atc			643
Ile Pro Asn Gly Val Glu Thr Ser Met Phe Lys Ala Ala Arg Gln Ile			
	170	175	180
gaa ccg aat gat cct gta gag atc gtc ttt ttg ggt cgc ctc gat gag			691
Glu Pro Asn Asp Pro Val Glu Ile Val Phe Leu Gly Arg Leu Asp Glu			
	185	190	195
tcc cgc aaa ggc ctc gac atc ctc ctg cgc gct ctg acc agg ctg gat			739
Ser Arg Lys Gly Leu Asp Ile Leu Leu Arg Ala Leu Thr Arg Leu Asp			
	200	205	210
cgc ccg ttt acc tgc acc gtc att ggc ggc ggc acc ccg cga gaa gtc			787
Arg Pro Phe Thr Cys Thr Val Ile Gly Gly Gly Thr Pro Arg Glu Val			
	215	220	225
gcc ggc atc aac ttt gtg ggc cgc gtc agc gat gag gaa aag gca gca			835
Ala Gly Ile Asn Phe Val Gly Arg Val Ser Asp Glu Glu Lys Ala Ala			
	230	235	240
atc tta ggt cgc gca gac atc tat gtc gca ccc aac acc ggc ggc gaa			883
Ile Leu Gly Arg Ala Asp Ile Tyr Val Ala Pro Asn Thr Gly Gly Glu			
	250	255	260
agc ttc ggc atc gtg cta gtt gaa gcg atg gcc gcg gga tgc gct gtc			931
Ser Phe Gly Ile Val Leu Val Glu Ala Met Ala Ala Gly Cys Ala Val			
	265	270	275
gtc gcc agc gac cta gaa gcg ttc tcc ctg gtc acc gat tct gaa gcc			979
Val Ala Ser Asp Leu Glu Ala Phe Ser Leu Val Thr Asp Ser Glu Ala			
	280	285	290
gca cag cca gcg ggc gtg cta ttt aaa acc ggc tca gac gcc gac cta			1027
Ala Gln Pro Ala Gly Val Leu Phe Lys Thr Gly Ser Asp Ala Asp Leu			
	295	300	305

gcc aaa aaa ctt caa gcg ctt atc gac gac ccc tcc tcc cgt tcc acg 1075
 Ala Lys Lys Leu Gln Ala Leu Ile Asp Asp Pro Ser Ser Arg Ser Thr
 310 315 320 325

ctt atc gcc gcg ggg cta aag cgc gca aac gcc tac gac tgg tgg aca 1123
 Leu Ile Ala Ala Gly Leu Lys Arg Ala Asn Ala Tyr Asp Trp Ser Thr
 330 335 340

gta tcc acc cag gtc atg gca gtc tat gaa acc att gcg atc gac aaa 1171
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 345 350 355

gtg agg ctt gga tgacccttgt ttacctcctc atc 1206
 Val Arg Leu Gly
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<210> 64
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 64
 Val Arg Ile Gly Met Val Cys Pro Tyr Ser Phe Asp Glu Pro Gly Gly
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Val Gln Ala His Ile Leu Asp Leu Ala Arg Thr Phe Ile Ala Gln Gly
 20 25 30

His Glu Val Gln Val Leu Gly Pro Cys Ser Ala Asp Thr Gln Val Pro
 35 40 45

Asp Phe Val Val Arg Gly Gly Gly Ser Ile Pro Ile Pro Tyr Asn Gly
 50 55 60

Ser Val Ala Arg Leu Ser Phe Gly Pro Lys Met Phe Lys Ala Val Arg
 65 70 75 80

Thr Phe Leu Arg Glu Gly Asn Phe Asp Val Leu His Ile His Glu Pro
 85 90 95

Asn Ser Pro Ser Phe Ser Met Ala Ala Leu Arg Phe Ala Glu Gly Pro
 100 105 110

Ile Val Ala Thr Tyr His Ala Ser Ser Ser Gly Ser Lys Leu Leu Lys
 115 120 125

Ala Phe Leu Pro Val Leu Ser Pro Met Leu Glu Lys Val Arg Ala Gly
 130 135 140

Ile Ala Val Ser Glu Met Ala Arg Arg Trp Gln Val Glu Gln Val Gly
 145 150 155 160

Gly Asp Pro Val Leu Ile Pro Asn Gly Val Glu Thr Ser Met Phe Lys
 165 170 175

Ala Ala Arg Gln Ile Glu Pro Asn Asp Pro Val Glu Ile Val Phe Leu
 180 185 190

Gly Arg Leu Asp Glu Ser Arg Lys Gly Leu Asp Ile Leu Leu Arg Ala

195	200	205
Leu Thr Arg Leu Asp Arg Pro Phe Thr Cys Thr Val Ile Gly Gly Gly 210 215 220		
Thr Pro Arg Glu Val Ala Gly Ile Asn Phe Val Gly Arg Val Ser Asp 225 230 235 240		
Glu Glu Lys Ala Ala Ile Leu Gly Arg Ala Asp Ile Tyr Val Ala Pro 245 250 255		
Asn Thr Gly Gly Glu Ser Phe Gly Ile Val Leu Val Glu Ala Met Ala 260 265 270		
Ala Gly Cys Ala Val Val Ala Ser Asp Leu Glu Ala Phe Ser Leu Val 275 280 285		
Thr Asp Ser Glu Ala Ala Gln Pro Ala Gly Val Leu Phe Lys Thr Gly 290 295 300		
Ser Asp Ala Asp Leu Ala Lys Lys Leu Gln Ala Leu Ile Asp Asp Pro 305 310 315 320		
Ser Ser Arg Ser Thr Leu Ile Ala Ala Gly Leu Lys Arg Ala Asn Ala 325 330 335		
Tyr Asp Trp Ser Thr Val Ser Thr Gln Val Met Ala Val Tyr Glu Thr 340 345 350		
Ile Ala Ile Asp Lys Val Arg Leu Gly 355 360		

<210> 65
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(789)
 <223> FRXA00934

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gct act tac cac gcc tcc agt agc gga tcg aag ctg ctc aag gct ttc Ala Thr Tyr His Ala Ser Ser Ser Gly Ser Lys Leu Leu Lys Ala Phe 20 25 30	96
tta cca gtg ctt tcg ccc atg ctg gag aaa gtg cgc gca ggc atc gcc Leu Pro Val Leu Ser Pro Met Leu Glu Lys Val Arg Ala Gly Ile Ala 35 40 45	144
gtg tct gaa atg gct cgg cgc tgg cag gtg gag caa gtc ggc ggc gat Val Ser Glu Met Ala Arg Arg Trp Gln Val Glu Gln Val Gly Gly Asp 50 55 60	192
ccc gtg ctg atc ccc aac ggg gta gag acc tcc atg ttc aaa gcc gcg	240

Pro Val Leu Ile Pro Asn Gly Val Glu Thr Ser Met Phe Lys Ala Ala
 65 70 75 80
 cgc caa atc gaa ccg aat gat cct gta gag atc gtc ttt ttg ggt cgc 288
 Arg Gln Ile Glu Pro Asn Asp Pro Val Glu Ile Val Phe Leu Gly Arg
 85 90 95
 ctc gat gag tcc cgc aaa ggc ctc gac atc ctc ctg cgc gct ctg acc 336
 Leu Asp Glu Ser Arg Lys Gly Leu Asp Ile Leu Leu Arg Ala Leu Thr
 100 105 110
 agg ctg gat cgc ccg ttt acc tgc acc gtc att ggc ggc ggc acc ccg 384
 Arg Leu Asp Arg Pro Phe Thr Cys Thr Val Ile Gly Gly Gly Thr Pro
 115 120 125
 cga gaa gtc gcc ggc atc aac ttt gtg ggc cgc gtc agc gat gag gaa 432
 Arg Glu Val Ala Gly Ile Asn Phe Val Gly Arg Val Ser Asp Glu Glu
 130 135 140
 aag gca gca atc tta ggt cgc gca gac atc tat gtc gca ccc aac acc 480
 Lys Ala Ala Ile Leu Gly Arg Ala Asp Ile Tyr Val Ala Pro Asn Thr
 145 150 155 160
 ggc ggc gaa agc ttc ggc atc gtg cta gtt gaa gcg atg gcc gcg gga 528
 Gly Gly Glu Ser Phe Gly Ile Val Leu Val Glu Ala Met Ala Ala Gly
 165 170 175
 tgc gct gtc gtc gcc agc gac cta gaa gcg ttc tcc ctg gtc acc gat 576
 Cys Ala Val Val Ala Ser Asp Leu Glu Ala Phe Ser Leu Val Thr Asp
 180 185 190
 tct gaa gcc gca cag cca gcg ggc gtg cta ttt aaa acc ggc tca gac 624
 Ser Glu Ala Ala Gln Pro Ala Gly Val Leu Phe Lys Thr Gly Ser Asp
 195 200 205
 gcc gac cta gcc aaa aaa ctt caa gcg ctt atc gac gac ccc tcc tcc 672
 Ala Asp Leu Ala Lys Lys Leu Gln Ala Leu Ile Asp Asp Pro Ser Ser
 210 215 220
 cgt tcc acg ctt atc gcc gcg ggg cta aag cgc gca aac gcc tac gac 720
 Arg Ser Thr Leu Ile Ala Ala Gly Leu Lys Arg Ala Asn Ala Tyr Asp
 225 230 235 240
 tgg tcg aca gta tcc acc cag gtc atg gca gtc tat gaa acc att gcg 768
 Trp Ser Thr Val Ser Thr Gln Val Met Ala Val Tyr Glu Thr Ile Ala
 245 250 255
 atc gac aaa gtg agg ctt gga tgacccttgt ttacctcctc atc 812
 Ile Asp Lys Val Arg Leu Gly
 260

<210> 66

<211> 263

<212> PRT

<213> Corynebacterium glutamicum

<400> 66

Pro Ser Phe Ser Met Ala Ala Leu Pro Phe Ala Glu Gly Pro Ile Val
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Ala Thr Tyr His Ala Ser Ser Ser Gly Ser Lys Leu Leu Lys Ala Phe
 20 25 30
 Leu Pro Val Leu Ser Pro Met Leu Glu Lys Val Arg Ala Gly Ile Ala
 35 40 45
 Val Ser Glu Met Ala Arg Arg Trp Gln Val Glu Gln Val Gly Gly Asp
 50 55 60
 Pro Val Leu Ile Pro Asn Gly Val Glu Thr Ser Met Phe Lys Ala Ala
 65 70 75 80
 Arg Gln Ile Glu Pro Asn Asp Pro Val Glu Ile Val Phe Leu Gly Arg
 85 90 95
 Leu Asp Glu Ser Arg Lys Gly Leu Asp Ile Leu Leu Arg Ala Leu Thr
 100 105 110
 Arg Leu Asp Arg Pro Phe Thr Cys Thr Val Ile Gly Gly Gly Thr Pro
 115 120 125
 Arg Glu Val Ala Gly Ile Asn Phe Val Gly Arg Val Ser Asp Glu Glu
 130 135 140
 Lys Ala Ala Ile Leu Gly Arg Ala Asp Ile Tyr Val Ala Pro Asn Thr
 145 150 155 160
 Gly Gly Glu Ser Phe Gly Ile Val Leu Val Glu Ala Met Ala Ala Gly
 165 170 175
 Cys Ala Val Val Ala Ser Asp Leu Glu Ala Phe Ser Leu Val Thr Asp
 180 185 190
 Ser Glu Ala Ala Gln Pro Ala Gly Val Leu Phe Lys Thr Gly Ser Asp
 195 200 205
 Ala Asp Leu Ala Lys Lys Leu Gln Ala Leu Ile Asp Asp Pro Ser Ser
 210 215 220
 Arg Ser Thr Leu Ile Ala Ala Gly Leu Lys Arg Ala Asn Ala Tyr Asp
 225 230 235 240
 Trp Ser Thr Val Ser Thr Gln Val Met Ala Val Tyr Glu Thr Ile Ala
 245 250 255
 Ile Asp Lys Val Arg Leu Gly
 260

<210> 67

<211> 618

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(595)

<223> RXA02605

<400> 67

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gagcagaact tcggcggttg gcgaaacaac aactccattg gtg gcc tgt cca tgg 115
Val Ala Cys Pro Trp
1 5

gcg gga act gcc gcg ctg aac ctc gca gca aag cac cca gat cag ttc 163
Ala Gly Thr Ala Ala Leu Asn Leu Ala Ala Lys His Pro Asp Gln Phe
10 15 20

cgc cag gct atg tct tgg tcc ggc tac ttg aac acc act gcg cca ggc 211
Arg Gln Ala Met Ser Trp Ser Gly Tyr Leu Asn Thr Thr Ala Pro Gly
25 30 35

atg caa acc ctg ctg cgt gtg gcc atg ctg gac acc ggt gga ttc aac 259
Met Gln Thr Leu Leu Arg Val Ala Met Leu Asp Thr Gly Gly Phe Asn
40 45 50

gtc aac gca atg tat ggc tca atc att aac cca cgt cgt ttt gaa aac 307
Val Asn Ala Met Tyr Gly Ser Ile Ile Asn Pro Arg Arg Phe Glu Asn
55 60 65

gac cca ttc tgg aac atg ggc ggc ttg gct aac acc gac gtc tac atc 355
Asp Pro Phe Trp Asn Met Gly Gly Leu Ala Asn Thr Asp Val Tyr Ile
70 75 80 85

tct gca gct tcc ggc ctg tgg agc cct cag gat gat gga gtt cgc gta 403
Ser Ala Ala Ser Gly Leu Trp Ser Pro Gln Asp Asp Gly Val Arg Val
90 95 100

gac cac cgc ctc act ggt tct gtg ctt gaa ttc gtg gca atg aca tcc 451
Asp His Arg Leu Thr Gly Ser Val Leu Glu Phe Val Ala Met Thr Ser
105 110 115

acc agg att tgg gaa gca aag gca agg ctt cag ggt ctg aac cca act 499
Thr Arg Ile Trp Glu Ala Lys Ala Arg Leu Gln Gly Leu Asn Pro Thr
120 125 130

gcg gat tac cca atg tat ggc att cac ggc tgg gct cag ttc aac tcc 547
Ala Asp Tyr Pro Met Tyr Gly Ile His Gly Trp Ala Gln Phe Asn Ser
135 140 145

cag ctg gag aga act cag ggt cgt gtt cta gac gtc atg aac gcc tgg 595
Gln Leu Glu Arg Thr Gln Gly Arg Val Leu Asp Val Met Asn Ala Trp
150 155 160 165

tagagccaca ccaaaggcca cac 618

<210> 68
<211> 165
<212> PRT
<213> Corynebacterium glutamicum

<400> 68
Val Ala Cys Pro Trp Ala Gly Thr Ala Ala Leu Asn Leu Ala Ala Lys
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His Pro Asp Gln Phe Arg Gln Ala Met Ser Trp Ser Gly Tyr Leu Asn
20 25 30
Thr Thr Ala Pro Gly Met Gln Thr Leu Leu Arg Val Ala Met Leu Asp

35	40	45
Thr Gly Gly Phe Asn Val Asn Ala Met Tyr Gly Ser Ile Ile Asn Pro		
50	55	60
Arg Arg Phe Glu Asn Asp Pro Phe Trp Asn Met Gly Gly Leu Ala Asn		
65	70	75 80
Thr Asp Val Tyr Ile Ser Ala Ala Ser Gly Leu Trp Ser Pro Gln Asp		
	85	90 95
Asp Gly Val Arg Val Asp His Arg Leu Thr Gly Ser Val Leu Glu Phe		
	100	105 110
Val Ala Met Thr Ser Thr Arg Ile Trp Glu Ala Lys Ala Arg Leu Gln		
	115	120 125
Gly Leu Asn Pro Thr Ala Asp Tyr Pro Met Tyr Gly Ile His Gly Trp		
	130	135 140
Ala Gln Phe Asn Ser Gln Leu Glu Arg Thr Gln Gly Arg Val Leu Asp		
145	150	155 160
Val Met Asn Ala Trp		
	165	

<210> 69
 <211> 1386
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1363)
 <223> RXN00525

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 tggttgacgg gcgcattcatt gggctctgagg tgaaacactc atg agc ctt gca gaa 115
 Met Ser Leu Ala Glu
 1 5
 tca att ctt ttg gcg ctc acc agc ctg aga agc aac aag atg cgt gca 163
 Ser Ile Leu Leu Ala Leu Thr Ser Leu Arg Ser Asn Lys Met Arg Ala
 10 15 20
 ttg ttg acg ctg tta gga gtc atc att ggt atc gca tca gtc atc gga 211
 Leu Leu Thr Leu Leu Gly Val Ile Ile Gly Ile Ala Ser Val Ile Gly
 25 30 35
 att ttg acc att ggt aaa gcc ctg cag gat caa act ttg aat agt ttg 259
 Ile Leu Thr Ile Gly Lys Ala Leu Gln Asp Gln Thr Leu Asn Ser Leu
 40 45 50
 gaa agc ttg ggc gcg aat gat ctg tcg gcg cag gtg gag gaa cgc ccc 307
 Glu Ser Leu Gly Ala Asn Asp Leu Ser Ala Gln Val Glu Glu Arg Pro
 55 60 65
 gac gaa gat tcc ccc gaa ccc gat atg ttc gct ttt tct ggg gct gca 355

Asp	Glu	Asp	Ser	Pro	Glu	Pro	Asp	Met	Phe	Ala	Phe	Ser	Gly	Ala	Ala			
70					75					80					85			
aac	tct	agt	ggc	aat	ctg	att	ccg	gaa	gaa	aca	gtt	gat	acg	ctg	cgc		403	
Asn	Ser	Ser	Gly	Asn	Leu	Ile	Pro	Glu	Glu	Thr	Val	Asp	Thr	Leu	Arg			
				90					95					100				
gat	cgt	ttc	gca	ggc	agc	atc	acg	gga	atc	agc	gtt	ggc	gga	atg	ggc		451	
Asp	Arg	Phe	Ala	Gly	Ser	Ile	Thr	Gly	Ile	Ser	Val	Gly	Gly	Met	Gly			
			105					110					115					
acg	caa	ggc	act	ctc	atc	ggc	gac	acc	gca	gat	ctt	aaa	tcc	gat	ctc		499	
Thr	Gln	Gly	Thr	Leu	Ile	Gly	Asp	Thr	Ala	Asp	Leu	Lys	Ser	Asp	Leu			
		120					125					130						
ctc	ggc	gtc	aac	gag	gat	tat	atg	tgg	atg	aat	ggc	gtc	gaa	atg	aac		547	
Leu	Gly	Val	Asn	Glu	Asp	Tyr	Met	Trp	Met	Asn	Gly	Val	Glu	Met	Asn			
	135					140					145							
tac	ggc	cgc	gcc	atc	acg	caa	gac	gat	gtt	gcc	gct	cag	cgc	ccc	gtt		595	
Tyr	Gly	Arg	Ala	Ile	Thr	Gln	Asp	Asp	Val	Ala	Ala	Gln	Arg	Pro	Val			
150					155				160						165			
gcg	gtc	atc	gcc	cca	gac	acc	ttt	aat	acg	ctt	ttc	gac	gca	aac	ccc		643	
Ala	Val	Ile	Ala	Pro	Asp	Thr	Phe	Asn	Thr	Leu	Phe	Asp	Ala	Asn	Pro			
				170					175					180				
aac	ctc	gct	ctg	ggg	tcc	gaa	gta	gct	ttt	gaa	ctc	aac	ggc	caa	gag		691	
Asn	Leu	Ala	Leu	Gly	Ser	Glu	Val	Ala	Phe	Glu	Leu	Asn	Gly	Gln	Glu			
			185					190					195					
aca	ttt	ttg	cgg	gtt	atc	ggc	gtg	tat	aaa	gaa	gcc	gca	gca	ggc	gga		739	
Thr	Phe	Leu	Arg	Val	Ile	Gly	Val	Tyr	Lys	Glu	Ala	Ala	Ala	Gly	Gly			
		200					205					210						
ctt	gtg	gga	agc	aat	cca	acc	gtc	cac	acc	tac	acc	cca	tat	acg	gtg		787	
Leu	Val	Gly	Ser	Asn	Pro	Thr	Val	His	Thr	Tyr	Thr	Pro	Tyr	Thr	Val			
	215					220					225							
gcc	aat	gac	atc	acc	cac	acg	gaa	gat	gga	ttg	aac	acg	tta	agt	atc		835	
Ala	Asn	Asp	Ile	Thr	His	Thr	Glu	Asp	Gly	Leu	Asn	Thr	Leu	Ser	Ile			
230					235				240						245			
cgt	gca	gct	cag	ggc	gta	gac	cag	gat	tca	ctt	aag	ggc	tca	ctg	caa		883	
Arg	Ala	Ala	Gln	Gly	Val	Asp	Gln	Asp	Ser	Leu	Lys	Gly	Ser	Leu	Gln			
			250					255						260				
acc	tac	ttc	gac	gcg	ctg	tac	gcc	aac	aat	gac	tcg	cac	cac	gtt	gcc		931	
Thr	Tyr	Phe	Asp	Ala	Leu	Tyr	Ala	Asn	Asn	Asp	Ser	His	His	Val	Ala			
			265					270					275					
atg	ttg	gac	ttc	cgt	aaa	cag	atc	gaa	gag	ttc	aac	acc	att	ctc	ggc		979	
Met	Leu	Asp	Phe	Arg	Lys	Gln	Ile	Glu	Glu	Phe	Asn	Thr	Ile	Leu	Gly			
		280					285					290						
gca	atg	agt	ttg	ggc	atc	tca	gcc	atc	ggc	gga	att	tcc	ttg	ctt	gtc		1027	
Ala	Met	Ser	Leu	Gly	Ile	Ser	Ala	Ile	Gly	Gly	Ile	Ser	Leu	Leu	Val			
	295					300					305							
ggc	ggc	atc	gga	gtg	atg	aac	att	atg	ttg	gtg	tct	gtc	acc	gag	cga		1075	
Gly	Gly	Ile	Gly	Val	Met	Asn	Ile	Met	Leu	Val	Ser	Val	Thr	Glu	Arg			

310	315	320	325	
acc cgc gaa atc ggt gtc cga aaa gcc ctc ggc gct cgt cga cgt gac				1123
Thr Arg Glu Ile Gly Val Arg Lys Ala Leu Gly Ala Arg Arg Arg Asp	330	335	340	
att cgc ctg caa ttc gtc gtt gaa gcc atg atc att tgt ttc atc ggt				1171
Ile Arg Leu Gln Phe Val Val Glu Ala Met Ile Ile Cys Phe Ile Gly	345	350	355	
ggc atc ctc ggc gtg ctt ttg ggc ggc att ttg gga ttg atc atg tcc				1219
Gly Ile Leu Gly Val Leu Leu Gly Gly Ile Leu Gly Leu Ile Met Ser	360	365	370	
agc gct att ggc tac att tcc ttg cca cca ctg agt gga atc gtg atc				1267
Ser Ala Ile Gly Tyr Ile Ser Leu Pro Pro Leu Ser Gly Ile Val Ile	375	380	385	
gcc ttg gta ttt tcc atg gct atc ggc ctg ttt ttc ggc tac tac ccc				1315
Ala Leu Val Phe Ser Met Ala Ile Gly Leu Phe Phe Gly Tyr Tyr Pro	390	395	400	405
gcc aac aag gca gca aag ctc gat cca att gac gcc ttg cgt tat gag				1363
Ala Asn Lys Ala Ala Lys Leu Asp Pro Ile Asp Ala Leu Arg Tyr Glu	410	415	420	
taaaagcctc gtttttaagg tag				1386

<210> 70
 <211> 421
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 70
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 Asn Lys Met Arg Ala Leu Leu Thr Leu Leu Gly Val Ile Ile Gly Ile
 20 25 30
 Ala Ser Val Ile Gly Ile Leu Thr Ile Gly Lys Ala Leu Gln Asp Gln
 35 40 45
 Thr Leu Asn Ser Leu Glu Ser Leu Gly Ala Asn Asp Leu Ser Ala Gln
 50 55 60
 Val Glu Glu Arg Pro Asp Glu Asp Ser Pro Glu Pro Asp Met Phe Ala
 65 70 75 80
 Phe Ser Gly Ala Ala Asn Ser Ser Gly Asn Leu Ile Pro Glu Glu Thr
 85 90 95
 Val Asp Thr Leu Arg Asp Arg Phe Ala Gly Ser Ile Thr Gly Ile Ser
 100 105 110
 Val Gly Gly Met Gly Thr Gln Gly Thr Leu Ile Gly Asp Thr Ala Asp
 115 120 125
 Leu Lys Ser Asp Leu Leu Gly Val Asn Glu Asp Tyr Met Trp Met Asn
 130 135 140

Gly Val Glu Met Asn Tyr Gly Arg Ala Ile Thr Gln Asp Asp Val Ala
 145 150 155 160
 Ala Gln Arg Pro Val Ala Val Ile Ala Pro Asp Thr Phe Asn Thr Leu
 165 170 175
 Phe Asp Ala Asn Pro Asn Leu Ala Leu Gly Ser Glu Val Ala Phe Glu
 180 185 190
 Leu Asn Gly Gln Glu Thr Phe Leu Arg Val Ile Gly Val Tyr Lys Glu
 195 200 205
 Ala Ala Ala Gly Gly Leu Val Gly Ser Asn Pro Thr Val His Thr Tyr
 210 215 220
 Thr Pro Tyr Thr Val Ala Asn Asp Ile Thr His Thr Glu Asp Gly Leu
 225 230 235 240
 Asn Thr Leu Ser Ile Arg Ala Ala Gln Gly Val Asp Gln Asp Ser Leu
 245 250 255
 Lys Gly Ser Leu Gln Thr Tyr Phe Asp Ala Leu Tyr Ala Asn Asn Asp
 260 265 270
 Ser His His Val Ala Met Leu Asp Phe Arg Lys Gln Ile Glu Glu Phe
 275 280 285
 Asn Thr Ile Leu Gly Ala Met Ser Leu Gly Ile Ser Ala Ile Gly Gly
 290 295 300
 Ile Ser Leu Leu Val Gly Gly Ile Gly Val Met Asn Ile Met Leu Val
 305 310 315 320
 Ser Val Thr Glu Arg Thr Arg Glu Ile Gly Val Arg Lys Ala Leu Gly
 325 330 335
 Ala Arg Arg Arg Asp Ile Arg Leu Gln Phe Val Val Glu Ala Met Ile
 340 345 350
 Ile Cys Phe Ile Gly Gly Ile Leu Gly Val Leu Leu Gly Gly Ile Leu
 355 360 365
 Gly Leu Ile Met Ser Ser Ala Ile Gly Tyr Ile Ser Leu Pro Pro Leu
 370 375 380
 Ser Gly Ile Val Ile Ala Leu Val Phe Ser Met Ala Ile Gly Leu Phe
 385 390 395 400
 Phe Gly Tyr Tyr Pro Ala Asn Lys Ala Ala Lys Leu Asp Pro Ile Asp
 405 410 415
 Ala Leu Arg Tyr Glu
 420

<210> 71

<211> 760

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(760)

<223> FRXA00525

<400> 71

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                                   Met Ser Leu Ala Glu
                                   1 5

tca att ctt ttg gcg ctc acc agc ctg aga agc aac aag atg cgt gca 163
Ser Ile Leu Leu Ala Leu Thr Ser Leu Arg Ser Asn Lys Met Arg Ala
              10              15              20

ttg ttg acg ctg tta gga gtc atc att ggt atc gca tca gtc atc gga 211
Leu Leu Thr Leu Leu Gly Val Ile Ile Gly Ile Ala Ser Val Ile Gly
              25              30              35

att ttg acc att ggt aaa gcc ctg cag gat caa act ttg aat agt ttg 259
Ile Leu Thr Ile Gly Lys Ala Leu Gln Asp Gln Thr Leu Asn Ser Leu
              40              45              50

gaa agc ttg ggc gcg aat gat ctg tcg gcg cag gtg gag gaa cgc ccc 307
Glu Ser Leu Gly Ala Asn Asp Leu Ser Ala Gln Val Glu Glu Arg Pro
              55              60              65

gac gaa gat tcc ccc gaa ccc gat atg ttc gct ttt tct ggg gct gca 355
Asp Glu Asp Ser Pro Glu Pro Asp Met Phe Ala Phe Ser Gly Ala Ala
              70              75              80              85

aac tct agt ggc aat ctg att ccg gaa gaa aca gtt gat acg ctg cgc 403
Asn Ser Ser Gly Asn Leu Ile Pro Glu Glu Thr Val Asp Thr Leu Arg
              90              95              100

gat cgt ttc gca ggc agc atc acg gga atc agc gtt ggc gga atg ggt 451
Asp Arg Phe Ala Gly Ser Ile Thr Gly Ile Ser Val Gly Gly Met Gly
              105              110              115

acg caa ggc act ctc atc ggc gac acc gca gat ctt aaa tcc gat ctc 499
Thr Gln Gly Thr Leu Ile Gly Asp Thr Ala Asp Leu Lys Ser Asp Leu
              120              125              130

ctc ggc gtc aac gag gat tat atg tgg atg aat ggc gtc gaa atg aac 547
Leu Gly Val Asn Glu Asp Tyr Met Trp Met Asn Gly Val Glu Met Asn
              135              140              145

tac ggc cgc gcc atc acg caa gac gat gtt gcc gct cag cgc ccc gtt 595
Tyr Gly Arg Ala Ile Thr Gln Asp Asp Val Ala Ala Gln Arg Pro Val
              150              155              160              165

gcg gtc atc gcc cca gac acc ttt aat acg ctt ttc gac gca aac ccc 643
Ala Val Ile Ala Pro Asp Thr Phe Asn Thr Leu Phe Asp Ala Asn Pro
              170              175              180

aac ctc gct ctg ggg tcc gaa gta gct ttt gaa ctc aac ggt caa gag 691
Asn Leu Ala Leu Gly Ser Glu Val Ala Phe Glu Leu Asn Gly Gln Glu
              185              190              195

aca ttt ttg cgg gtt atc ggt gtg tat aaa gaa gcc gca gca ggt gga 739

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Thr Phe Leu Arg Val Ile Gly Val Tyr Lys Glu Ala Ala Ala Gly Gly
 200 205 210

ctt gtg gga agc aat cca acc
 Leu Val Gly Ser Asn Pro Thr
 215 220

760

<210> 72
 <211> 220
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 72
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 Ala Ser Val Ile Gly Ile Leu Thr Ile Gly Lys Ala Leu Gln Asp Gln
 35 40 45
 Thr Leu Asn Ser Leu Glu Ser Leu Gly Ala Asn Asp Leu Ser Ala Gln
 50 55 60
 Val Glu Glu Arg Pro Asp Glu Asp Ser Pro Glu Pro Asp Met Phe Ala
 65 70 75 80
 Phe Ser Gly Ala Ala Asn Ser Ser Gly Asn Leu Ile Pro Glu Glu Thr
 85 90 95
 Val Asp Thr Leu Arg Asp Arg Phe Ala Gly Ser Ile Thr Gly Ile Ser
 100 105 110
 Val Gly Gly Met Gly Thr Gln Gly Thr Leu Ile Gly Asp Thr Ala Asp
 115 120 125
 Leu Lys Ser Asp Leu Leu Gly Val Asn Glu Asp Tyr Met Trp Met Asn
 130 135 140
 Gly Val Glu Met Asn Tyr Gly Arg Ala Ile Thr Gln Asp Asp Val Ala
 145 150 155 160
 Ala Gln Arg Pro Val Ala Val Ile Ala Pro Asp Thr Phe Asn Thr Leu
 165 170 175
 Phe Asp Ala Asn Pro Asn Leu Ala Leu Gly Ser Glu Val Ala Phe Glu
 180 185 190
 Leu Asn Gly Gln Glu Thr Phe Leu Arg Val Ile Gly Val Tyr Lys Glu
 195 200 205
 Ala Ala Ala Gly Gly Leu Val Gly Ser Asn Pro Thr
 210 215 220

<210> 73
 <211> 617
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(594)

<223> FRXA00556

<400> 73

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Leu Asn Thr Leu Ser Ile Arg Ala Ala Gln Gly Val Asp Gln Asp Ser	
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ctt aag ggt tca ctg caa acc tac ttc gac gcg ctg tac gcc aac aat	144
Leu Lys Gly Ser Leu Gln Thr Tyr Phe Asp Ala Leu Tyr Ala Asn Asn	
35 40 45	
gac tcg cac cac gtt gcc atg ttg gac ttc cgt aaa cag atc gaa gag	192
Asp Ser His His Val Ala Met Leu Asp Phe Arg Lys Gln Ile Glu Glu	
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Phe Asn Thr Ile Leu Gly Ala Met Ser Leu Gly Ile Ser Ala Ile Gly	
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Gly Ile Ser Leu Leu Val Gly Gly Ile Gly Val Met Asn Ile Met Leu	
85 90 95	
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Val Ser Val Thr Glu Arg Thr Arg Glu Ile Gly Val Arg Lys Ala Leu	
100 105 110	
ggc gct cgt cga cgt gac att cgc ctg caa ttc gtc gtt gaa gcc atg	384
Gly Ala Arg Arg Arg Asp Ile Arg Leu Gln Phe Val Val Glu Ala Met	
115 120 125	
atc att tgt ttc atc ggt ggc atc ctg ggc gtg ctt ttg ggc ggc att	432
Ile Ile Cys Phe Ile Gly Gly Ile Leu Gly Val Leu Leu Gly Gly Ile	
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Leu Gly Leu Ile Met Ser Ser Ala Ile Gly Tyr Ile Ser Leu Pro Pro	
145 150 155 160	
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Leu Ser Gly Ile Val Ile Ala Leu Val Phe Ser Met Ala Ile Gly Leu	
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Phe Phe Gly Tyr Tyr Pro Ala Asn Lys Ala Ala Lys Leu Asp Pro Ile	
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Asp Ala Leu Arg Tyr Glu	
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Met Ala Val Leu Phe
1 5
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tcc atc atg ggt gcg ctc atc ctt ttg gtc ctg tac gtg ctg ttt tta	163
Ser Ile Met Gly Ala Leu Ile Leu Leu Val Leu Tyr Val Leu Phe Leu	
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gga aaa ctg caa att gac ggt ctc atg gtg gat cta cct gac tca gcc	211
Gly Lys Leu Gln Ile Asp Gly Leu Met Val Asp Leu Pro Asp Ser Ala	
25 30 35	
cga gac gat gtt gaa gga ttc gtc ttc aat tgg gtg ttt tcc gga att	259
Arg Asp Asp Val Glu Gly Phe Val Phe Asn Trp Val Phe Ser Gly Ile	
40 45 50	
ctc atc acg tcc gca atc act gtt ccg caa gca gca ctt gga gtg ctg	307
Leu Ile Thr Ser Ala Ile Thr Val Pro Gln Ala Ala Leu Gly Val Leu	
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Val Glu Asp Arg Thr Arg Gly Gly Ile Lys Asp Phe Leu Val Ala Pro	
70 75 80 85	
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Val Ser Arg Thr Thr Leu Thr Val Ser Tyr Ile Phe Ala Ala Val Ile	
90 95 100	
gtc gcc atg acg att ttg atc ttt gaa atc gtg gtg gga agt att ggt	451
Val Ala Met Thr Ile Leu Ile Phe Glu Ile Val Val Gly Ser Ile Gly	
105 110 115	
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Leu Ala Ile Leu Gly His Phe Ser Met Ser Ile Ala Arg Val Leu Glu	
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Leu Val Val Ala Leu Leu Leu Leu Thr Leu Val Phe Ser Ala Ile Ala	
135 140 145	
gca ttt ctg atc acc ttg gtg aaa tct caa ggc gga atg tct gcg ctt	595
Ala Phe Leu Ile Thr Leu Val Lys Ser Gln Gly Gly Met Ser Ala Leu	
150 155 160 165	
tca agc ctg gta ggc acc ctg gcg ggc ttt tta tct gct gct tat att	643
Ser Ser Leu Val Gly Thr Leu Ala Gly Phe Leu Ser Ala Ala Tyr Ile	
170 175 180	
cca ccc atc gca ttg cct gaa gca gtg aca aac gtg ttg aac ttc ctc	691
Pro Pro Ile Ala Leu Pro Glu Ala Val Thr Asn Val Leu Asn Phe Leu	
185 190 195	
ccg ttt acc cca gct gga atg ttg atc aga caa att gtg gtt gcc cca	739
Pro Phe Thr Pro Ala Gly Met Leu Ile Arg Gln Ile Val Val Ala Pro	
200 205 210	
gca ttg gac gcg att tca ctt cca ccc gaa gcc ttc gat atc ttc caa	787
Ala Leu Asp Ala Ile Ser Leu Pro Pro Glu Ala Phe Asp Ile Phe Gln	
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Phe Gly Tyr Gly Leu Lys Leu Glu Met Phe Gly Glu Pro Val Ser Thr	
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ttc 939

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Leu	Pro	Asp	Ser	Ala	Arg	Asp	Asp	Val	Glu	Gly	Phe	Val	Phe	Asn	Trp
		35					40					45			
Val	Phe	Ser	Gly	Ile	Leu	Ile	Thr	Ser	Ala	Ile	Thr	Val	Pro	Gln	Ala
	50					55					60				
Ala	Leu	Gly	Val	Leu	Val	Glu	Asp	Arg	Thr	Arg	Gly	Gly	Ile	Lys	Asp
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Phe	Leu	Val	Ala	Pro	Val	Ser	Arg	Thr	Thr	Leu	Thr	Val	Ser	Tyr	Ile
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			100					105					110		
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		115					120					125			
Ala	Arg	Val	Leu	Glu	Leu	Val	Val	Ala	Leu	Leu	Leu	Leu	Thr	Leu	Val
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Gly	Met	Ser	Ala	Leu	Ser	Ser	Leu	Val	Gly	Thr	Leu	Ala	Gly	Phe	Leu
				165					170					175	
Ser	Ala	Ala	Tyr	Ile	Pro	Pro	Ile	Ala	Leu	Pro	Glu	Ala	Val	Thr	Asn
			180					185					190		
Val	Leu	Asn	Phe	Leu	Pro	Phe	Thr	Pro	Ala	Gly	Met	Leu	Ile	Arg	Gln
		195					200					205			
Ile	Val	Val	Ala	Pro	Ala	Leu	Asp	Ala	Ile	Ser	Leu	Pro	Pro	Glu	Ala
	210					215					220				
Phe	Asp	Ile	Phe	Gln	Phe	Gly	Tyr	Gly	Leu	Lys	Leu	Glu	Met	Phe	Gly
225					230					235					240

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<211> 1815

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(1792)

<223> RXN02096

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Met Gly Leu Asp Val
1 5

agt gat gag cag atc gaa cac gca gcc agg ctt gcc cag gct cat gat 163
Ser Asp Glu Gln Ile Glu His Ala Ala Arg Leu Ala Gln Ala His Asp
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ttt atc gat cgc ctt cca aac aaa tac gag gaa gtc att ggc gaa cgc 211
Phe Ile Asp Arg Leu Pro Asn Lys Tyr Glu Glu Val Ile Gly Glu Arg
25 30 35

ggc ctg acg ctt tct ggt ggt caa cgc caa cgc atc gcc ctc gca cgg 259
Gly Leu Thr Leu Ser Gly Gly Gln Arg Gln Arg Ile Ala Leu Ala Arg
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gct ttc ctg gcg cat ccc aaa gtg ttg gtg ctt gat gat gcc acc tct 307
Ala Phe Leu Ala His Pro Lys Val Leu Val Leu Asp Asp Ala Thr Ser
55 60 65

gcc att gat gcc tcc act gag gac cgc att ttc cag gcc ttg cgc gaa 355
Ala Ile Asp Ala Ser Thr Glu Asp Arg Ile Phe Gln Ala Leu Arg Glu
70 75 80 85

gaa ctg cac gat gtc acc att ttg atc atc gcg cac cgc cac tcc act 403
Glu Leu His Asp Val Thr Ile Leu Ile Ile Ala His Arg His Ser Thr
90 95 100

ttg gag ctc ggc gat cgg gtt ggt ctg gtc gaa gat gga cgg gta aca 451
Leu Glu Leu Gly Asp Arg Val Gly Leu Val Glu Asp Gly Arg Val Thr
105 110 115

gca ctg gga ccg ttg agt gag atg cgt gat cac gct cgt ttc tcg cat 499
Ala Leu Gly Pro Leu Ser Glu Met Arg Asp His Ala Arg Phe Ser His
120 125 130

ctg atg gct ctt gat ttc cag gat tct cac gat ccg gaa ttc acc ctc 547
Leu Met Ala Leu Asp Phe Gln Asp Ser His Asp Pro Glu Phe Thr Leu
135 140 145

gac aac ggt tca cta ccc agc caa gag caa ttg tgg ccg gag gtc tcc	595
Asp Asn Gly Ser Leu Pro Ser Gln Glu Gln Leu Trp Pro Glu Val Ser	
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Thr Glu Lys Gln Tyr Lys Ile Leu Ala Pro Ala Pro Gly Arg Gly Arg	
170 175 180	
ggc atg tcc atg cca gca acc cct gag ctg ctc gcc cag att gag gcg	691
Gly Met Ser Met Pro Ala Thr Pro Glu Leu Leu Ala Gln Ile Glu Ala	
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Leu Pro Ala Ala Thr Glu Glu Thr Arg Val Asp Ala Gly Arg Leu Arg	
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Thr Ser Thr Ser Gly Phe Lys Leu Leu Ser Leu Phe Lys Gln Val Arg	
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Trp Leu Val Val Ala Val Ile Ala Leu Leu Leu Val Gly Val Ala Ala	
230 235 240 245	
gat cta gca ttt cca aca ctg atg cgc gca gcc atc gac aac ggt gtg	883
Asp Leu Ala Phe Pro Thr Leu Met Arg Ala Ala Ile Asp Asn Gly Val	
250 255 260	
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Gln Ala Gln Ser Thr Ser Thr Leu Trp Trp Ile Ala Ile Ala Gly Ser	
265 270 275	
gta gta gtc ctt ctg tcc tgg gcc gcc gcc gcg atc aac acg att atc	979
Val Val Val Leu Leu Ser Trp Ala Ala Ala Ala Ile Asn Thr Ile Ile	
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Thr Ala Arg Thr Gly Glu Arg Leu Leu Tyr Gly Leu Arg Leu Arg Ser	
295 300 305	
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Phe Val His Leu Leu Arg Leu Ser Met Ser Tyr Phe Glu Arg Thr Met	
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tcc ggc cgc atc atg acg cgc atg acc acc gac atc gac aac ctc tcg	1123
Ser Gly Arg Ile Met Thr Arg Met Thr Thr Asp Ile Asp Asn Leu Ser	
330 335 340	
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Ser Phe Leu Gln Ser Gly Leu Ala Gln Thr Val Val Ser Val Gly Thr	
345 350 355	
ctc atc ggt gtg gtc acc atg ctc gcc atc acc gac gca caa cta gca	1219
Leu Ile Gly Val Val Thr Met Leu Ala Ile Thr Asp Ala Gln Leu Ala	
360 365 370	
ctc gtt gcg ctg tcc gtg gtg ccg atc atc atc gtg ctc act ctc att	1267
Leu Val Ala Leu Ser Val Val Pro Ile Ile Ile Val Leu Thr Leu Ile	
375 380 385	
ttc cga cgc atc agc tcc agg ctg tac acc gct tca cgc gag caa gcc	1315

Phe Arg Arg Ile Ser Ser Arg Leu Tyr Thr Ala Ser Arg Glu Gln Ala
 390 395 400 405
 agc cag gtc aac gcg gta ttc cac gag tcc atc gcc ggt tta cgc acc 1363
 Ser Gln Val Asn Ala Val Phe His Glu Ser Ile Ala Gly Leu Arg Thr
 410 415 420
 gcg cag atg cac cgc atg gaa gac caa gtc ttt gac aat tat gcg ggc 1411
 Ala Gln Met His Arg Met Glu Asp Gln Val Phe Asp Asn Tyr Ala Gly
 425 430 435
 gaa gca gag gaa ttc cga cgc ctg cgt gtg aaa tcc cag acg gcc atc 1459
 Glu Ala Glu Glu Phe Arg Arg Leu Arg Val Lys Ser Gln Thr Ala Ile
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 gcc atc tac ttc ccc ggc ctt ggc gcg ctc tct gaa atc gcc cag gca 1507
 Ala Ile Tyr Phe Pro Gly Leu Gly Ala Leu Ser Glu Ile Ala Gln Ala
 455 460 465
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 Leu Val Leu Gly Phe Gly Ala Leu Gln Val Thr Arg Gly Asp Ile Ser
 470 475 480 485
 acc ggc gta ctc gtg gca ttc gtg ctg tac atg ggc ctg atg ttc ggc 1603
 Thr Gly Val Leu Val Ala Phe Val Leu Tyr Met Gly Leu Met Phe Gly
 490 495 500
 ccc atc caa caa cta agc caa atc ttc gac tcc tac caa caa gcc gcc 1651
 Pro Ile Gln Gln Leu Ser Gln Ile Phe Asp Ser Tyr Gln Gln Ala Ala
 505 510 515
 gtc ggc ttc cgt cgc atc acc gaa ctg ctc gca acg cag ccc agc gtc 1699
 Val Gly Phe Arg Arg Ile Thr Glu Leu Leu Ala Thr Gln Pro Ser Val
 520 525 530
 cag atc tgg gca cca aca ggc acg cta ggc agg ctg cca cgc agc ctt 1747
 Gln Ile Trp Ala Pro Thr Gly Thr Leu Gly Arg Leu Pro Arg Ser Leu
 535 540 545
 tat tgc ttg acg acg tca cct tcg gct att cag acg atc cga tcc 1792
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<213> Corynebacterium glutamicum

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Ile Ala Leu Ala Arg Ala Phe Leu Ala His Pro Lys Val Leu Val Leu
 50 55 60
 Asp Asp Ala Thr Ser Ala Ile Asp Ala Ser Thr Glu Asp Arg Ile Phe
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 Gln Ala Leu Arg Glu Glu Leu His Asp Val Thr Ile Leu Ile Ile Ala
 85 90 95
 His Arg His Ser Thr Leu Glu Leu Gly Asp Arg Val Gly Leu Val Glu
 100 105 110
 Asp Gly Arg Val Thr Ala Leu Gly Pro Leu Ser Glu Met Arg Asp His
 115 120 125
 Ala Arg Phe Ser His Leu Met Ala Leu Asp Phe Gln Asp Ser His Asp
 130 135 140
 Pro Glu Phe Thr Leu Asp Asn Gly Ser Leu Pro Ser Gln Glu Gln Leu
 145 150 155 160
 Trp Pro Glu Val Ser Thr Glu Lys Gln Tyr Lys Ile Leu Ala Pro Ala
 165 170 175
 Pro Gly Arg Gly Arg Gly Met Ser Met Pro Ala Thr Pro Glu Leu Leu
 180 185 190
 Ala Gln Ile Glu Ala Leu Pro Ala Ala Thr Glu Glu Thr Arg Val Asp
 195 200 205
 Ala Gly Arg Leu Arg Thr Ser Thr Ser Gly Phe Lys Leu Leu Ser Leu
 210 215 220
 Phe Lys Gln Val Arg Trp Leu Val Val Ala Val Ile Ala Leu Leu Leu
 225 230 235 240
 Val Gly Val Ala Ala Asp Leu Ala Phe Pro Thr Leu Met Arg Ala Ala
 245 250 255
 Ile Asp Asn Gly Val Gln Ala Gln Ser Thr Ser Thr Leu Trp Trp Ile
 260 265 270
 Ala Ile Ala Gly Ser Val Val Val Leu Leu Ser Trp Ala Ala Ala Ala
 275 280 285
 Ile Asn Thr Ile Ile Thr Ala Arg Thr Gly Glu Arg Leu Leu Tyr Gly
 290 295 300
 Leu Arg Leu Arg Ser Phe Val His Leu Leu Arg Leu Ser Met Ser Tyr
 305 310 315 320
 Phe Glu Arg Thr Met Ser Gly Arg Ile Met Thr Arg Met Thr Thr Asp
 325 330 335
 Ile Asp Asn Leu Ser Ser Phe Leu Gln Ser Gly Leu Ala Gln Thr Val
 340 345 350
 Val Ser Val Gly Thr Leu Ile Gly Val Val Thr Met Leu Ala Ile Thr
 355 360 365
 Asp Ala Gln Leu Ala Leu Val Ala Leu Ser Val Val Pro Ile Ile Ile

370	375	380
Val Leu Thr Leu Ile Phe Arg Arg Ile Ser Ser Arg Leu Tyr Thr Ala		
385	390	395 400
Ser Arg Glu Gln Ala Ser Gln Val Asn Ala Val Phe His Glu Ser Ile		
	405	410 415
Ala Gly Leu Arg Thr Ala Gln Met His Arg Met Glu Asp Gln Val Phe		
	420	425 430
Asp Asn Tyr Ala Gly Glu Ala Glu Glu Phe Arg Arg Leu Arg Val Lys		
	435	440 445
Ser Gln Thr Ala Ile Ala Ile Tyr Phe Pro Gly Leu Gly Ala Leu Ser		
	450	455 460
Glu Ile Ala Gln Ala Leu Val Leu Gly Phe Gly Ala Leu Gln Val Thr		
	465	470 475 480
Arg Gly Asp Ile Ser Thr Gly Val Leu Val Ala Phe Val Leu Tyr Met		
	485	490 495
Gly Leu Met Phe Gly Pro Ile Gln Gln Leu Ser Gln Ile Phe Asp Ser		
	500	505 510
Tyr Gln Gln Ala Ala Val Gly Phe Arg Arg Ile Thr Glu Leu Leu Ala		
	515	520 525
Thr Gln Pro Ser Val Gln Ile Trp Ala Pro Thr Gly Thr Leu Gly Arg		
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Leu Pro Arg Ser Leu Tyr Cys Leu Thr Thr Ser Pro Ser Ala Ile Gln		
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 Met Gly Leu Asp Val
 1 5
 agt gat gag cag atc gaa cac gca gcc agg ctt gcc cag gct cat gat 163
 Ser Asp Glu Gln Ile Glu His Ala Ala Arg Leu Ala Gln Ala His Asp
 10 15 20
 ttt atc gat cgc ctt cca aac aaa tac gag gaa gtc att ggc gaa cgc 211

Phe	Ile	Asp	Arg	Leu	Pro	Asn	Lys	Tyr	Glu	Glu	Val	Ile	Gly	Glu	Arg		
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Gly	Leu	Thr	Leu	Ser	Gly	Gly	Gln	Arg	Gln	Arg	Ile	Ala	Leu	Ala	Arg		
		40					45					50					
gct	ttc	ctg	gcg	cat	ccc	aaa	gtg	ttg	gtg	ctt	gat	gat	gcc	acc	tct	307	
Ala	Phe	Leu	Ala	His	Pro	Lys	Val	Leu	Val	Leu	Asp	Asp	Ala	Thr	Ser		
	55					60					65						
gcc	att	gat	gcc	tcc	act	gag	gac	cgc	att	ttc	cag	gcc	ttg	cgc	gaa	355	
Ala	Ile	Asp	Ala	Ser	Thr	Glu	Asp	Arg	Ile	Phe	Gln	Ala	Leu	Arg	Glu		
70					75				80						85		
gaa	ctg	cac	gat	gtc	acc	att	ttg	atc	atc	gcg	cac	cgc	cac	tcc	act	403	
Glu	Leu	His	Asp	Val	Thr	Ile	Leu	Ile	Ile	Ala	His	Arg	His	Ser	Thr		
				90				95						100			
ttg	gag	ctc	ggc	gat	cgg	gtt	ggt	ctg	gtc	gaa	gat	gga	cgg	gta	aca	451	
Leu	Glu	Leu	Gly	Asp	Arg	Val	Gly	Leu	Val	Glu	Asp	Gly	Arg	Val	Thr		
			105				110						115				
gca	ctg	gga	cgc	ttg	agt	gag	atg	cgt	gat	cac	gct	cgt	ttc	tcg	cat	499	
Ala	Leu	Gly	Pro	Leu	Ser	Glu	Met	Arg	Asp	His	Ala	Arg	Phe	Ser	His		
		120					125					130					
ctg	atg	gct	ctt	gat	ttc	cag	gat	tct	cac	gat	ccg	gaa	ttc	acc	ctc	547	
Leu	Met	Ala	Leu	Asp	Phe	Gln	Asp	Ser	His	Asp	Pro	Glu	Phe	Thr	Leu		
	135					140					145						
gac	aac	ggt	tca	cta	ccc	agc	caa	gag	caa	ttg	tgg	cgc	gag	gtc	tcc	595	
Asp	Asn	Gly	Ser	Leu	Pro	Ser	Gln	Glu	Gln	Leu	Trp	Pro	Glu	Val	Ser		
150					155					160					165		
aca	gaa	aag	cag	tac	aag	att	ctt	gcg	cct	gcc	cct	ggt	cga	ggc	cgt	643	
Thr	Glu	Lys	Gln	Tyr	Lys	Ile	Leu	Ala	Pro	Ala	Pro	Gly	Arg	Gly	Arg		
			170					175						180			
ggc	atg	tcc	atg	cca	gca	acc	cct	gag	ctg	ctc	gcc	cag	att	gag	gcg	691	
Gly	Met	Ser	Met	Pro	Ala	Thr	Pro	Glu	Leu	Leu	Ala	Gln	Ile	Glu	Ala		
			185				190						195				
ctg	cca	gca	gca	acg	gaa	gaa	aca	cga	gtt	gat	gcc	ggg	agg	cta	cgc	739	
Leu	Pro	Ala	Ala	Thr	Glu	Glu	Thr	Arg	Val	Asp	Ala	Gly	Arg	Leu	Arg		
		200					205					210					
acc	agt	acc	tcc	ggt	ttc	aaa	ttg	ctc	agt	tta	ttc	aag	cag	gtc	cgt	787	
Thr	Ser	Thr	Ser	Gly	Phe	Lys	Leu	Leu	Ser	Leu	Phe	Lys	Gln	Val	Arg		
	215					220					225						
tgg	ctc	gtc	gtc	gcg	gtc	atc	gcg	ttg	ttg	ctg	gtg	ggc	gta	gcc	gcc	835	
Trp	Leu	Val	Val	Ala	Val	Ile	Ala	Leu	Leu	Leu	Val	Gly	Val	Ala	Ala		
230					235					240					245		
gat	cta	gca	ttt	cca	aca	ctg	atg	cgc	gca	gcc	atc	gac	aac	ggt	gtg	883	
Asp	Leu	Ala	Phe	Pro	Thr	Leu	Met	Arg	Ala	Ala	Ile	Asp	Asn	Gly	Val		
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caa	gca	caa	agc	acc	tcc	acg	ttg	tgg	tgg	atc	gcc	atc	gca	ggc	agc	931	
Gln	Ala	Gln	Ser	Thr	Ser	Thr	Leu	Trp	Trp	Ile	Ala	Ile	Ala	Gly	Ser		

265	270	275	
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Val Val Val Leu Leu Ser Trp Ala Ala Ala Ala Ile Asn Thr Ile Ile			
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Thr Ala Arg Thr Gly Glu Arg Leu Leu Tyr Gly Leu Arg Leu Arg Ser			
295	300	305	
ttt gtg cat cta ttg cgc ctg tcc atg agc tat ttc gaa cgc acc atg			1075
Phe Val His Leu Leu Arg Leu Ser Met Ser Tyr Phe Glu Arg Thr Met			
310	315	320	325
tcc ggc cgc atc atg acg cgc atg acc acc gac atc gac aac ctc tcg			1123
Ser Gly Arg Ile Met Thr Arg Met Thr Thr Asp Ile Asp Asn Leu Ser			
330	335	340	
tcc ttc ctc caa tca ggt ctg gcg caa aca gtt gtc tct gtg ggc acg			1171
Ser Phe Leu Gln Ser Gly Leu Ala Gln Thr Val Val Ser Val Gly Thr			
345	350	355	
ctc atc ggt gtg gtc acc atg ctc gcc atc acc gac gca caa cta gca			1219
Leu Ile Gly Val Val Thr Met Leu Ala Ile Thr Asp Ala Gln Leu Ala			
360	365	370	
ctc gtt gcg ctg tcc gtg gtg ccg atc atc atc gtg ctc act ctc att			1267
Leu Val Ala Leu Ser Val Val Pro Ile Ile Ile Val Leu Thr Leu Ile			
375	380	385	
ttc cga cgc atc agc tcc agg ctg tac acc gct tca cgc gag caa gcc			1315
Phe Arg Arg Ile Ser Ser Arg Leu Tyr Thr Ala Ser Arg Glu Gln Ala			
390	395	400	405
agc cag gtc aac gcg gta ttc cac gag tcc atc gcc ggt tta cgc acc			1363
Ser Gln Val Asn Ala Val Phe His Glu Ser Ile Ala Gly Leu Arg Thr			
410	415	420	
gcg cag atg cac cgc atg gaa gac caa gtc ttt gac aat tat gcg ggc			1411
Ala Gln Met His Arg Met Glu Asp Gln Val Phe Asp Asn Tyr Ala Gly			
425	430	435	
gaa gca			1417
Glu Ala			

<210> 80

<211> 439

<212> PRT

<213> Corynebacterium glutamicum

<400> 80

Met Gly Leu Asp Val Ser Asp Glu Gln Ile Glu His Ala Ala Arg Leu
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Ala Gln Ala His Asp Phe Ile Asp Arg Leu Pro Asn Lys Tyr Glu Glu
20 25 30

Val Ile Gly Glu Arg Gly Leu Thr Leu Ser Gly Gly Gln Arg Gln Arg
35 40 45

Ile Ala Leu Ala Arg Ala Phe Leu Ala His Pro Lys Val Leu Val Leu
 50 55 60
 Asp Asp Ala Thr Ser Ala Ile Asp Ala Ser Thr Glu Asp Arg Ile Phe
 65 70 75 80
 Gln Ala Leu Arg Glu Glu Leu His Asp Val Thr Ile Leu Ile Ile Ala
 85 90 95
 His Arg His Ser Thr Leu Glu Leu Gly Asp Arg Val Gly Leu Val Glu
 100 105 110
 Asp Gly Arg Val Thr Ala Leu Gly Pro Leu Ser Glu Met Arg Asp His
 115 120 125
 Ala Arg Phe Ser His Leu Met Ala Leu Asp Phe Gln Asp Ser His Asp
 130 135 140
 Pro Glu Phe Thr Leu Asp Asn Gly Ser Leu Pro Ser Gln Glu Gln Leu
 145 150 155 160
 Trp Pro Glu Val Ser Thr Glu Lys Gln Tyr Lys Ile Leu Ala Pro Ala
 165 170 175
 Pro Gly Arg Gly Arg Gly Met Ser Met Pro Ala Thr Pro Glu Leu Leu
 180 185 190
 Ala Gln Ile Glu Ala Leu Pro Ala Ala Thr Glu Glu Thr Arg Val Asp
 195 200 205
 Ala Gly Arg Leu Arg Thr Ser Thr Ser Gly Phe Lys Leu Leu Ser Leu
 210 215 220
 Phe Lys Gln Val Arg Trp Leu Val Val Ala Val Ile Ala Leu Leu Leu
 225 230 235 240
 Val Gly Val Ala Ala Asp Leu Ala Phe Pro Thr Leu Met Arg Ala Ala
 245 250 255
 Ile Asp Asn Gly Val Gln Ala Gln Ser Thr Ser Thr Leu Trp Trp Ile
 260 265 270
 Ala Ile Ala Gly Ser Val Val Val Leu Leu Ser Trp Ala Ala Ala Ala
 275 280 285
 Ile Asn Thr Ile Ile Thr Ala Arg Thr Gly Glu Arg Leu Leu Tyr Gly
 290 295 300
 Leu Arg Leu Arg Ser Phe Val His Leu Leu Arg Leu Ser Met Ser Tyr
 305 310 315 320
 Phe Glu Arg Thr Met Ser Gly Arg Ile Met Thr Arg Met Thr Thr Asp
 325 330 335
 Ile Asp Asn Leu Ser Ser Phe Leu Gln Ser Gly Leu Ala Gln Thr Val
 340 345 350
 Val Ser Val Gly Thr Leu Ile Gly Val Val Thr Met Leu Ala Ile Thr
 355 360 365

Asp Ala Gln Leu Ala Leu Val Ala Leu Ser Val Val Pro Ile Ile Ile
 370 375 380
 Val Leu Thr Leu Ile Phe Arg Arg Ile Ser Ser Arg Leu Tyr Thr Ala
 385 390 395 400
 Ser Arg Glu Gln Ala Ser Gln Val Asn Ala Val Phe His Glu Ser Ile
 405 410 415
 Ala Gly Leu Arg Thr Ala Gln Met His Arg Met Glu Asp Gln Val Phe
 420 425 430
 Asp Asn Tyr Ala Gly Glu Ala
 435

<210> 81
 <211> 843
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(820)
 <223> RXA02562

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 tgagcagatt tatttgggct tttgtctagg gtggggagct atg ttc ttg aca aag 115
 Met Phe Leu Thr Lys
 1 5
 gtt tcg ctg ctt gat cat ccg gag tca ttg ccg ggg tat tta tcg agc 163
 Val Ser Leu Leu Asp His Pro Glu Ser Leu Pro Gly Tyr Leu Ser Ser
 10 15 20
 ctg gcg atc gtg gaa tat ctg cat gaa cag ccg ttg gag ttt cgt gca 211
 Leu Ala Ile Val Glu Tyr Leu His Glu Gln Pro Leu Glu Phe Arg Ala
 25 30 35
 ccg att act gtg att act ggt gaa aat ggg gtg ggt aaa tcc acg ttg 259
 Pro Ile Thr Val Ile Thr Gly Glu Asn Gly Val Gly Lys Ser Thr Leu
 40 45 50
 gtt gag gct ttg gcg gtg ggg atg cgc ctt aat ccg tct ggt ggc tct 307
 Val Glu Ala Leu Ala Val Gly Met Arg Leu Asn Pro Ser Gly Gly Ser
 55 60 65
 agg cat gca aac ttt ggc agg gaa ggc gat att gtg tcg tcg ctt cat 355
 Arg His Ala Asn Phe Gly Arg Glu Gly Asp Ile Val Ser Ser Leu His
 70 75 80 85
 cag tcg ttg aag ttg gtg cgg aga gaa aac cct ccg gat gcg ttc ttt 403
 Gln Ser Leu Lys Leu Val Arg Arg Glu Asn Pro Arg Asp Ala Phe Phe
 90 95 100
 ttt cgg ggt gag acg atg tat aac gtg gct tcc tat tat gag gag tta 451
 Phe Arg Gly Glu Thr Met Tyr Asn Val Ala Ser Tyr Tyr Glu Glu Leu
 105 110 115

atg ggg gaa aag aac atg cat gat ctt cac aag atg agc cat ggc gaa 499
Met Gly Glu Lys Asn Met His Asp Leu His Lys Met Ser His Gly Glu
120 125 130

tcg gta ttt gcg gtg att gat cgg cgt ttt aac aat caa gga ttt ttt 547
Ser Val Phe Ala Val Ile Asp Arg Arg Phe Asn Asn Gln Gly Phe Phe
135 140 145

gtt ttg gac gag cct gag gca ggc ctt tcc atg ctg agg cag ttg gag 595
Val Leu Asp Glu Pro Glu Ala Gly Leu Ser Met Leu Arg Gln Leu Glu
150 155 160 165

ttg ttg gga aag ttg ggc aac ctt gct cga ggt ggt gcg cag atc atc 643
Leu Leu Gly Lys Leu Gly Asn Leu Ala Arg Gly Gly Ala Gln Ile Ile
170 175 180

atg gct acg cac tct cca ata ttg ttg gct att ccg ggg gca gag atc 691
Met Ala Thr His Ser Pro Ile Leu Leu Ala Ile Pro Gly Ala Glu Ile
185 190 195

ctt gaa att aca tct tcg ggt gtt gca aag gtg aat ttt gag gat gcg 739
Leu Glu Ile Thr Ser Ser Gly Val Ala Lys Val Asn Phe Glu Asp Ala
200 205 210

gag gct gtt cgt gcg gct cgg gaa ttt gtg gca gat ccg cga ggt acg 787
Glu Ala Val Arg Ala Ala Arg Glu Phe Val Ala Asp Pro Arg Gly Thr
215 220 225

gcg gcg ttt ctg act gcg gag gag gat cac caa tgatgccgta tatcaccgat 840
Ala Ala Phe Leu Thr Ala Glu Glu Asp His Gln
230 235 240

att 843

<210> 82

<211> 240

<212> PRT

<213> Corynebacterium glutamicum

<400> 82

Met Phe Leu Thr Lys Val Ser Leu Leu Asp His Pro Glu Ser Leu Pro
1 5 10 15

Gly Tyr Leu Ser Ser Leu Ala Ile Val Glu Tyr Leu His Glu Gln Pro
20 25 30

Leu Glu Phe Arg Ala Pro Ile Thr Val Ile Thr Gly Glu Asn Gly Val
35 40 45

Gly Lys Ser Thr Leu Val Glu Ala Leu Ala Val Gly Met Arg Leu Asn
50 55 60

Pro Ser Gly Gly Ser Arg His Ala Asn Phe Gly Arg Glu Gly Asp Ile
65 70 75 80

Val Ser Ser Leu His Gln Ser Leu Lys Leu Val Arg Arg Glu Asn Pro
85 90 95

Arg Asp Ala Phe Phe Phe Arg Gly Glu Thr Met Tyr Asn Val Ala Ser
100 105 110

Tyr Tyr Glu Glu Leu Met Gly Glu Lys Asn Met His Asp Leu His Lys
 115 120 125
 Met Ser His Gly Glu Ser Val Phe Ala Val Ile Asp Arg Arg Phe Asn
 130 135 140
 Asn Gln Gly Phe Phe Val Leu Asp Glu Pro Glu Ala Gly Leu Ser Met
 145 150 155 160
 Leu Arg Gln Leu Glu Leu Leu Gly Lys Leu Gly Asn Leu Ala Arg Gly
 165 170 175
 Gly Ala Gln Ile Ile Met Ala Thr His Ser Pro Ile Leu Leu Ala Ile
 180 185 190
 Pro Gly Ala Glu Ile Leu Glu Ile Thr Ser Ser Gly Val Ala Lys Val
 195 200 205
 Asn Phe Glu Asp Ala Glu Ala Val Arg Ala Ala Arg Glu Phe Val Ala
 210 215 220
 Asp Pro Arg Gly Thr Ala Ala Phe Leu Thr Ala Glu Glu Asp His Gln
 225 230 235 240

<210> 83
 <211> 1029
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1006)
 <223> RXA00950

<400> 83
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 tctgctgatt tttgtctcca agtggagttg aatgagagtt atg aac act ccg gca 115
 Met Asn Thr Pro Ala
 1 5
 gtt cag gtt caa aat cta agt ttg agt ttt ggg tcg ttc aca gct gtc 163
 Val Gln Val Gln Asn Leu Ser Leu Ser Phe Gly Ser Phe Thr Ala Val
 10 15 20
 aac ggc ctc agc ctc acg gtg gag cag ggg agc att cac ggc ttc ctc 211
 Asn Gly Leu Ser Leu Thr Val Glu Gln Gly Ser Ile His Gly Phe Leu
 25 30 35
 ggc ccc aac ggt gca gga aag tca aca acc atc agg gca ctc att gga 259
 Gly Pro Asn Gly Ala Gly Lys Ser Thr Thr Ile Arg Ala Leu Ile Gly
 40 45 50
 gtg cta aaa ccc caa aca ggt tca gtc gct att ctc ggc caa gat cct 307
 Val Leu Lys Pro Gln Thr Gly Ser Val Ala Ile Leu Gly Gln Asp Pro
 55 60 65
 gtt gct cac ccc gat gtc ctt cga aga gtt ggc tac gtt cca gga gat 355
 Val Ala His Pro Asp Val Leu Arg Arg Val Gly Tyr Val Pro Gly Asp

70	75	80	85	
gcc aca ctg tgg gac aac ctc act ggg gcg gaa gtt ttc agg gcg ctc				403
Ala Thr Leu Trp Asp Asn Leu Thr Gly Ala Glu Val Phe Arg Ala Leu	90	95	100	
gaa tca ctc cgc aag act cca tcc aac cga gct cta gaa aac gag ctc				451
Glu Ser Leu Arg Lys Thr Pro Ser Asn Arg Ala Leu Glu Asn Glu Leu	105	110	115	
att gac gcc ttc caa ttg gat ccc tcg aag aag atc cgc gaa tac tcg				499
Ile Asp Ala Phe Gln Leu Asp Pro Ser Lys Lys Ile Arg Glu Tyr Ser	120	125	130	
aca ggt aac aga agg aaa gtc agt ctc atc gcg gcg ctc agt cat gag				547
Thr Gly Asn Arg Arg Lys Val Ser Leu Ile Ala Ala Leu Ser His Glu	135	140	145	
ccc gag ctc ctc atc gtt gac gag ccc acc gca ggc ttg gat ccc atc				595
Pro Glu Leu Leu Ile Val Asp Glu Pro Thr Ala Gly Leu Asp Pro Ile	150	155	160	165
atg gag caa gtc ttt gtc acc tat gtc cgc aag gca cga acc aac ggc				643
Met Glu Gln Val Phe Val Thr Tyr Val Arg Lys Ala Arg Thr Asn Gly	170	175	180	
gcg tcc gtg tta ctc agc agc cac att ctc agt gag gtg gag cag ctg				691
Ala Ser Val Leu Leu Ser Ser His Ile Leu Ser Glu Val Glu Gln Leu	185	190	195	
tgt gat tac gtc acg gtc ctt aaa gag ggg cga gca gtt gca tct aat				739
Cys Asp Tyr Val Thr Val Leu Lys Glu Gly Arg Ala Val Ala Ser Asn	200	205	210	
gag gtg agc tat ctg agg aag atc tcc gct cac cgc att act gcc acg				787
Glu Val Ser Tyr Leu Arg Lys Ile Ser Ala His Arg Ile Thr Ala Thr	215	220	225	
att ccg gcg gta cct caa cac ctt gct ggc agg gga gaa gtg gat ttc				835
Ile Pro Ala Val Pro Gln His Leu Ala Gly Arg Gly Glu Val Asp Phe	230	235	240	245
gat gct ggc cat ctc agc atc acc tgc gat gcc tcc gag gtt ccc gat				883
Asp Ala Gly His Leu Ser Ile Thr Cys Asp Ala Ser Glu Val Pro Asp	250	255	260	
att ttg cgc atc atc atc gac gct ggc ggc cag gac atc atc agc acc				931
Ile Leu Arg Ile Ile Ile Asp Ala Gly Gly Gln Asp Ile Ile Ser Thr	265	270	275	
gcg gcg tcg ctg gag gag atc ttc ttg cgt cac tat gga gaa acc gtg				979
Ala Ala Ser Leu Glu Glu Ile Phe Leu Arg His Tyr Gly Glu Thr Val	280	285	290	
agt ggt tca gaa agc aag gca tca caa tgatccgtct taatctacgt ctt				1029
Ser Gly Ser Glu Ser Lys Ala Ser Gln	295	300		

<210> 84

<211> 302

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 84

Met	Asn	Thr	Pro	Ala	Val	Gln	Val	Gln	Asn	Leu	Ser	Leu	Ser	Phe	Gly	1	5	10	15
Ser	Phe	Thr	Ala	Val	Asn	Gly	Leu	Ser	Leu	Thr	Val	Glu	Gln	Gly	Ser	20	25	30	
Ile	His	Gly	Phe	Leu	Gly	Pro	Asn	Gly	Ala	Gly	Lys	Ser	Thr	Thr	Ile	35	40	45	
Arg	Ala	Leu	Ile	Gly	Val	Leu	Lys	Pro	Gln	Thr	Gly	Ser	Val	Ala	Ile	50	55	60	
Leu	Gly	Gln	Asp	Pro	Val	Ala	His	Pro	Asp	Val	Leu	Arg	Arg	Val	Gly	65	70	75	80
Tyr	Val	Pro	Gly	Asp	Ala	Thr	Leu	Trp	Asp	Asn	Leu	Thr	Gly	Ala	Glu	85	90	95	
Val	Phe	Arg	Ala	Leu	Glu	Ser	Leu	Arg	Lys	Thr	Pro	Ser	Asn	Arg	Ala	100	105	110	
Leu	Glu	Asn	Glu	Leu	Ile	Asp	Ala	Phe	Gln	Leu	Asp	Pro	Ser	Lys	Lys	115	120	125	
Ile	Arg	Glu	Tyr	Ser	Thr	Gly	Asn	Arg	Arg	Lys	Val	Ser	Leu	Ile	Ala	130	135	140	
Ala	Leu	Ser	His	Glu	Pro	Glu	Leu	Leu	Ile	Val	Asp	Glu	Pro	Thr	Ala	145	150	155	160
Gly	Leu	Asp	Pro	Ile	Met	Glu	Gln	Val	Phe	Val	Thr	Tyr	Val	Arg	Lys	165	170	175	
Ala	Arg	Thr	Asn	Gly	Ala	Ser	Val	Leu	Leu	Ser	Ser	His	Ile	Leu	Ser	180	185	190	
Glu	Val	Glu	Gln	Leu	Cys	Asp	Tyr	Val	Thr	Val	Leu	Lys	Glu	Gly	Arg	195	200	205	
Ala	Val	Ala	Ser	Asn	Glu	Val	Ser	Tyr	Leu	Arg	Lys	Ile	Ser	Ala	His	210	215	220	
Arg	Ile	Thr	Ala	Thr	Ile	Pro	Ala	Val	Pro	Gln	His	Leu	Ala	Gly	Arg	225	230	235	240
Gly	Glu	Val	Asp	Phe	Asp	Ala	Gly	His	Leu	Ser	Ile	Thr	Cys	Asp	Ala	245	250	255	
Ser	Glu	Val	Pro	Asp	Ile	Leu	Arg	Ile	Ile	Ile	Asp	Ala	Gly	Gly	Gln	260	265	270	
Asp	Ile	Ile	Ser	Thr	Ala	Ala	Ser	Leu	Glu	Glu	Ile	Phe	Leu	Arg	His	275	280	285	
Tyr	Gly	Glu	Thr	Val	Ser	Gly	Ser	Glu	Ser	Lys	Ala	Ser	Gln	290	295	300			

<400> 85															60	
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gcttaaattg cttgtcgacg cctagtgcca caatggagac										atg acc gaa aca ctt		115				
										Met Thr Glu Thr Leu		5				
										1						
gtg	gtg	aat	ggc	ctt	gca	ggc	ggc	tat	ggg	cac	cgc	aca	tta	ttt	aac	163
Val	Val	Asn	Gly	Leu	Ala	Gly	Gly	Tyr	Gly	His	Arg	Thr	Leu	Phe	Asn	20
				10						15						
gat	gtg	aat	ctc	acc	gta	gct	gcc	ggc	gat	gtc	gtg	ggc	gtt	gtc	ggc	211
Asp	Val	Asn	Leu	Thr	Val	Ala	Ala	Gly	Asp	Val	Val	Gly	Val	Val	Gly	35
				25						30						
gtc	aat	ggc	gct	ggg	aaa	tcc	aca	ttt	cta	aaa	att	ctg	gcg	ggc	gtg	259
Val	Asn	Gly	Ala	Gly	Lys	Ser	Thr	Phe	Leu	Lys	Ile	Leu	Ala	Gly	Val	50
				40						45						
gaa	aag	cca	ctg	gct	gga	act	atc	gcg	ctt	tcg	cca	gcc	gat	gct	ttt	307
Glu	Lys	Pro	Leu	Ala	Gly	Thr	Ile	Ala	Leu	Ser	Pro	Ala	Asp	Ala	Phe	65
				55						60						
gtg	ggc	tac	ttg	cca	cag	gaa	cac	acc	cgc	acg	tct	gga	gag	acg	atc	355
Val	Gly	Tyr	Leu	Pro	Gln	Glu	His	Thr	Arg	Thr	Ser	Gly	Glu	Thr	Ile	85
				70						75						
gca	gtt	tac	att	gct	cgt	cga	acc	ggc	tgc	caa	gct	gca	aca	act	gcc	403
Ala	Val	Tyr	Ile	Ala	Arg	Arg	Thr	Gly	Cys	Gln	Ala	Ala	Thr	Thr	Ala	100
				90						95						
atg	gat	gac	acc	gcc	gaa	gcg	ttt	ggg	gcg	gat	cca	gac	aac	gct	gcc	451
Met	Asp	Asp	Thr	Ala	Glu	Ala	Phe	Gly	Ala	Asp	Pro	Asp	Asn	Ala	Ala	115
				105						110						
ttg	gcc	gat	gca	tac	gcc	gag	gcg	ctg	gat	cgg	tgg	atg	gcc	agt	ggc	499
Leu	Ala	Asp	Ala	Tyr	Ala	Glu	Ala	Leu	Asp	Arg	Trp	Met	Ala	Ser	Gly	130
				120						125						
gca	gcc	gat	ttg	gat	gaa	cgc	atc	ccc	atc	gtg	ctc	gct	gat	ttg	ggc	547
Ala	Ala	Asp	Leu	Asp	Glu	Arg	Ile	Pro	Ile	Val	Leu	Ala	Asp	Leu	Gly	145
				135						140						
ttt	gag	ctt	ccc	acc	tcg	acg	ctg	atg	gaa	gga	ctt	tca	ggc	ggg	cag	595
Phe	Glu	Leu	Pro	Thr	Ser	Thr	Leu	Met	Glu	Gly	Leu	Ser	Gly	Gly	Gln	165
				150						155						
gca	gcc	cgg	gtc	ggg	ctg	gcg	gcg	tta	ctg	ttg	tca	cgt	ttt	gac	att	643
Ala	Ala	Arg	Val	Gly	Leu	Ala	Ala	Leu	Leu	Leu	Ser	Arg	Phe	Asp	Ile	180
				170						175						

gtg ctt ctc gac gag ccc acc aac gat ttg gat ctc gac ggt ctt gag	691
Val Leu Leu Asp Glu Pro Thr Asn Asp Leu Asp Leu Asp Gly Leu Glu	
185 190 195	
caa ctg gag aat ttt gtt cag ggg ctt cgc ggg gga gtc gta ctg gtc	739
Gln Leu Glu Asn Phe Val Gln Gly Leu Arg Gly Gly Val Val Leu Val	
200 205 210	
agc cat gat cgt gag ttt ctt tcc agg tgt gtg acc act gtg ctg gaa	787
Ser His Asp Arg Glu Phe Leu Ser Arg Cys Val Thr Thr Val Leu Glu	
215 220 225	
ctc gat ctg cac caa aat tcc cac cat gtt tat ggc ggt gga tat gat	835
Leu Asp Leu His Gln Asn Ser His His Val Tyr Gly Gly Gly Tyr Asp	
230 235 240 245	
tcc tac ctt gag gaa cgc gca gtg cta cgc cag cac gcc cgt gac caa	883
Ser Tyr Leu Glu Glu Arg Ala Val Leu Arg Gln His Ala Arg Asp Gln	
250 255 260	
tat gag gaa ttt gcg gaa aag aag aag gac ctt gtg gca cgt gct cga	931
Tyr Glu Glu Phe Ala Glu Lys Lys Lys Asp Leu Val Ala Arg Ala Arg	
265 270 275	
acg cag cgt gaa tgg tct agt cac ggt gtc cgc aat gct att aaa cgt	979
Thr Gln Arg Glu Trp Ser Ser His Gly Val Arg Asn Ala Ile Lys Arg	
280 285 290	
gca cct gac aac gac aaa ctt cgg aag aaa gcc gct gcg gaa tcc agt	1027
Ala Pro Asp Asn Asp Lys Leu Arg Lys Lys Ala Ala Ala Glu Ser Ser	
295 300 305	
gaa aag cag gct caa aaa gtc cgc cag atg gaa agc cgc atc gct cgg	1075
Glu Lys Gln Ala Gln Lys Val Arg Gln Met Glu Ser Arg Ile Ala Arg	
310 315 320 325	
tta gaa gaa gtt gaa gag cca cgt aaa gaa tgg aaa ctg cag ttc agc	1123
Leu Glu Glu Val Glu Glu Pro Arg Lys Glu Trp Lys Leu Gln Phe Ser	
330 335 340	
gtc ggt aag gcg tcg cgg tca agt tct gtt gtt tcc acg ttg aat gat	1171
Val Gly Lys Ala Ser Arg Ser Ser Ser Val Val Ser Thr Leu Asn Asp	
345 350 355	
gca agc ttc acc caa ggc gat ttc acc ttg gga cca gta tcc atc caa	1219
Ala Ser Phe Thr Gln Gly Asp Phe Thr Leu Gly Pro Val Ser Ile Gln	
360 365 370	
gta aat gct ggc gat cgc att ggc atc aca gga ccc aac ggt gct ggt	1267
Val Asn Ala Gly Asp Arg Ile Gly Ile Thr Gly Pro Asn Gly Ala Gly	
375 380 385	
aaa tcc aca ttg ctg cgc gga cta ttg gga aac caa gaa ccc acc agc	1315
Lys Ser Thr Leu Leu Arg Gly Leu Leu Gly Asn Gln Glu Pro Thr Ser	
390 395 400 405	
ggt act gcc acg atg ggc acg agc gtg gcg atc gga gaa atc gat cag	1363
Gly Thr Ala Thr Met Gly Thr Ser Val Ala Ile Gly Glu Ile Asp Gln	
410 415 420	

gca cga gcg tta ctt gat cca cag ttg cca ctg att tct gcg ttt gaa 1411
 Ala Arg Ala Leu Leu Asp Pro Gln Leu Pro Leu Ile Ser Ala Phe Glu
 425 430 435

aag cat gtt cca gac tta ccg atc agt gag gtg cgc aca ctg ctc gcg 1459
 Lys His Val Pro Asp Leu Pro Ile Ser Glu Val Arg Thr Leu Leu Ala
 440 445 450

aaa ttt ggg ctg aat gat aat cat gtg gaa cgg gac gtc gaa aag cta 1507
 Lys Phe Gly Leu Asn Asp Asn His Val Glu Arg Asp Val Glu Lys Leu
 455 460 465

tct cct ggc gag cgc acg cgc gcc gga ctt gcg ctg cta cag gtg cgg 1555
 Ser Pro Gly Glu Arg Thr Arg Ala Gly Leu Ala Leu Leu Gln Val Arg
 470 475 480 485

ggc gtc aac gtg ctt gtt ctt gat gag ccc acc aac cac ctt gac ctg 1603
 Gly Val Asn Val Leu Val Leu Asp Glu Pro Thr Asn His Leu Asp Leu
 490 495 500

gag gcc atc gag caa ttg gag caa gcg ttg gcc tcg tat gat ggt gtg 1651
 Glu Ala Ile Glu Gln Leu Glu Gln Ala Leu Ala Ser Tyr Asp Gly Val
 505 510 515

ttg ctg ctg gtc acg cac gat cgt cgc atg ttg gac gct gtg cag acc 1699
 Leu Leu Leu Val Thr His Asp Arg Arg Met Leu Asp Ala Val Gln Thr
 520 525 530

aat cgt cgt tgg cat gtc gag gct ggc gaa gtt agg gag cta 1741
 Asn Arg Arg Trp His Val Glu Ala Gly Glu Val Arg Glu Leu
 535 540 545

taaccgtttc cgtattgatg cca 1764

<210> 86
 <211> 547
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 86
 Met Thr Glu Thr Leu Val Val Asn Gly Leu Ala Gly Gly Tyr Gly His
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Arg Thr Leu Phe Asn Asp Val Asn Leu Thr Val Ala Ala Gly Asp Val
 20 25 30

Val Gly Val Val Gly Val Asn Gly Ala Gly Lys Ser Thr Phe Leu Lys
 35 40 45

Ile Leu Ala Gly Val Glu Lys Pro Leu Ala Gly Thr Ile Ala Leu Ser
 50 55 60

Pro Ala Asp Ala Phe Val Gly Tyr Leu Pro Gln Glu His Thr Arg Thr
 65 70 75 80

Ser Gly Glu Thr Ile Ala Val Tyr Ile Ala Arg Arg Thr Gly Cys Gln
 85 90 95

Ala Ala Thr Thr Ala Met Asp Asp Thr Ala Glu Ala Phe Gly Ala Asp
 100 105 110

Pro Asp Asn Ala Ala Leu Ala Asp Ala Tyr Ala Glu Ala Leu Asp Arg
 115 120 125
 Trp Met Ala Ser Gly Ala Ala Asp Leu Asp Glu Arg Ile Pro Ile Val
 130 135 140
 Leu Ala Asp Leu Gly Phe Glu Leu Pro Thr Ser Thr Leu Met Glu Gly
 145 150 155 160
 Leu Ser Gly Gly Gln Ala Ala Arg Val Gly Leu Ala Ala Leu Leu Leu
 165 170 175
 Ser Arg Phe Asp Ile Val Leu Leu Asp Glu Pro Thr Asn Asp Leu Asp
 180 185 190
 Leu Asp Gly Leu Glu Gln Leu Glu Asn Phe Val Gln Gly Leu Arg Gly
 195 200 205
 Gly Val Val Leu Val Ser His Asp Arg Glu Phe Leu Ser Arg Cys Val
 210 215 220
 Thr Thr Val Leu Glu Leu Asp Leu His Gln Asn Ser His His Val Tyr
 225 230 235 240
 Gly Gly Gly Tyr Asp Ser Tyr Leu Glu Glu Arg Ala Val Leu Arg Gln
 245 250 255
 His Ala Arg Asp Gln Tyr Glu Glu Phe Ala Glu Lys Lys Lys Asp Leu
 260 265 270
 Val Ala Arg Ala Arg Thr Gln Arg Glu Trp Ser Ser His Gly Val Arg
 275 280 285
 Asn Ala Ile Lys Arg Ala Pro Asp Asn Asp Lys Leu Arg Lys Lys Ala
 290 295 300
 Ala Ala Glu Ser Ser Glu Lys Gln Ala Gln Lys Val Arg Gln Met Glu
 305 310 315 320
 Ser Arg Ile Ala Arg Leu Glu Glu Val Glu Glu Pro Arg Lys Glu Trp
 325 330 335
 Lys Leu Gln Phe Ser Val Gly Lys Ala Ser Arg Ser Ser Ser Val Val
 340 345 350
 Ser Thr Leu Asn Asp Ala Ser Phe Thr Gln Gly Asp Phe Thr Leu Gly
 355 360 365
 Pro Val Ser Ile Gln Val Asn Ala Gly Asp Arg Ile Gly Ile Thr Gly
 370 375 380
 Pro Asn Gly Ala Gly Lys Ser Thr Leu Leu Arg Gly Leu Leu Gly Asn
 385 390 395 400
 Gln Glu Pro Thr Ser Gly Thr Ala Thr Met Gly Thr Ser Val Ala Ile
 405 410 415
 Gly Glu Ile Asp Gln Ala Arg Ala Leu Leu Asp Pro Gln Leu Pro Leu
 420 425 430

Ile Ser Ala Phe Glu Lys His Val Pro Asp Leu Pro Ile Ser Glu Val
 435 440 445

Arg Thr Leu Leu Ala Lys Phe Gly Leu Asn Asp Asn His Val Glu Arg
 450 455 460

Asp Val Glu Lys Leu Ser Pro Gly Glu Arg Thr Arg Ala Gly Leu Ala
 465 470 475 480

Leu Leu Gln Val Arg Gly Val Asn Val Leu Val Leu Asp Glu Pro Thr
 485 490 495

Asn His Leu Asp Leu Glu Ala Ile Glu Gln Leu Glu Gln Ala Leu Ala
 500 505 510

Ser Tyr Asp Gly Val Leu Leu Leu Val Thr His Asp Arg Arg Met Leu
 515 520 525

Asp Ala Val Gln Thr Asn Arg Arg Trp His Val Glu Ala Gly Glu Val
 530 535 540

Arg Glu Leu
 545

<210> 87
 <211> 981
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(958)
 <223> RXA01185

<400> 87
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 Met Thr Asp Pro Glu
 1 5

aac tcg caa gga acc cca cag att tgt ccg act gat ccg act acg caa 163
 Asn Ser Gln Gly Thr Pro Gln Ile Cys Pro Thr Asp Pro Thr Thr Gln
 10 15 20

gca tta gca gtt cgg ggc tta acc aag tcc tat ggt gat gca aca gta 211
 Ala Leu Ala Val Arg Gly Leu Thr Lys Ser Tyr Gly Asp Ala Thr Val
 25 30 35

gtg aac aat atc aat ctg gac atc ccc aaa gga gcc att tac ggc atc 259
 Val Asn Asn Ile Asn Leu Asp Ile Pro Lys Gly Ala Ile Tyr Gly Ile
 40 45 50

gtt gga cct aat ggt gca ggt aaa acc acc atg ctg tcc atg gca acg 307
 Val Gly Pro Asn Gly Ala Gly Lys Thr Thr Met Leu Ser Met Ala Thr
 55 60 65

ggt tta ctg agg ccg aat aaa ggc acc gcg tgg att tcg ggt ttc aat 355
 Gly Leu Leu Arg Pro Asn Lys Gly Thr Ala Trp Ile Ser Gly Phe Asn
 70 75 80 85

gtg tgg gaa gag cca aac gat gca aaa cga agc atg gga ttg ttg gca 403
Val Trp Glu Glu Pro Asn Asp Ala Lys Arg Ser Met Gly Leu Leu Ala
90 95 100

gat ggc ttg ccc atc ttt gat cgc ttg act ggc aaa gaa ctg ctc aca 451
Asp Gly Leu Pro Ile Phe Asp Arg Leu Thr Gly Lys Glu Leu Leu Thr
105 110 115

tat gtc ggg gca ttg cgt gag ttg gat gaa ggc att gtt gat caa cgt 499
Tyr Val Gly Ala Leu Arg Glu Leu Asp Glu Gly Ile Val Asp Gln Arg
120 125 130

agt gag gaa ttg ctg gag gcc ctc ggg ctt aaa gaa gca gcg ggc aag 547
Ser Glu Glu Leu Leu Glu Ala Leu Gly Leu Lys Glu Ala Ala Gly Lys
135 140 145

aga gtc gtc gac tat tcc gcc ggc atg acg aag aag att ctt ttg gcc 595
Arg Val Val Asp Tyr Ser Ala Gly Met Thr Lys Lys Ile Leu Leu Ala
150 155 160 165

cag gcc ctc att cac aat ccg aaa gtg ctc atc ctt gat gaa cct ttg 643
Gln Ala Leu Ile His Asn Pro Lys Val Leu Ile Leu Asp Glu Pro Leu
170 175 180

gaa gcg gtt gat ccg gtg tct ggt cgt ttg att cag cag att ttg aag 691
Glu Ala Val Asp Pro Val Ser Gly Arg Leu Ile Gln Gln Ile Leu Lys
185 190 195

aac ttt gcg caa acg ggt gga acc gtc gtt ttg agt tcg cat gtc atg 739
Asn Phe Ala Gln Thr Gly Gly Thr Val Val Leu Ser Ser His Val Met
200 205 210

gaa ttg gtt gag ggg ttg tgc gat cac gtt gcc atc atc aac agg gga 787
Glu Leu Val Glu Gly Leu Cys Asp His Val Ala Ile Ile Asn Arg Gly
215 220 225

gtg gtg gag att gcc gga cat gtg aat gag gtt cgt cgg ggc aga tct 835
Val Val Glu Ile Ala Gly His Val Asn Glu Val Arg Arg Gly Arg Ser
230 235 240 245

tac cgg atg tct tcg tta atg cgg ttg aag gcg ctg ctc ttc aag agg 883
Tyr Arg Met Ser Ser Leu Met Arg Leu Lys Ala Leu Leu Phe Lys Arg
250 255 260

ggt cac tat ctt ggt tgg gtg cgt ccg aag gcc ata gcg aag gcc aaa 931
Gly His Tyr Leu Gly Trp Val Arg Pro Lys Ala Ile Ala Lys Ala Lys
265 270 275

atc aga acg agg atc ggg ctg agt aaa tgactaaaac acttctgaaa cta 981
Ile Arg Thr Arg Ile Gly Leu Ser Lys
280 285

<210> 88

<211> 286

<212> PRT

<213> Corynebacterium glutamicum

<400> 88

Met Thr Asp Pro Glu Asn Ser Gln Gly Thr Pro Gln Ile Cys Pro Thr

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Asp Pro Thr Thr Gln Ala Leu Ala Val Arg Gly Leu Thr Lys Ser Tyr	20	25	30
Gly Asp Ala Thr Val Val Asn Asn Ile Asn Leu Asp Ile Pro Lys Gly	35	40	45
Ala Ile Tyr Gly Ile Val Gly Pro Asn Gly Ala Gly Lys Thr Thr Met	50	55	60
Leu Ser Met Ala Thr Gly Leu Leu Arg Pro Asn Lys Gly Thr Ala Trp	65	70	75
Ile Ser Gly Phe Asn Val Trp Glu Glu Pro Asn Asp Ala Lys Arg Ser	85	90	95
Met Gly Leu Leu Ala Asp Gly Leu Pro Ile Phe Asp Arg Leu Thr Gly	100	105	110
Lys Glu Leu Leu Thr Tyr Val Gly Ala Leu Arg Glu Leu Asp Glu Gly	115	120	125
Ile Val Asp Gln Arg Ser Glu Glu Leu Leu Glu Ala Leu Gly Leu Lys	130	135	140
Glu Ala Ala Gly Lys Arg Val Val Asp Tyr Ser Ala Gly Met Thr Lys	145	150	155
Lys Ile Leu Leu Ala Gln Ala Leu Ile His Asn Pro Lys Val Leu Ile	165	170	175
Leu Asp Glu Pro Leu Glu Ala Val Asp Pro Val Ser Gly Arg Leu Ile	180	185	190
Gln Gln Ile Leu Lys Asn Phe Ala Gln Thr Gly Gly Thr Val Val Leu	195	200	205
Ser Ser His Val Met Glu Leu Val Glu Gly Leu Cys Asp His Val Ala	210	215	220
Ile Ile Asn Arg Gly Val Val Glu Ile Ala Gly His Val Asn Glu Val	225	230	235
Arg Arg Gly Arg Ser Tyr Arg Met Ser Ser Leu Met Arg Leu Lys Ala	245	250	255
Leu Leu Phe Lys Arg Gly His Tyr Leu Gly Trp Val Arg Pro Lys Ala	260	265	270
Ile Ala Lys Ala Lys Ile Arg Thr Arg Ile Gly Leu Ser Lys	275	280	285

<210> 89

<211> 1203

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1180)

<223> RXN00412

<400> 89

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cttttgtccc ccgacttttg tacgaatcga ggacaccgtc gtg tca cac acc gcg 115
Val Ser His Thr Ala
1 5

tcc aca ccg acg cca gag gaa tac tcc gcg cag caa ccc agc acc cag 163
Ser Thr Pro Thr Pro Glu Glu Tyr Ser Ala Gln Gln Pro Ser Thr Gln
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ggc act cgc gtt gag ttc cgc ggc ata acc aaa gtc ttt agc aac aat 211
Gly Thr Arg Val Glu Phe Arg Gly Ile Thr Lys Val Phe Ser Asn Asn
25 30 35

aaa tct gct aaa acc acc gcg ctt gat aat gtc act ctc acc gta gaa 259
Lys Ser Ala Lys Thr Thr Ala Leu Asp Asn Val Thr Leu Thr Val Glu
40 45 50

ccc ggt gag gta atc ggc atc atc ggt tac tct ggc gcc ggc aag tcc 307
Pro Gly Glu Val Ile Gly Ile Ile Gly Tyr Ser Gly Ala Gly Lys Ser
55 60 65

act ctt gtc cgc ctc atc aat ggc ctt gac tcc ccc acg agc ggt tcg 355
Thr Leu Val Arg Leu Ile Asn Gly Leu Asp Ser Pro Thr Ser Gly Ser
70 75 80 85

ttg ctg ctc aac ggc acc gac atc gtc gga atg ccc gag tct aag ctg 403
Leu Leu Leu Asn Gly Thr Asp Ile Val Gly Met Pro Glu Ser Lys Leu
90 95 100

cgt aaa ctg cgc agt aat atc ggc atg att ttc cag cag ttc aac ctg 451
Arg Lys Leu Arg Ser Asn Ile Gly Met Ile Phe Gln Gln Phe Asn Leu
105 110 115

ttc cag tcg cgt act gcg gct gga aat gtg gag tac ccg ctg gaa gtt 499
Phe Gln Ser Arg Thr Ala Ala Gly Asn Val Glu Tyr Pro Leu Glu Val
120 125 130

gcc aag atg gac aag gca gct cgt aaa gct cgc gtg caa gaa atg ctc 547
Ala Lys Met Asp Lys Ala Ala Arg Lys Ala Arg Val Gln Glu Met Leu
135 140 145

gag ttc gtc ggc ctg ggc gac aaa ggc aaa aac tac ccc gag cag ctg 595
Glu Phe Val Gly Leu Gly Asp Lys Gly Lys Asn Tyr Pro Glu Gln Leu
150 155 160 165

tcg ggc ggc cag aag cag cgc gtc ggc att gcc cgt gca ctg gcc acc 643
Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala Arg Ala Leu Ala Thr
170 175 180

aat cca acg ctt ttg ctt gcc gac gaa gcc acc tcc gct ttg gac cca 691
Asn Pro Thr Leu Leu Leu Ala Asp Glu Ala Thr Ser Ala Leu Asp Pro
185 190 195

gaa acc acc cat gaa gtt ctg gag ctg ctg cgc aag gta aac cgc gaa 739
Glu Thr Thr His Glu Val Leu Glu Leu Leu Arg Lys Val Asn Arg Glu
200 205 210

ctg ggc atc acc atc gtt gtg atc acc cac gaa atg gaa gtt gtg cgt 787
 Leu Gly Ile Thr Ile Val Val Ile Thr His Glu Met Glu Val Val Arg
 215 220 225

tcc atc gca gac aag gtt gct gtg atg gaa tcc ggc aaa gtt gtg gaa 835
 Ser Ile Ala Asp Lys Val Ala Val Met Glu Ser Gly Lys Val Val Glu
 230 235 240 245

tac ggc agc gtc tac gag gtg ttc tcc aat cca caa aca cag gtt gct 883
 Tyr Gly Ser Val Tyr Glu Val Phe Ser Asn Pro Gln Thr Gln Val Ala
 250 255 260

caa aag ttc gtg gcc acc gcg ctg cgt aac acc cca gac caa gtg gaa 931
 Gln Lys Phe Val Ala Thr Ala Leu Arg Asn Thr Pro Asp Gln Val Glu
 265 270 275

tcg gaa gat ctg ctt agc cat gag gga cgt ctg ttc acc att gat ctg 979
 Ser Glu Asp Leu Leu Ser His Glu Gly Arg Leu Phe Thr Ile Asp Leu
 280 285 290

act gaa acg tcc ggc ttc ttt gca gca acc gct cgt gct gcc gaa caa 1027
 Thr Glu Thr Ser Gly Phe Phe Ala Ala Thr Ala Arg Ala Ala Glu Gln
 295 300 305

ggt gct ttt gtc aac atc gtt cac ggt ggc gtg acc acc ttg caa cgc 1075
 Gly Ala Phe Val Asn Ile Val His Gly Gly Val Thr Thr Leu Gln Arg
 310 315 320 325

caa tca ttt ggc aaa atg act gtt cga ctc acc ggc aac acc gct gcg 1123
 Gln Ser Phe Gly Lys Met Thr Val Arg Leu Thr Gly Asn Thr Ala Ala
 330 335 340

att gaa gag ttc tat caa acc ttg acc aag acc acg acc atc aag gag 1171
 Ile Glu Glu Phe Tyr Gln Thr Leu Thr Lys Thr Thr Thr Ile Lys Glu
 345 350 355

atc acc cga tgaacgagat gatcctcgca gct 1203
 Ile Thr Arg
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<210> 90

<211> 360

<212> PRT

<213> Corynebacterium glutamicum

<400> 90

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Gln Pro Ser Thr Gln Gly Thr Arg Val Glu Phe Arg Gly Ile Thr Lys
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Val Phe Ser Asn Asn Lys Ser Ala Lys Thr Thr Ala Leu Asp Asn Val
 35 40 45

Thr Leu Thr Val Glu Pro Gly Glu Val Ile Gly Ile Ile Gly Tyr Ser
 50 55 60

Gly Ala Gly Lys Ser Thr Leu Val Arg Leu Ile Asn Gly Leu Asp Ser

65	70	75	80
Pro Thr Ser Gly Ser Leu Leu Leu Asn Gly Thr Asp Ile Val Gly Met	85	90	95
Pro Glu Ser Lys Leu Arg Lys Leu Arg Ser Asn Ile Gly Met Ile Phe	100	105	110
Gln Gln Phe Asn Leu Phe Gln Ser Arg Thr Ala Ala Gly Asn Val Glu	115	120	125
Tyr Pro Leu Glu Val Ala Lys Met Asp Lys Ala Ala Arg Lys Ala Arg	130	135	140
Val Gln Glu Met Leu Glu Phe Val Gly Leu Gly Asp Lys Gly Lys Asn	145	150	155
Tyr Pro Glu Gln Leu Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala	165	170	175
Arg Ala Leu Ala Thr Asn Pro Thr Leu Leu Leu Ala Asp Glu Ala Thr	180	185	190
Ser Ala Leu Asp Pro Glu Thr Thr His Glu Val Leu Glu Leu Leu Arg	195	200	205
Lys Val Asn Arg Glu Leu Gly Ile Thr Ile Val Val Ile Thr His Glu	210	215	220
Met Glu Val Val Arg Ser Ile Ala Asp Lys Val Ala Val Met Glu Ser	225	230	235
Gly Lys Val Val Glu Tyr Gly Ser Val Tyr Glu Val Phe Ser Asn Pro	245	250	255
Gln Thr Gln Val Ala Gln Lys Phe Val Ala Thr Ala Leu Arg Asn Thr	260	265	270
Pro Asp Gln Val Glu Ser Glu Asp Leu Leu Ser His Glu Gly Arg Leu	275	280	285
Phe Thr Ile Asp Leu Thr Glu Thr Ser Gly Phe Phe Ala Ala Thr Ala	290	295	300
Arg Ala Ala Glu Gln Gly Ala Phe Val Asn Ile Val His Gly Gly Val	305	310	315
Thr Thr Leu Gln Arg Gln Ser Phe Gly Lys Met Thr Val Arg Leu Thr	325	330	335
Gly Asn Thr Ala Ala Ile Glu Glu Phe Tyr Gln Thr Leu Thr Lys Thr	340	345	350
Thr Thr Ile Lys Glu Ile Thr Arg	355	360	

<210> 91

<211> 1203

<212> DNA

<213> Corynebacterium glutamicum

<223> FRXA00412

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Asn Pro Thr Leu Leu Ala Asp Glu Ala Thr Ser Ala Leu Asp Pro
185 190 195

gaa acc acc cat gaa gtt ctg gag ctg ctg cgc aag gta aac cgc gaa 739
 Glu Thr Thr His Glu Val Leu Glu Leu Leu Arg Lys Val Asn Arg Glu
 200 205 210

 ctg ggc atc acc atc gtt gtg atc acc cac gaa atg gaa gtt gtg cgt 787
 Leu Gly Ile Thr Ile Val Val Ile Thr His Glu Met Glu Val Val Arg
 215 220 225

 tcc atc gca gac aag gtt gct gtg atg gaa tcc ggc aaa gtt gtg gaa 835
 Ser Ile Ala Asp Lys Val Ala Val Met Glu Ser Gly Lys Val Val Glu
 230 235 240 245

 tac ggc agc gtc tac gag gtg ttc tcc aat cca caa aca cag gtt gct 883
 Tyr Gly Ser Val Tyr Glu Val Phe Ser Asn Pro Gln Thr Gln Val Ala
 250 255 260

 caa aag ttc gtg gcc acc gcg ctg cgt aac acc cca gac caa gtg gaa 931
 Gln Lys Phe Val Ala Thr Ala Leu Arg Asn Thr Pro Asp Gln Val Glu
 265 270 275

 tcg gaa gat ctg ctt agc cat gag gga cgt ctg ttc acc att gat ctg 979
 Ser Glu Asp Leu Leu Ser His Glu Gly Arg Leu Phe Thr Ile Asp Leu
 280 285 290

 act gaa acg tcc ggc ttc ttt gca gca acc gct cgt gct gcc gaa caa 1027
 Thr Glu Thr Ser Gly Phe Phe Ala Ala Thr Ala Arg Ala Ala Glu Gln
 295 300 305

 ggt gct ttt gtc aac atc gtt cac ggt ggc gtg acc acc ttg caa cgc 1075
 Gly Ala Phe Val Asn Ile Val His Gly Gly Val Thr Thr Leu Gln Arg
 310 315 320 325

 caa tca ttt ggc aaa atg act gtt cga ctc acc ggc aac acc gct gcg 1123
 Gln Ser Phe Gly Lys Met Thr Val Arg Leu Thr Gly Asn Thr Ala Ala
 330 335 340

 att gaa gag ttc tat caa acc ttg acc aag acc acg acc atc aag gag 1171
 Ile Glu Glu Phe Tyr Gln Thr Leu Thr Lys Thr Thr Thr Ile Lys Glu
 345 350 355

 atc acc cga tgaacgagat gatcctcgca gct 1203
 Ile Thr Arg
 360

<210> 92

<211> 360

<212> PRT

<213> Corynebacterium glutamicum

<400> 92

Val Ser His Thr Ala Ser Thr Pro Thr Pro Glu Glu Tyr Ser Ala Gln
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Gln Pro Ser Thr Gln Gly Thr Arg Val Glu Phe Arg Gly Ile Thr Lys
 20 25 30

Val Phe Ser Asn Asn Lys Ser Ala Lys Thr Thr Ala Leu Asp Asn Val
 35 40 45

Thr Leu Thr Val Glu Pro Gly Glu Val Ile Gly Ile Ile Gly Tyr Ser

50	55	60
Gly Ala Gly Lys Ser Thr Leu Val Arg Leu Ile Asn Gly Leu Asp Ser 65 70 75 80		
Pro Thr Ser Gly Ser Leu Leu Leu Asn Gly Thr Asp Ile Val Gly Met 85 90 95		
Pro Glu Ser Lys Leu Arg Lys Leu Arg Ser Asn Ile Gly Met Ile Phe 100 105 110		
Gln Gln Phe Asn Leu Phe Gln Ser Arg Thr Ala Ala Gly Asn Val Glu 115 120 125		
Tyr Pro Leu Glu Val Ala Lys Met Asp Lys Ala Ala Arg Lys Ala Arg 130 135 140		
Val Gln Glu Met Leu Glu Phe Val Gly Leu Gly Asp Lys Gly Lys Asn 145 150 155 160		
Tyr Pro Glu Gln Leu Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala 165 170 175		
Arg Ala Leu Ala Thr Asn Pro Thr Leu Leu Leu Ala Asp Glu Ala Thr 180 185 190		
Ser Ala Leu Asp Pro Glu Thr Thr His Glu Val Leu Glu Leu Leu Arg 195 200 205		
Lys Val Asn Arg Glu Leu Gly Ile Thr Ile Val Val Ile Thr His Glu 210 215 220		
Met Glu Val Val Arg Ser Ile Ala Asp Lys Val Ala Val Met Glu Ser 225 230 235 240		
Gly Lys Val Val Glu Tyr Gly Ser Val Tyr Glu Val Phe Ser Asn Pro 245 250 255		
Gln Thr Gln Val Ala Gln Lys Phe Val Ala Thr Ala Leu Arg Asn Thr 260 265 270		
Pro Asp Gln Val Glu Ser Glu Asp Leu Leu Ser His Glu Gly Arg Leu 275 280 285		
Phe Thr Ile Asp Leu Thr Glu Thr Ser Gly Phe Phe Ala Ala Thr Ala 290 295 300		
Arg Ala Ala Glu Gln Gly Ala Phe Val Asn Ile Val His Gly Gly Val 305 310 315 320		
Thr Thr Leu Gln Arg Gln Ser Phe Gly Lys Met Thr Val Arg Leu Thr 325 330 335		
Gly Asn Thr Ala Ala Ile Glu Glu Phe Tyr Gln Thr Leu Thr Lys Thr 340 345 350		
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<211> 2340
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(2317)
 <223> RXN02925

<400> 93

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                                         Met Ser Thr Pro His
                                         1           5

cac cac ggt gat cac ccc gct ccg gaa aca gac cac acc cac cac ccg 163
His His Gly Asp His Pro Ala Pro Glu Thr Asp His Thr His His Pro
              10              15              20

aat cat gcc ggt cac gag cac cat gcg gat gcc gcc acc cac ggc cag 211
Asn His Ala Gly His Glu His His Ala Asp Ala Ala Thr His Gly Gln
              25              30              35

gcc atg ccg cac gat cat ccg cat tcc act gtc gat gaa gaa cat cag 259
Ala Met Pro His Asp His Pro His Ser Thr Val Asp Glu Glu His Gln
              40              45              50

gtc cac agt cac ggt gaa cac gcc ggc cac agc gcc gcg atg ttc ccg 307
Val His Ser His Gly Glu His Ala Gly His Ser Ala Ala Met Phe Arg
              55              60              65

gac cgc ttc tgg tgg tcg ctg atc ctg tcg gtt ccg gtg gtg ttc ttc 355
Asp Arg Phe Trp Trp Ser Leu Ile Leu Ser Val Pro Val Val Phe Phe
              70              75              80              85

agc ccg atg ttc gcc gac ctg ctg gga tat aat att ccg gag att ccg 403
Ser Pro Met Phe Ala Asp Leu Leu Gly Tyr Asn Ile Pro Glu Ile Pro
              90              95              100

gga gcc tac tgg att cct ccg gtc ctg ggc acg atc atc ttc ctc tac 451
Gly Ala Tyr Trp Ile Pro Pro Val Leu Gly Thr Ile Ile Phe Leu Tyr
              105              110              115

ggc ggc acc ccc ttc ctc aag ggc gca atg acc gag ctg aaa tcc cgc 499
Gly Gly Thr Pro Phe Leu Lys Gly Ala Met Thr Glu Leu Lys Ser Arg
              120              125              130

caa ccg ggc atg atg ctc ctg atc gcc atg gcg atc acc gtg gcg ttt 547
Gln Pro Gly Met Met Leu Leu Ile Ala Met Ala Ile Thr Val Ala Phe
              135              140              145

atc gcc tcc tgg gtc acc acc ctg ggg ctg ggc ggc ttc cac cta gat 595
Ile Ala Ser Trp Val Thr Thr Leu Gly Leu Gly Gly Phe His Leu Asp
              150              155              160              165

ttc tgg tgg gaa ctg gcc ctg ctg gtg acc atc atg ctg ttg ggc cac 643
Phe Trp Trp Glu Leu Ala Leu Leu Val Thr Ile Met Leu Leu Gly His
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tgg ctg gag atg cgc gct ctt ggt gca gcc tcc tcc gcg ctt gac gcg 691

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Leu	Ala	Ala	Leu	Leu	Pro	Asp	Glu	Ala	Glu	Lys	Val	Val	Asp	Gly	Thr		
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acc	cgc	acc	gta	gcg	atc	tca	gag	ctg	gcc	gtc	gac	gat	gtc	gtg	ctg	787	
Thr	Arg	Thr	Val	Ala	Ile	Ser	Glu	Leu	Ala	Val	Asp	Asp	Val	Val	Leu		
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gtc	cga	gca	ggt	gcc	cgc	gtc	ccg	gcc	gac	ggg	acc	atc	atc	gac	gga	835	
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tac	cgg	gat	acc	ggt	gag	acc	gtg	gtg	gcc	ggc	acc	gtg	gcc	acc	gac	931	
Tyr	Arg	Asp	Thr	Gly	Glu	Thr	Val	Val	Ala	Gly	Thr	Val	Ala	Thr	Asp		
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Asn	Thr	Val	Arg	Ile	Arg	Val	Glu	Ala	Thr	Gly	Gly	Asp	Thr	Ala	Leu		
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gca	ggc	atc	cag	cgc	atg	gtc	gcc	gac	gcc	cag	gcc	tcc	tcc	tcc	cgg	1027	
Ala	Gly	Ile	Gln	Arg	Met	Val	Ala	Asp	Ala	Gln	Ala	Ser	Ser	Ser	Arg		
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Ala	Gln	Ala	Leu	Ala	Asp	Arg	Ala	Ala	Ala	Leu	Leu	Phe	Trp	Phe	Ala		
310					315					320					325		
ctg	atc	acg	gcc	ctg	atc	acc	gcc	gtg	gtc	tgg	acc	atc	atc	ggc	agc	1123	
Leu	Ile	Thr	Ala	Leu	Ile	Thr	Ala	Val	Val	Trp	Thr	Ile	Ile	Gly	Ser		
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ccc	gac	gat	gcc	gtg	gtc	cgc	gcg	gtg	acc	gtg	ctg	atc	atc	gcc	tgc	1171	
Pro	Asp	Asp	Ala	Val	Val	Arg	Ala	Val	Thr	Val	Leu	Ile	Ile	Ala	Cys		
			345				350						355				
ccg	cac	gcc	ctg	ggc	ctg	gcc	atc	ccg	ctg	gtc	atc	gcg	atc	tcc	tcc	1219	
Pro	His	Ala	Leu	Gly	Leu	Ala	Ile	Pro	Leu	Val	Ile	Ala	Ile	Ser	Ser		
			360			365						370					
gag	cgc	gcc	gcg	aaa	tcc	ggg	gtg	ctc	atc	aag	gac	cgc	atg	gca	ctc	1267	
Glu	Arg	Ala	Ala	Lys	Ser	Gly	Val	Leu	Ile	Lys	Asp	Arg	Met	Ala	Leu		
			375			380					385						
gag	cac	atg	cgc	acc	atc	gac	gtc	gtc	ttg	ttc	gat	aag	acc	ggc	acc	1315	
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390					395				400					405			
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Lys	Ile	Arg	Pro	Glu	Ser	Arg	Ala	Ala	Val	Arg	Ala	Leu	Gln	Ala	Arg	
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Pro	Gln	Asp	Lys	Asp	Thr	Lys	Val	Thr	Gln	Leu	Gln	Glu	Arg	Gly	Leu	
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tcg	atg	atc	gag	ctc	tcc	cat	gcc	agc	tac	cgc	aag	atg	gtc	cag	aac	2083
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Val Thr Pro Ile Phe Phe Trp Gly Gly Ser Pro Phe His Lys Ala Thr
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tcc gtc acc gac gtc acc gcc atc aac tac agc gaa acc gaa atc ctc Ser Val Thr Asp Val Thr Ala Ile Asn Tyr Ser Glu Thr Glu Ile Leu 470 475 480 485	1555
gaa ttc gct gca gcc gtc gag tcc gcc tcc gaa cac ccc atc gcc cag Glu Phe Ala Ala Ala Val Glu Ser Ala Ser Glu His Pro Ile Ala Gln 490 495 500	1603
gca atc gcc aag gcc gcc gaa cac gag caa gtc acc gac ttc caa aac Ala Ile Ala Lys Ala Ala Glu His Glu Gln Val Thr Asp Phe Gln Asn 505 510 515	1651
acc gca ggt cag gaa gtc acc ggt gta gtc cgc gga cac gag gtc cgc Thr Ala Gly Gln Glu Val Thr Gly Val Val Arg Gly His Glu Val Arg 520 525 530	1699
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caa cac gcc caa aaa atc ggc gga acc ccc gta gtc gtc acg att gac Gln His Ala Gln Lys Ile Gly Gly Thr Pro Val Val Val Thr Ile Asp 550 555 560 565	1795
ggc gta gat tcc gga ata atc acg gtc cgc gac acc gtc aaa gac acc Gly Val Asp Ser Gly Ile Ile Thr Val Arg Asp Thr Val Lys Asp Thr 570 575 580	1843
tcc gcc gaa gca atc cgc gga ctc aag gaa ctg gga ctc acc cca atc Ser Ala Glu Ala Ile Arg Gly Leu Lys Glu Leu Gly Leu Thr Pro Ile 585 590 595	1891
cta ctc acc gga gac aat gaa ggc gca gct aaa tcc gta gcc gct gaa Leu Leu Thr Gly Asp Asn Glu Gly Ala Ala Lys Ser Val Ala Ala Glu 600 605 610	1939
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caa aac gta gaa gcc ctc caa gca caa ggc aaa aac gtt gcg atg gtc Gln Asn Val Glu Ala Leu Gln Ala Gln Gly Lys Asn Val Ala Met Val 630 635 640 645	2035
ggc gac ggc gtc aac gat gcc gca gct ctt gcc caa gct gac ctc gga Gly Asp Gly Val Asn Asp Ala Ala Ala Leu Ala Gln Ala Asp Leu Gly 650 655 660	2083
ctc gcc atg gga gcc ggc acc gac gta gcc atc gaa gcc tcc gac atc Leu Ala Met Gly Ala Gly Thr Asp Val Ala Ile Glu Ala Ser Asp Ile 665 670 675	2131
acc ctc atg aac aac gac ctc cga tcc gca gtc gac gcc atc cga ctg Thr Leu Met Asn Asn Asp Leu Arg Ser Ala Val Asp Ala Ile Arg Leu 680 685 690	2179
tcc cgt aaa acc ctc ggc acc atc aag gga aac ctt ttc tgg gct ttc	2227

Ser Arg Lys Thr Leu Gly Thr Ile Lys Gly Asn Leu Phe Trp Ala Phe
 695 700 705
 gcc tac aat gtt gca cta atc cca gta gcg gcg atc gga ctc ctc aac 2275
 Ala Tyr Asn Val Ala Leu Ile Pro Val Ala Ala Ile Gly Leu Leu Asn
 710 715 720 725
 cca atg ctt gcc ggc att gcg atg gcc ttc agt tca gtt ttc gtc gtc 2323
 Pro Met Leu Ala Gly Ile Ala Met Ala Phe Ser Ser Val Phe Val Val
 730 735 740
 tcc aat tcc ttg cgt ctg cga gga ttc aaa gca agg agc aac 2365
 Ser Asn Ser Leu Arg Leu Arg Gly Phe Lys Ala Arg Ser Asn
 745 750 755
 taatgtccaa cagcgaatgc cac 2388

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 <213> Corynebacterium glutamicum

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 Val Glu Arg Lys Leu Asn Lys Leu Asp Gly Val Glu Ala Thr Val Asn
 35 40 45
 Tyr Ala Thr Glu Ser Ala Gln Val Ser Tyr Asp Pro Ser Lys Val Ser
 50 55 60
 Pro Glu Gln Leu Ile Lys Thr Val Glu Asp Thr Gly Tyr Gly Ala Phe
 65 70 75 80
 Thr Met Ala Ser Ala Ala Ala Glu Ser Glu Glu Asp Asn Ala Pro Ala
 85 90 95
 Asp Ser Gly Gln Ser Arg Ile Asp Ala Ala Arg Asp His Glu Ala Ala
 100 105 110
 Asp Leu Lys His Arg Val Ile Val Ser Ala Leu Leu Ser Val Pro Val
 115 120 125
 Val Leu Val Ser Met Ile Pro Ala Leu Gln Phe Asn Asn Trp Gln Trp
 130 135 140
 Ala Val Leu Thr Leu Val Thr Pro Ile Phe Phe Trp Gly Gly Ser Pro
 145 150 155 160
 Phe His Lys Ala Thr Trp Ala Asn Leu Lys Arg Gly Ser Phe Thr Met
 165 170 175
 Asn Thr Leu Val Ser Leu Gly Thr Ser Ala Ala Asp Leu Trp Ser Leu
 180 185 190
 Trp Ala Leu Phe Ile Glu Asn Ala Gly His Pro Gly Met Lys Met Glu

195					200					205					
Met	His	Leu	Leu	Pro	Ser	Ala	Ser	Thr	Met	Asp	Glu	Ile	Tyr	Leu	Glu
210						215					220				
Thr	Val	Ala	Val	Val	Ile	Thr	Phe	Leu	Leu	Leu	Gly	Arg	Trp	Phe	Glu
225					230					235					240
Thr	Lys	Ala	Lys	Gly	Gln	Ser	Ser	Glu	Ala	Leu	Arg	Lys	Leu	Leu	Asp
				245					250						255
Met	Gly	Ala	Lys	Asp	Ala	Val	Val	Leu	Arg	Asp	Gly	Ala	Glu	Val	Arg
			260					265					270		
Val	Pro	Val	Asn	Gln	Leu	Lys	Leu	Gly	Asp	Val	Phe	Ile	Thr	Arg	Pro
			275				280					285			
Gly	Glu	Lys	Ile	Ala	Thr	Asp	Gly	Glu	Val	Asp	Glu	Gly	Ser	Ser	Ala
	290					295					300				
Val	Asp	Glu	Ser	Met	Leu	Thr	Gly	Glu	Ser	Ile	Pro	Val	Glu	Val	Thr
305					310					315					320
Lys	Gly	Ser	Lys	Val	Thr	Gly	Ala	Thr	Leu	Asn	Thr	Ser	Gly	Arg	Leu
				325					330					335	
Met	Val	Lys	Val	Thr	Arg	Ile	Gly	Ala	Asp	Thr	Thr	Leu	Ser	Gln	Met
			340					345						350	
Ala	Lys	Leu	Val	Thr	Asp	Ala	Gln	Ser	Lys	Lys	Ala	Pro	Val	Gln	Arg
		355					360					365			
Leu	Val	Asp	Gln	Ile	Ser	Gln	Val	Phe	Val	Pro	Val	Val	Ile	Val	Ile
	370					375					380				
Ala	Ile	Ala	Thr	Leu	Ile	Ala	His	Leu	Val	Phe	Thr	Asp	Ala	Gly	Leu
385					390					395					400
Ala	Pro	Ala	Phe	Thr	Ala	Ala	Val	Ala	Val	Leu	Ile	Ile	Ala	Cys	Pro
				405				410						415	
Cys	Ala	Leu	Gly	Leu	Ala	Thr	Pro	Thr	Ala	Leu	Leu	Val	Gly	Thr	Gly
		420						425					430		
Arg	Gly	Ala	Gln	Leu	Gly	Leu	Leu	Ile	Lys	Gly	Pro	Glu	Ile	Leu	Glu
		435					440					445			
Ser	Thr	Lys	Lys	Val	Asp	Thr	Ile	Val	Leu	Asp	Lys	Thr	Gly	Thr	Val
	450					455					460				
Thr	Thr	Gly	Thr	Met	Ser	Val	Thr	Asp	Val	Thr	Ala	Ile	Asn	Tyr	Ser
465					470					475					480
Glu	Thr	Glu	Ile	Leu	Glu	Phe	Ala	Ala	Ala	Val	Glu	Ser	Ala	Ser	Glu
				485				490						495	
His	Pro	Ile	Ala	Gln	Ala	Ile	Ala	Lys	Ala	Ala	Glu	His	Glu	Gln	Val
			500					505					510		
Thr	Asp	Phe	Gln	Asn	Thr	Ala	Gly	Gln	Glu	Val	Thr	Gly	Val	Val	Arg
			515				520					525			

Gly His Glu Val Arg Val Gly Arg Pro Ser Ser Thr Leu Ile Asp Ala
 530 535 540
 Leu Leu His Pro Phe Gln His Ala Gln Lys Ile Gly Gly Thr Pro Val
 545 550 555 560
 Val Val Thr Ile Asp Gly Val Asp Ser Gly Ile Ile Thr Val Arg Asp
 565 570 575
 Thr Val Lys Asp Thr Ser Ala Glu Ala Ile Arg Gly Leu Lys Glu Leu
 580 585 590
 Gly Leu Thr Pro Ile Leu Leu Thr Gly Asp Asn Glu Gly Ala Ala Lys
 595 600 605
 Ser Val Ala Ala Glu Val Gly Ile Asp Gln Val Ile Ala Asn Val Leu
 610 615 620
 Pro His Glu Lys Val Gln Asn Val Glu Ala Leu Gln Ala Gln Gly Lys
 625 630 635 640
 Asn Val Ala Met Val Gly Asp Gly Val Asn Asp Ala Ala Ala Leu Ala
 645 650 655
 Gln Ala Asp Leu Gly Leu Ala Met Gly Ala Gly Thr Asp Val Ala Ile
 660 665 670
 Glu Ala Ser Asp Ile Thr Leu Met Asn Asn Asp Leu Arg Ser Ala Val
 675 680 685
 Asp Ala Ile Arg Leu Ser Arg Lys Thr Leu Gly Thr Ile Lys Gly Asn
 690 695 700
 Leu Phe Trp Ala Phe Ala Tyr Asn Val Ala Leu Ile Pro Val Ala Ala
 705 710 715 720
 Ile Gly Leu Leu Asn Pro Met Leu Ala Gly Ile Ala Met Ala Phe Ser
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 Ser Val Phe Val Val Ser Asn Ser Leu Arg Leu Arg Gly Phe Lys Ala
 740 745 750
 Arg Ser Asn
 755

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 <212> DNA
 <213> *Corynebacterium glutamicum*

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 <223> FRXA01323

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 cagtgagtca tgtaaacata ctgcagaag gagcgatccc atg gct cag aca ccc 115

	Met	Ala	Gln	Thr	Pro	
	1				5	
gcc aaa atc ccg gcg gca ctg aat ttc att gac gtc gac ctc ggc gtt						163
Ala Lys Ile Pro Ala Ala Leu Asn Phe Ile Asp Val Asp Leu Gly Val						
	10			15	20	
acc ggc atg acc tgc act tct tgc tcc gcc cgc gtc gag cgc aaa ctg						211
Thr Gly Met Thr Cys Thr Ser Cys Ser Ala Arg Val Glu Arg Lys Leu						
	25			30	35	
aac aag ctc gac ggc gtt gaa gca acc gtc aac tac gcg acg gaa tcc						259
Asn Lys Leu Asp Gly Val Glu Ala Thr Val Asn Tyr Ala Thr Glu Ser						
	40		45		50	
gca cag gtc agc tac gac ccc tca aag gtc agc cct gaa cag ctg att						307
Ala Gln Val Ser Tyr Asp Pro Ser Lys Val Ser Pro Glu Gln Leu Ile						
	55		60		65	
aag act gtt gag gac acc ggc tac ggt gct ttc acg atg gct tcc gca						355
Lys Thr Val Glu Asp Thr Gly Tyr Gly Ala Phe Thr Met Ala Ser Ala						
	70		75		80	85
gct gcc gaa tca gaa gag gac aac gct cca gct gac agc ggc cag tcc						403
Ala Ala Glu Ser Glu Glu Asp Asn Ala Pro Ala Asp Ser Gly Gln Ser						
	90			95		100
cgc atc gac gca gct cgc gac cac gaa gca gcc gac ctg aaa cac cgc						451
Arg Ile Asp Ala Ala Arg Asp His Glu Ala Ala Asp Leu Lys His Arg						
	105			110		115
gtg atc gtc tct gca ctg ttg tca gtt cct gtg gtt ttg gtc agc atg						499
Val Ile Val Ser Ala Leu Leu Ser Val Pro Val Val Leu Val Ser Met						
	120			125		130
atc ccg gcg ctg caa ttc aac aac tgg cag tgg gcc gta ctc act ttg						547
Ile Pro Ala Leu Gln Phe Asn Asn Trp Gln Trp Ala Val Leu Thr Leu						
	135			140		145
gtc acc ccg att ttc ttc tgg ggc ggt tca ccg ttc cac aag gca acg						595
Val Thr Pro Ile Phe Phe Trp Gly Gly Ser Pro Phe His Lys Ala Thr						
	150		155		160	165
tgg gca aac ctg aag cgc ggt tcc ttc acc atg aac acc ctg gtt tca						643
Trp Ala Asn Leu Lys Arg Gly Ser Phe Thr Met Asn Thr Leu Val Ser						
	170			175		180
ctc ggc acg tcc gct gct gac ctg tgg tcc ctg tgg gct ttg ttc att						691
Leu Gly Thr Ser Ala Ala Asp Leu Trp Ser Leu Trp Ala Leu Phe Ile						
	185			190		195
gaa aat gct ggt cac cct gcc atg aag atg gag atg cac ctg ctg ccg						739
Glu Asn Ala Gly His Pro Gly Met Lys Met Glu Met His Leu Leu Pro						
	200		205		210	
tcg gcc tcc acg atg gat gag att tac ctc gaa acc gtc gcg gtc gtt						787
Ser Ala Ser Thr Met Asp Glu Ile Tyr Leu Glu Thr Val Ala Val Val						
	215		220		225	
att acg ttc ctg ctg ctt gga cgc tgg ttt gag aca aaa gct aag ggc						835
Ile Thr Phe Leu Leu Leu Gly Arg Trp Phe Glu Thr Lys Ala Lys Gly						

230	235	240	245	
caa tct tcg gaa gct ctg cgc aag ctg ctg gac atg ggc gcc aaa gat				883
Gln Ser Ser Glu Ala Leu Arg Lys Leu Leu Asp Met Gly Ala Lys Asp	250	255	260	
gca gtc gtc tta cgt gac ggc gcc gaa gtc cgc gtt cct gtg aat cag				931
Ala Val Val Leu Arg Asp Gly Ala Glu Val Arg Val Pro Val Asn Gln	265	270	275	
ctt aaa ctc ggc gac gtt ttc atc acc cgc ccc ggc gag aaa atc gcc				979
Leu Lys Leu Gly Asp Val Phe Ile Thr Arg Pro Gly Glu Lys Ile Ala	280	285	290	
acc gac ggt gaa gtc gac gaa ggt tcc tcc gca gtc gac gaa tcc atg				1027
Thr Asp Gly Glu Val Asp Glu Gly Ser Ser Ala Val Asp Glu Ser Met	295	300	305	
ctc acc ggc gaa tcc atc ccc gtt gaa gtc acc aag ggc tcc aaa gtt				1075
Leu Thr Gly Glu Ser Ile Pro Val Glu Val Thr Lys Gly Ser Lys Val	310	315	320	325
acc ggc gca acg ctg aac act tcc ggc cgc ctc atg gtg aaa gta acc				1123
Thr Gly Ala Thr Leu Asn Thr Ser Gly Arg Leu Met Val Lys Val Thr	330	335	340	
cgc atc ggc gcc gac acc acc ctg tcg caa atg gct aaa ctg gtc acg				1171
Arg Ile Gly Ala Asp Thr Thr Leu Ser Gln Met Ala Lys Leu Val Thr	345	350	355	
gac gca cag tcc aaa aag gcc cct gtc cag cgt ctt gtt gac caa atc				1219
Asp Ala Gln Ser Lys Lys Ala Pro Val Gln Arg Leu Val Asp Gln Ile	360	365	370	
tcg cag gtt ttc gtt ccc gtt gtc atc gta att gct att gcg acg ctg				1267
Ser Gln Val Phe Val Pro Val Val Ile Val Ile Ala Ile Ala Thr Leu	375	380	385	
atc gcg cac ctc gtc ttc acc gac gcc ggc ctc gcc cca gca ttc acc				1315
Ile Ala His Leu Val Phe Thr Asp Ala Gly Leu Ala Pro Ala Phe Thr	390	395	400	405
gca gca gtc gcc gtc ctc att atc gcc tgc cct tgt gcc ctc ggc ctg				1363
Ala Ala Val Ala Val Leu Ile Ile Ala Cys Pro Cys Ala Leu Gly Leu	410	415	420	
gca acc cca acc gca ctt ctg gtc gga acc ggc cgc ggc gcg caa ctt				1411
Ala Thr Pro Thr Ala Leu Leu Val Gly Thr Gly Arg Gly Ala Gln Leu	425	430	435	
ggt ctg ttg atc aag ggc cct gaa atc ctc gaa tcc acc aaa aaa gtc				1459
Gly Leu Leu Ile Lys Gly Pro Glu Ile Leu Glu Ser Thr Lys Lys Val	440	445	450	
gac acc atc gtc ctc gac aaa acc ggc acc gtc acc acc ggc acc atg				1507
Asp Thr Ile Val Leu Asp Lys Thr Gly Thr Val Thr Thr Gly Thr Met	455	460	465	
tcc gtc acc gac gtc acc gcc atc aac tac agc gaa acc gaa atc ctc				1555
Ser Val Thr Asp Val Thr Ala Ile Asn Tyr Ser Glu Thr Glu Ile Leu	470	475	480	485

gaa ttc gct gca gcc gtc gag tcc gcc tcc gaa cac ccc atc gcc cag Glu Phe Ala Ala Ala Val Glu Ser Ala Ser Glu His Pro Ile Ala Gln 490 495 500	1603
gca atc gcc aag gcc gcc gaa cac gag caa gtc acc gac ttc caa aac Ala Ile Ala Lys Ala Ala Glu His Glu Gln Val Thr Asp Phe Gln Asn 505 510 515	1651
acc gca ggt cag gaa gtc acc ggt gta gtc cgc gga cac gag gtc cgc Thr Ala Gly Gln Glu Val Thr Gly Val Val Arg Gly His Glu Val Arg 520 525 530	1699
gtg ggc agg cct tca agc acg ctt atc gac gcc ctc ctc cac ccc ttc Val Gly Arg Pro Ser Ser Thr Leu Ile Asp Ala Leu Leu His Pro Phe 535 540 545	1747
caa cac gcc caa aaa atc ggc gga acc ccc gta gtc gtc acg att gac Gln His Ala Gln Lys Ile Gly Gly Thr Pro Val Val Val Thr Ile Asp 550 555 560 565	1795
ggc gta gat tcc gga ata atc acg gtc cgc gac acc gtc aaa gac acc Gly Val Asp Ser Gly Ile Ile Thr Val Arg Asp Thr Val Lys Asp Thr 570 575 580	1843
tcc gcc gaa gca atc cgc gga ctc aag gaa ctg gga ctc acc cca atc Ser Ala Glu Ala Ile Arg Gly Leu Lys Glu Leu Gly Leu Thr Pro Ile 585 590 595	1891
cta ctc acc gga gac aat gaa ggc gca gct aaa tcc gta gcc gct gaa Leu Leu Thr Gly Asp Asn Glu Gly Ala Ala Lys Ser Val Ala Ala Glu 600 605 610	1939
gtc ggc atc gac caa gtc atc gcc aac gtc ctc ccc cac gaa aaa gtc Val Gly Ile Asp Gln Val Ile Ala Asn Val Leu Pro His Glu Lys Val 615 620 625	1987
caa aac gta gaa gcc ctc caa gca caa ggc aaa aac gtt gcg atg gtc Gln Asn Val Glu Ala Leu Gln Ala Gln Gly Lys Asn Val Ala Met Val 630 635 640 645	2035
ggc gac ggc gtc aac gat gcc gca gct ctt gcc caa gct gac ctc gga Gly Asp Gly Val Asn Asp Ala Ala Ala Leu Ala Gln Ala Asp Leu Gly 650 655 660	2083
ctc gcc atg gga gcc ggc acc gac gta gcc atc gaa gcc tcc gac atc Leu Ala Met Gly Ala Gly Thr Asp Val Ala Ile Glu Ala Ser Asp Ile 665 670 675	2131
acc ctc atg aac aac gac ctc cga tcc gca gtc gac gcc atc cga ctg Thr Leu Met Asn Asn Asp Leu Arg Ser Ala Val Asp Ala Ile Arg Leu 680 685 690	2179
tcc cgt aaa acc ctc ggc acc atc aag gga aac ctt ttc tgg gct ttc Ser Arg Lys Thr Leu Gly Thr Ile Lys Gly Asn Leu Phe Trp Ala Phe 695 700 705	2227
gcc tac aat gtt gca cta atc cca gta gcg gcg atc gga ctc ctc aac Ala Tyr Asn Val Ala Leu Ile Pro Val Ala Ala Ile Gly Leu Leu Asn 710 715 720 725	2275

cca atg ctt gcc ggc att gcg atg gcc ttc agt tca gtt ttc gtc gtc 2323
 Pro Met Leu Ala Gly Ile Ala Met Ala Phe Ser Ser Val Phe Val Val
 730 735 740

tcc aat tcc ttg cgt ctg cga gga ttc aaa gca agg agc aac 2365
 Ser Asn Ser Leu Arg Leu Arg Gly Phe Lys Ala Arg Ser Asn
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taatgtccaa cagcgaatgc cac 2388

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<211> 755

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 102

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 20 25 30

Val Glu Arg Lys Leu Asn Lys Leu Asp Gly Val Glu Ala Thr Val Asn
 35 40 45

Tyr Ala Thr Glu Ser Ala Gln Val Ser Tyr Asp Pro Ser Lys Val Ser
 50 55 60

Pro Glu Gln Leu Ile Lys Thr Val Glu Asp Thr Gly Tyr Gly Ala Phe
 65 70 75 80

Thr Met Ala Ser Ala Ala Ala Glu Ser Glu Glu Asp Asn Ala Pro Ala
 85 90 95

Asp Ser Gly Gln Ser Arg Ile Asp Ala Ala Arg Asp His Glu Ala Ala
 100 105 110

Asp Leu Lys His Arg Val Ile Val Ser Ala Leu Leu Ser Val Pro Val
 115 120 125

Val Leu Val Ser Met Ile Pro Ala Leu Gln Phe Asn Asn Trp Gln Trp
 130 135 140

Ala Val Leu Thr Leu Val Thr Pro Ile Phe Phe Trp Gly Gly Ser Pro
 145 150 155 160

Phe His Lys Ala Thr Trp Ala Asn Leu Lys Arg Gly Ser Phe Thr Met
 165 170 175

Asn Thr Leu Val Ser Leu Gly Thr Ser Ala Ala Asp Leu Trp Ser Leu
 180 185 190

Trp Ala Leu Phe Ile Glu Asn Ala Gly His Pro Gly Met Lys Met Glu
 195 200 205

Met His Leu Leu Pro Ser Ala Ser Thr Met Asp Glu Ile Tyr Leu Glu
 210 215 220

Thr Val Ala Val Val Ile Thr Phe Leu Leu Leu Gly Arg Trp Phe Glu
 225 230 235 240

Thr Lys Ala Lys Gly Gln Ser Ser Glu Ala Leu Arg Lys Leu Leu Asp
 245 250 255
 Met Gly Ala Lys Asp Ala Val Val Leu Arg Asp Gly Ala Glu Val Arg
 260 265 270
 Val Pro Val Asn Gln Leu Lys Leu Gly Asp Val Phe Ile Thr Arg Pro
 275 280 285
 Gly Glu Lys Ile Ala Thr Asp Gly Glu Val Asp Glu Gly Ser Ser Ala
 290 295 300
 Val Asp Glu Ser Met Leu Thr Gly Glu Ser Ile Pro Val Glu Val Thr
 305 310 315 320
 Lys Gly Ser Lys Val Thr Gly Ala Thr Leu Asn Thr Ser Gly Arg Leu
 325 330 335
 Met Val Lys Val Thr Arg Ile Gly Ala Asp Thr Thr Leu Ser Gln Met
 340 345 350
 Ala Lys Leu Val Thr Asp Ala Gln Ser Lys Lys Ala Pro Val Gln Arg
 355 360 365
 Leu Val Asp Gln Ile Ser Gln Val Phe Val Pro Val Val Ile Val Ile
 370 375 380
 Ala Ile Ala Thr Leu Ile Ala His Leu Val Phe Thr Asp Ala Gly Leu
 385 390 395 400
 Ala Pro Ala Phe Thr Ala Ala Val Ala Val Leu Ile Ile Ala Cys Pro
 405 410 415
 Cys Ala Leu Gly Leu Ala Thr Pro Thr Ala Leu Leu Val Gly Thr Gly
 420 425 430
 Arg Gly Ala Gln Leu Gly Leu Leu Ile Lys Gly Pro Glu Ile Leu Glu
 435 440 445
 Ser Thr Lys Lys Val Asp Thr Ile Val Leu Asp Lys Thr Gly Thr Val
 450 455 460
 Thr Thr Gly Thr Met Ser Val Thr Asp Val Thr Ala Ile Asn Tyr Ser
 465 470 475 480
 Glu Thr Glu Ile Leu Glu Phe Ala Ala Ala Val Glu Ser Ala Ser Glu
 485 490 495
 His Pro Ile Ala Gln Ala Ile Ala Lys Ala Ala Glu His Glu Gln Val
 500 505 510
 Thr Asp Phe Gln Asn Thr Ala Gly Gln Glu Val Thr Gly Val Val Arg
 515 520 525
 Gly His Glu Val Arg Val Gly Arg Pro Ser Ser Thr Leu Ile Asp Ala
 530 535 540
 Leu Leu His Pro Phe Gln His Ala Gln Lys Ile Gly Gly Thr Pro Val
 545 550 555 560

Val Val Thr Ile Asp Gly Val Asp Ser Gly Ile Ile Thr Val Arg Asp
 565 570 575

Thr Val Lys Asp Thr Ser Ala Glu Ala Ile Arg Gly Leu Lys Glu Leu
 580 585 590

Gly Leu Thr Pro Ile Leu Leu Thr Gly Asp Asn Glu Gly Ala Ala Lys
 595 600 605

Ser Val Ala Ala Glu Val Gly Ile Asp Gln Val Ile Ala Asn Val Leu
 610 615 620

Pro His Glu Lys Val Gln Asn Val Glu Ala Leu Gln Ala Gln Gly Lys
 625 630 635 640

Asn Val Ala Met Val Gly Asp Gly Val Asn Asp Ala Ala Ala Leu Ala
 645 650 655

Gln Ala Asp Leu Gly Leu Ala Met Gly Ala Gly Thr Asp Val Ala Ile
 660 665 670

Glu Ala Ser Asp Ile Thr Leu Met Asn Asn Asp Leu Arg Ser Ala Val
 675 680 685

Asp Ala Ile Arg Leu Ser Arg Lys Thr Leu Gly Thr Ile Lys Gly Asn
 690 695 700

Leu Phe Trp Ala Phe Ala Tyr Asn Val Ala Leu Ile Pro Val Ala Ala
 705 710 715 720

Ile Gly Leu Leu Asn Pro Met Leu Ala Gly Ile Ala Met Ala Phe Ser
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Ser Val Phe Val Val Ser Asn Ser Leu Arg Leu Arg Gly Phe Lys Ala
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Arg Ser Asn
 755

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 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1807)
 <223> RXN00702

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 Met Ser Ala Pro Phe
 1 5

agc gcg cgc act gcg tgg tcg acg gac ccc gtg ctg gaa ctg gaa agc 163
 Ser Ala Arg Thr Ala Trp Ser Thr Asp Pro Val Leu Glu Leu Glu Ser
 10 15 20

gtc gct gcc tcg tat tat gac gat gag cgc acg ctg gcg gcg ccg cag	211
Val Ala Ala Ser Tyr Tyr Asp Asp Glu Arg Thr Leu Ala Ala Pro Gln	
25 30 35	
atc agc gac gtg aat ctg acg ctt ttt gaa ggc gaa atc ctg ctg gtt	259
Ile Ser Asp Val Asn Leu Thr Leu Phe Glu Gly Glu Ile Leu Leu Val	
40 45 50	
gtg ggg cgc acc ggc tcc ggc aaa tcg acg ctg ctg aac gcg atg tcc	307
Val Gly Arg Thr Gly Ser Gly Lys Ser Thr Leu Leu Asn Ala Met Ser	
55 60 65	
ggc gcg atg ccg cat gcg acc ggc ggc cga ctt gat ggg cgc gtg cgc	355
Gly Ala Met Pro His Ala Thr Gly Gly Arg Leu Asp Gly Arg Val Arg	
70 75 80 85	
gtg gtc ggc cgg gat acg cgt gat ttc cca cca cgc atg ctt tcc gac	403
Val Val Gly Arg Asp Thr Arg Asp Phe Pro Pro Arg Met Leu Ser Asp	
90 95 100	
gtg gtc ggc gtc gtt ggg caa gat ccg gcg gca agt ttt atc acc aac	451
Val Val Gly Val Val Gly Gln Asp Pro Ala Ala Ser Phe Ile Thr Asn	
105 110 115	
acg gtt gaa gaa gaa ctt gcc tac agc atg gag caa tta ggg ctc cca	499
Thr Val Glu Glu Glu Leu Ala Tyr Ser Met Glu Gln Leu Gly Leu Pro	
120 125 130	
cct gcg gtc atg cgc aag cgc gta gag gaa acc ctt gat ctt tta ggc	547
Pro Ala Val Met Arg Lys Arg Val Glu Glu Thr Leu Asp Leu Leu Gly	
135 140 145	
atc gcg gag ctg cga tac gtg cca ttg gcg gaa cta tct ggt ggt gag	595
Ile Ala Glu Leu Arg Tyr Val Pro Leu Ala Glu Leu Ser Gly Gly Glu	
150 155 160 165	
cag cag cgc gtg gcg att ggc gcg gtg ctg acc act cgc ccc gcg ctg	643
Gln Gln Arg Val Ala Ile Gly Ala Val Leu Thr Thr Arg Pro Ala Leu	
170 175 180	
att atc ttg gat gaa cca acc agc gct ttg gac cct aat ggt gcc gag	691
Ile Ile Leu Asp Glu Pro Thr Ser Ala Leu Asp Pro Asn Gly Ala Glu	
185 190 195	
gat gtg ctg gca acc gta acc aag ctg gct cat gac ttg gcg atg acc	739
Asp Val Leu Ala Thr Val Thr Lys Leu Ala His Asp Leu Ala Met Thr	
200 205 210	
gta gtg ctt gct gaa cac cgc atc gag cgc gta ctg cag tac gtg gac	787
Val Val Leu Ala Glu His Arg Ile Glu Arg Val Leu Gln Tyr Val Asp	
215 220 225	
cgc gtg gcg cat gtg ggc gct gat ggg cac gtc act gtt ggg acg ccg	835
Arg Val Ala His Val Gly Ala Asp Gly His Val Thr Val Gly Thr Pro	
230 235 240 245	
gaa gaa atc atg gct gat tct gat gtg gca cca ccc att gtg gaa tta	883
Glu Glu Ile Met Ala Asp Ser Asp Val Ala Pro Pro Ile Val Glu Leu	
250 255 260	
gga cgc tgg gct ggc tgg gct ccc cta ccg cta tcg atc cgc gat gca	931

Gly Arg Trp Ala Gly Trp Ala Pro Leu Pro Leu Ser Ile Arg Asp Ala	
265 270 275	
cgc gca cac tcc gct gac atg cgc aaa cgc ctg tat cag cgt ggt tta	979
Arg Ala His Ser Ala Asp Met Arg Lys Arg Leu Tyr Gln Arg Gly Leu	
280 285 290	
gtg gtg aac aaa tta cac aac cac gct gtc cag cca ctt ttg atc gcc	1027
Val Val Asn Lys Leu His Asn His Ala Val Gln Pro Leu Leu Ile Ala	
295 300 305	
gaa gat atc atg gtt gat ttc ccc gaa atc cgt gcc gtt gac ggc gtg	1075
Glu Asp Ile Met Val Asp Phe Pro Glu Ile Arg Ala Val Asp Gly Val	
310 315 320 325	
aac ttg aat ctc aac tcc ggt gaa att acc gtg ctc atg ggc cga aac	1123
Asn Leu Asn Leu Asn Ser Gly Glu Ile Thr Val Leu Met Gly Arg Asn	
330 335 340	
ggc tgc gga aaa tca tcc ctg ctg tgg gct tta caa ggt tca ggg act	1171
Gly Cys Gly Lys Ser Ser Leu Leu Trp Ala Leu Gln Gly Ser Gly Thr	
345 350 355	
aga aat cag ggc tgc gtg cag gtg ctt gat gag gcc gcg gga ttt tgc	1219
Arg Asn Gln Gly Ser Val Gln Val Leu Asp Glu Ala Ala Gly Phe Ser	
360 365 370	
tgg aca gac ccc aaa act tta aag ccc gcc aag cgg cgc aat ctt gtg	1267
Trp Thr Asp Pro Lys Thr Leu Lys Pro Ala Lys Arg Arg Asn Leu Val	
375 380 385	
tcc atg gtt ccg caa aca ccg acc gat att ttg tat gaa tca acc gtg	1315
Ser Met Val Pro Gln Thr Pro Thr Asp Ile Leu Tyr Glu Ser Thr Val	
390 395 400 405	
cat gca gag ctc gca cgc tct gat aaa gat gcc gca gca ccc gcc ggc	1363
His Ala Glu Leu Ala Arg Ser Asp Lys Asp Ala Ala Ala Pro Ala Gly	
410 415 420	
acc acg cgg gaa atc ctg gat tca ctg gtc ccg aat atc ccg gac cat	1411
Thr Thr Arg Glu Ile Leu Asp Ser Leu Val Pro Asn Ile Pro Asp His	
425 430 435	
ctc cac cca cgt gat cta tca gaa ggc caa aag ctc tcc ctc gcg ctg	1459
Leu His Pro Arg Asp Leu Ser Glu Gly Gln Lys Leu Ser Leu Ala Leu	
440 445 450	
tcc atc caa ctc gcc gca aaa ccc cgc gtg gta ttt ttc gac gaa ccc	1507
Ser Ile Gln Leu Ala Ala Lys Pro Arg Val Val Phe Phe Asp Glu Pro	
455 460 465	
acc cgc ggc cta gac tac gac ggc aag aaa tcc ctc gcc cgc tcc ttc	1555
Thr Arg Gly Leu Asp Tyr Asp Gly Lys Lys Ser Leu Ala Arg Ser Phe	
470 475 480 485	
caa caa ctg gca gac gac ggc cac gcc att ttg gtg gtc acc cac gac	1603
Gln Gln Leu Ala Asp Asp Gly His Ala Ile Leu Val Val Thr His Asp	
490 495 500	
gtg gaa ttc tct gca ctg tgc gcc gac cga gtg ttg ttt atg gcc tct	1651
Val Glu Phe Ser Ala Leu Cys Ala Asp Arg Val Leu Phe Met Ala Ser	

505	510	515	
gga aag atc atc tcc gat ggc aca gcc gta gaa atc ctc ccc gca tca			1699
Gly Lys Ile Ile Ser Asp Gly Thr Ala Val Glu Ile Leu Pro Ala Ser			
520	525	530	
ccg gct tac gcc cca caa gtc gca aaa atc acc gcc ggc atc caa gag			1747
Pro Ala Tyr Ala Pro Gln Val Ala Lys Ile Thr Ala Gly Ile Gln Glu			
535	540	545	
gaa tca cac tgg ctc aca gtc tcg gcc gtg aaa gct gcg cta ggg cat			1795
Glu Ser His Trp Leu Thr Val Ser Ala Val Lys Ala Ala Leu Gly His			
550	555	560	565
ggt gaa atc tca tgatcaacgc catcacactc aag			1830
Gly Glu Ile Ser			

<210> 104

<211> 569

<212> PRT

<213> Corynebacterium glutamicum

<400> 104

Met Ser Ala Pro Phe Ser Ala Arg Thr Ala Trp Ser Thr Asp Pro Val			
1	5	10	15
Leu Glu Leu Glu Ser Val Ala Ala Ser Tyr Tyr Asp Asp Glu Arg Thr			
20	25	30	
Leu Ala Ala Pro Gln Ile Ser Asp Val Asn Leu Thr Leu Phe Glu Gly			
35	40	45	
Glu Ile Leu Leu Val Val Gly Arg Thr Gly Ser Gly Lys Ser Thr Leu			
50	55	60	
Leu Asn Ala Met Ser Gly Ala Met Pro His Ala Thr Gly Gly Arg Leu			
65	70	75	80
Asp Gly Arg Val Arg Val Val Gly Arg Asp Thr Arg Asp Phe Pro Pro			
85	90	95	
Arg Met Leu Ser Asp Val Val Gly Val Val Gly Gln Asp Pro Ala Ala			
100	105	110	
Ser Phe Ile Thr Asn Thr Val Glu Glu Glu Leu Ala Tyr Ser Met Glu			
115	120	125	
Gln Leu Gly Leu Pro Pro Ala Val Met Arg Lys Arg Val Glu Glu Thr			
130	135	140	
Leu Asp Leu Leu Gly Ile Ala Glu Leu Arg Tyr Val Pro Leu Ala Glu			
145	150	155	160
Leu Ser Gly Gly Glu Gln Gln Arg Val Ala Ile Gly Ala Val Leu Thr			
165	170	175	
Thr Arg Pro Ala Leu Ile Ile Leu Asp Glu Pro Thr Ser Ala Leu Asp			
180	185	190	

Pro Asn Gly Ala Glu Asp Val Leu Ala Thr Val Thr Lys Leu Ala His
 195 200 205
 Asp Leu Ala Met Thr Val Val Leu Ala Glu His Arg Ile Glu Arg Val
 210 215 220
 Leu Gln Tyr Val Asp Arg Val Ala His Val Gly Ala Asp Gly His Val
 225 230 235 240
 Thr Val Gly Thr Pro Glu Glu Ile Met Ala Asp Ser Asp Val Ala Pro
 245 250 255
 Pro Ile Val Glu Leu Gly Arg Trp Ala Gly Trp Ala Pro Leu Pro Leu
 260 265 270
 Ser Ile Arg Asp Ala Arg Ala His Ser Ala Asp Met Arg Lys Arg Leu
 275 280 285
 Tyr Gln Arg Gly Leu Val Val Asn Lys Leu His Asn His Ala Val Gln
 290 295 300
 Pro Leu Leu Ile Ala Glu Asp Ile Met Val Asp Phe Pro Glu Ile Arg
 305 310 315 320
 Ala Val Asp Gly Val Asn Leu Asn Leu Asn Ser Gly Glu Ile Thr Val
 325 330 335
 Leu Met Gly Arg Asn Gly Cys Gly Lys Ser Ser Leu Leu Trp Ala Leu
 340 345 350
 Gln Gly Ser Gly Thr Arg Asn Gln Gly Ser Val Gln Val Leu Asp Glu
 355 360 365
 Ala Ala Gly Phe Ser Trp Thr Asp Pro Lys Thr Leu Lys Pro Ala Lys
 370 375 380
 Arg Arg Asn Leu Val Ser Met Val Pro Gln Thr Pro Thr Asp Ile Leu
 385 390 395 400
 Tyr Glu Ser Thr Val His Ala Glu Leu Ala Arg Ser Asp Lys Asp Ala
 405 410 415
 Ala Ala Pro Ala Gly Thr Thr Arg Glu Ile Leu Asp Ser Leu Val Pro
 420 425 430
 Asn Ile Pro Asp His Leu His Pro Arg Asp Leu Ser Glu Gly Gln Lys
 435 440 445
 Leu Ser Leu Ala Leu Ser Ile Gln Leu Ala Ala Lys Pro Arg Val Val
 450 455 460
 Phe Phe Asp Glu Pro Thr Arg Gly Leu Asp Tyr Asp Gly Lys Lys Ser
 465 470 475 480
 Leu Ala Arg Ser Phe Gln Gln Leu Ala Asp Asp Gly His Ala Ile Leu
 485 490 495
 Val Val Thr His Asp Val Glu Phe Ser Ala Leu Cys Ala Asp Arg Val
 500 505 510
 Leu Phe Met Ala Ser Gly Lys Ile Ile Ser Asp Gly Thr Ala Val Glu

515

520

525

Ile Leu Pro Ala Ser Pro Ala Tyr Ala Pro Gln Val Ala Lys Ile Thr
 530 535 540

Ala Gly Ile Gln Glu Glu Ser His Trp Leu Thr Val Ser Ala Val Lys
 545 550 555 560

Ala Ala Leu Gly His Gly Glu Ile Ser
 565

<210> 105

<211> 1343

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1320)

<223> FRXA00702

<400> 105

tta ggg ctc cca cct gcg gtc atg cgc aag cgc gta gag gaa acc ctt 48
 Leu Gly Leu Pro Pro Ala Val Met Arg Lys Arg Val Glu Glu Thr Leu
 1 5 10 15

gat ctt tta ggc atc gcg gag ctg cga tac gtg cca ttg gcg gaa cta 96
 Asp Leu Leu Gly Ile Ala Glu Leu Arg Tyr Val Pro Leu Ala Glu Leu
 20 25 30

tct ggt ggt gag cag cag cgc gtg gcg att ggc gcg gtg ctg acc act 144
 Ser Gly Gly Glu Gln Gln Arg Val Ala Ile Gly Ala Val Leu Thr Thr
 35 40 45

cgc ccc gcg ctg att atc ttg gat gaa cca acc agc gct ttg gac cct 192
 Arg Pro Ala Leu Ile Ile Leu Asp Glu Pro Thr Ser Ala Leu Asp Pro
 50 55 60

aat ggt gcc gag gat gtg ctg gca acc gta acc aag ctg gct cat gac 240
 Asn Gly Ala Glu Asp Val Leu Ala Thr Val Thr Lys Leu Ala His Asp
 65 70 75 80

ttg gcg atg acc gta gtg ctt gct gaa cac cgc atc gag cgc gta ctg 288
 Leu Ala Met Thr Val Val Leu Ala Glu His Arg Ile Glu Arg Val Leu
 85 90 95

cag tac gtg gac cgc gtg gcg cat gtg ggc gct gat ggg cac gtc act 336
 Gln Tyr Val Asp Arg Val Ala His Val Gly Ala Asp Gly His Val Thr
 100 105 110

gtt ggg acg ccg gaa gaa atc atg gct gat tct gat gtg gca cca ccc 384
 Val Gly Thr Pro Glu Glu Ile Met Ala Asp Ser Asp Val Ala Pro Pro
 115 120 125

att gtg gaa tta gga cgc tgg gct ggc tgg gct ccc cta ccg cta tcg 432
 Ile Val Glu Leu Gly Arg Trp Ala Gly Trp Ala Pro Leu Pro Leu Ser
 130 135 140

atc cgc gat gca cgc gca cac tcc gct gac atg cgc aaa cgc ctg tat 480
 Ile Arg Asp Ala Arg Ala His Ser Ala Asp Met Arg Lys Arg Leu Tyr

145	150	155	160	
cag cgt ggt tta gtg gtg aac aaa tta cac aac cac gct gtc cag cca				528
Gln Arg Gly Leu Val Val Asn Lys Leu His Asn His Ala Val Gln Pro				
	165	170	175	
ctt ttg atc gcc gaa gat atc atg gtt gat ttc ccc gaa atc cgt gcc				576
Leu Leu Ile Ala Glu Asp Ile Met Val Asp Phe Pro Glu Ile Arg Ala				
	180	185	190	
gtt gac ggc gtg aac ttg aat ctc aac tcc ggt gaa att acc gtg ctc				624
Val Asp Gly Val Asn Leu Asn Leu Asn Ser Gly Glu Ile Thr Val Leu				
	195	200	205	
atg ggc cga aac ggc tgc gga aaa tca tcc ctg ctg tgg gct tta caa				672
Met Gly Arg Asn Gly Cys Gly Lys Ser Ser Leu Leu Trp Ala Leu Gln				
	210	215	220	
ggg tca ggg act aga aat cag ggc tgc gtg cag gtg ctt gat gag gcc				720
Gly Ser Gly Thr Arg Asn Gln Gly Ser Val Gln Val Leu Asp Glu Ala				
	225	230	235	240
gcg gga ttt tgc tgg aca gac ccc aaa act tta aag ccc gcc aag cgg				768
Ala Gly Phe Ser Trp Thr Asp Pro Lys Thr Leu Lys Pro Ala Lys Arg				
	245	250	255	
cgc aat ctt gtg tcc atg gtt ccg caa aca ccg acc gat att ttg tat				816
Arg Asn Leu Val Ser Met Val Pro Gln Thr Pro Thr Asp Ile Leu Tyr				
	260	265	270	
gaa tca acc gtg cat gca gag ctc gca cgc tct gat aaa gat gcc gca				864
Glu Ser Thr Val His Ala Glu Leu Ala Arg Ser Asp Lys Asp Ala Ala				
	275	280	285	
gca ccc gcc ggc acc acg cgg gaa atc ctg gat tca ctg gtc ccg aat				912
Ala Pro Ala Gly Thr Thr Arg Glu Ile Leu Asp Ser Leu Val Pro Asn				
	290	295	300	
atc ccg gac cat ctc cac cca cgt gat cta tca gaa ggc caa aag ctc				960
Ile Pro Asp His Leu His Pro Arg Asp Leu Ser Glu Gly Gln Lys Leu				
	305	310	315	320
tcc ctc gcg ctg tcc atc caa ctc gcc gca aaa ccc cgc gtg gta ttt				1008
Ser Leu Ala Leu Ser Ile Gln Leu Ala Ala Lys Pro Arg Val Val Phe				
	325	330	335	
ttc gac gaa ccc acc cgc ggc cta gac tac gac ggc aag aaa tcc ctc				1056
Phe Asp Glu Pro Thr Arg Gly Leu Asp Tyr Asp Gly Lys Lys Ser Leu				
	340	345	350	
gcc cgc tcc ttc caa caa ctc gca gac gac ggc cac gcc att ttg gtg				1104
Ala Arg Ser Phe Gln Gln Leu Ala Asp Asp Gly His Ala Ile Leu Val				
	355	360	365	
gtc acc cac gac gtg gaa ttc tct gca ctg tgc gcc gac cga gtg ttg				1152
Val Thr His Asp Val Glu Phe Ser Ala Leu Cys Ala Asp Arg Val Leu				
	370	375	380	
ttt atg gcc tct gga aag atc atc tcc gat ggc aca gcc gta gaa atc				1200
Phe Met Ala Ser Gly Lys Ile Ile Ser Asp Gly Thr Ala Val Glu Ile				
	385	390	395	400

ctc ccc gca tca ccg gct tac gcc cca caa gtc gca aaa atc acc gcc 1248
 Leu Pro Ala Ser Pro Ala Tyr Ala Pro Gln Val Ala Lys Ile Thr Ala
 405 410 415

ggc atc caa gag gaa tca cac tgg ctc aca gtc tcg gcc gtg aaa gct 1296
 Gly Ile Gln Glu Glu Ser His Trp Leu Thr Val Ser Ala Val Lys Ala
 420 425 430

gcg cta ggg cat ggt gaa atc tca tgatcaacgc catcacactc aag 1343
 Ala Leu Gly His Gly Glu Ile Ser
 435 440

<210> 106

<211> 440

<212> PRT

<213> Corynebacterium glutamicum

<400> 106

Leu Gly Leu Pro Pro Ala Val Met Arg Lys Arg Val Glu Glu Thr Leu
 1 5 10 15

Asp Leu Leu Gly Ile Ala Glu Leu Arg Tyr Val Pro Leu Ala Glu Leu
 20 25 30

Ser Gly Gly Glu Gln Gln Arg Val Ala Ile Gly Ala Val Leu Thr Thr
 35 40 45

Arg Pro Ala Leu Ile Ile Leu Asp Glu Pro Thr Ser Ala Leu Asp Pro
 50 55 60

Asn Gly Ala Glu Asp Val Leu Ala Thr Val Thr Lys Leu Ala His Asp
 65 70 75 80

Leu Ala Met Thr Val Val Leu Ala Glu His Arg Ile Glu Arg Val Leu
 85 90 95

Gln Tyr Val Asp Arg Val Ala His Val Gly Ala Asp Gly His Val Thr
 100 105 110

Val Gly Thr Pro Glu Glu Ile Met Ala Asp Ser Asp Val Ala Pro Pro
 115 120 125

Ile Val Glu Leu Gly Arg Trp Ala Gly Trp Ala Pro Leu Pro Leu Ser
 130 135 140

Ile Arg Asp Ala Arg Ala His Ser Ala Asp Met Arg Lys Arg Leu Tyr
 145 150 155 160

Gln Arg Gly Leu Val Val Asn Lys Leu His Asn His Ala Val Gln Pro
 165 170 175

Leu Leu Ile Ala Glu Asp Ile Met Val Asp Phe Pro Glu Ile Arg Ala
 180 185 190

Val Asp Gly Val Asn Leu Asn Leu Asn Ser Gly Glu Ile Thr Val Leu
 195 200 205

Met Gly Arg Asn Gly Cys Gly Lys Ser Ser Leu Leu Trp Ala Leu Gln
 210 215 220

Gly Ser Gly Thr Arg Asn Gln Gly Ser Val Gln Val Leu Asp Glu Ala
 225 230 235 240
 Ala Gly Phe Ser Trp Thr Asp Pro Lys Thr Leu Lys Pro Ala Lys Arg
 245 250 255
 Arg Asn Leu Val Ser Met Val Pro Gln Thr Pro Thr Asp Ile Leu Tyr
 260 265 270
 Glu Ser Thr Val His Ala Glu Leu Ala Arg Ser Asp Lys Asp Ala Ala
 275 280 285
 Ala Pro Ala Gly Thr Thr Arg Glu Ile Leu Asp Ser Leu Val Pro Asn
 290 295 300
 Ile Pro Asp His Leu His Pro Arg Asp Leu Ser Glu Gly Gln Lys Leu
 305 310 315 320
 Ser Leu Ala Leu Ser Ile Gln Leu Ala Ala Lys Pro Arg Val Val Phe
 325 330 335
 Phe Asp Glu Pro Thr Arg Gly Leu Asp Tyr Asp Gly Lys Lys Ser Leu
 340 345 350
 Ala Arg Ser Phe Gln Gln Leu Ala Asp Asp Gly His Ala Ile Leu Val
 355 360 365
 Val Thr His Asp Val Glu Phe Ser Ala Leu Cys Ala Asp Arg Val Leu
 370 375 380
 Phe Met Ala Ser Gly Lys Ile Ile Ser Asp Gly Thr Ala Val Glu Ile
 385 390 395 400
 Leu Pro Ala Ser Pro Ala Tyr Ala Pro Gln Val Ala Lys Ile Thr Ala
 405 410 415
 Gly Ile Gln Glu Glu Ser His Trp Leu Thr Val Ser Ala Val Lys Ala
 420 425 430
 Ala Leu Gly His Gly Glu Ile Ser
 435 440

<210> 107
 <211> 576
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(553)
 <223> RXN00828

<400> 107
 cgggtgatcac cgggccgaat ggcgctggaa aatccacact tgcgctgacc atgggtggat 60
 tgcttccgcg aaaagtgggc agctggaact ctctgacacg gtg cgc ggc ggc ctt 115
 Val Arg Gly Gly Leu
 1 5

aac acg ccc ccg cac aag tgg cgt tca gct gat cta gct gca cgt att 163
 Asn Thr Pro Pro His Lys Trp Arg Ser Ala Asp Leu Ala Ala Arg Ile
 10 15 20

ggc act gtc ttt cag gat cca gag cac caa ttt gtg gcg cgc act gtg 211
 Gly Thr Val Phe Gln Asp Pro Glu His Gln Phe Val Ala Arg Thr Val
 25 30 35

cgt gat gag cta gaa att ggg ccg aaa atc atg aaa gtc gat gca agc 259
 Arg Asp Glu Leu Glu Ile Gly Pro Lys Ile Met Lys Val Asp Ala Ser
 40 45 50

gag cgc atc gag gag ctg ctt gat cgt ttg cgc ctc cgc cac ttg gaa 307
 Glu Arg Ile Glu Glu Leu Leu Asp Arg Leu Arg Leu Arg His Leu Glu
 55 60 65

aac gcc aat ccg ttt acc ttg agt ggt gga gaa aag cgc cgc cta tct 355
 Asn Ala Asn Pro Phe Thr Leu Ser Gly Gly Glu Lys Arg Arg Leu Ser
 70 75 80 85

gtg gcg aca gcc ttg gtg gca gca ccg aaa ctt ctc att ttg gat gag 403
 Val Ala Thr Ala Leu Val Ala Ala Pro Lys Leu Leu Ile Leu Asp Glu
 90 95 100

cct acg ttt ggc caa gat ccc gag acc ttc aca gag ctg gtg acg atg 451
 Pro Thr Phe Gly Gln Asp Pro Glu Thr Phe Thr Glu Leu Val Thr Met
 105 110 115

ttg cgt gaa tta aca gac aac gga atc agc att gtg tcg gta acc cat 499
 Leu Arg Glu Leu Thr Asp Asn Gly Ile Ser Ile Val Ser Val Thr His
 120 125 130

gat cct gat ttc atc gca gcg ctg ggc gat cac cac att gag gtg agc 547
 Asp Pro Asp Phe Ile Ala Ala Leu Gly Asp His His Ile Glu Val Ser
 135 140 145

gcg aag tgaacctgct gatcaaaatt aat 576
 Ala Lys
 150

<210> 108

<211> 151

<212> PRT

<213> Corynebacterium glutamicum

<400> 108

Val Arg Gly Gly Leu Asn Thr Pro Pro His Lys Trp Arg Ser Ala Asp
 1 5 10 15

Leu Ala Ala Arg Ile Gly Thr Val Phe Gln Asp Pro Glu His Gln Phe
 20 25 30

Val Ala Arg Thr Val Arg Asp Glu Leu Glu Ile Gly Pro Lys Ile Met
 35 40 45

Lys Val Asp Ala Ser Glu Arg Ile Glu Glu Leu Leu Asp Arg Leu Arg
 50 55 60

Leu Arg His Leu Glu Asn Ala Asn Pro Phe Thr Leu Ser Gly Gly Glu
 65 70 75 80

Lys Arg Arg Leu Ser Val Ala Thr Ala Leu Val Ala Ala Pro Lys Leu
 85 90 95

Leu Ile Leu Asp Glu Pro Thr Phe Gly Gln Asp Pro Glu Thr Phe Thr
 100 105 110

Glu Leu Val Thr Met Leu Arg Glu Leu Thr Asp Asn Gly Ile Ser Ile
 115 120 125

Val Ser Val Thr His Asp Pro Asp Phe Ile Ala Ala Leu Gly Asp His
 130 135 140

His Ile Glu Val Ser Ala Lys
 145 150

<210> 109

<211> 392

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(369)

<223> FRXA00828

<400> 109

gag cac caa ttt gtg gcg cgc act gtg cgt gat gag cta gaa att ggt 48
 Glu His Gln Phe Val Ala Arg Thr Val Arg Asp Glu Leu Glu Ile Gly
 1 5 10 15

ccg aaa atc atg aaa gtt gat gca agc gag cgc atc gag gag ttg ctt 96
 Pro Lys Ile Met Lys Val Asp Ala Ser Glu Arg Ile Glu Glu Leu Leu
 20 25 30

gat cgg ttg cgc ctc cgc cac tta gaa aat gct aat ccg ttt acc ttg 144
 Asp Arg Leu Arg Leu Arg His Leu Glu Asn Ala Asn Pro Phe Thr Leu
 35 40 45

agt ggt gga gaa aag cgc cgc cta tct gtg gcg aca gcc ttg gtg gca 192
 Ser Gly Gly Glu Lys Arg Arg Leu Ser Val Ala Thr Ala Leu Val Ala
 50 55 60

gca ccg aaa ctt ctc att ttg gat gag cct acg ttt ggc caa gat ccc 240
 Ala Pro Lys Leu Leu Ile Leu Asp Glu Pro Thr Phe Gly Gln Asp Pro
 65 70 75 80

gag acc ttc aca gag ctg gtg acg atg ttg cgt gaa tta aca gac aac 288
 Glu Thr Phe Thr Glu Leu Val Thr Met Leu Arg Glu Leu Thr Asp Asn
 85 90 95

gga atc agc att gtg tca gta acc cat gat cct gat ttc atc gca gcg 336
 Gly Ile Ser Ile Val Ser Val Thr His Asp Pro Asp Phe Ile Ala Ala
 100 105 110

ctg ggc gat cac cac att gag gtg agc gcg aag tgaacctgct gatcaaaatt 389
 Leu Gly Asp His His Ile Glu Val Ser Ala Lys
 115 120

aat

392

<210> 110
 <211> 123
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 110
 Glu His Gln Phe Val Ala Arg Thr Val Arg Asp Glu Leu Glu Ile Gly
 1 5 10 15
 Pro Lys Ile Met Lys Val Asp Ala Ser Glu Arg Ile Glu Glu Leu Leu
 20 25 30
 Asp Arg Leu Arg Leu Arg His Leu Glu Asn Ala Asn Pro Phe Thr Leu
 35 40 45
 Ser Gly Gly Glu Lys Arg Arg Leu Ser Val Ala Thr Ala Leu Val Ala
 50 55 60
 Ala Pro Lys Leu Leu Ile Leu Asp Glu Pro Thr Phe Gly Gln Asp Pro
 65 70 75 80
 Glu Thr Phe Thr Glu Leu Val Thr Met Leu Arg Glu Leu Thr Asp Asn
 85 90 95
 Gly Ile Ser Ile Val Ser Val Thr His Asp Pro Asp Phe Ile Ala Ala
 100 105 110
 Leu Gly Asp His His Ile Glu Val Ser Ala Lys
 115 120

<210> 111
 <211> 703
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(703)
 <223> RXN03020

<400> 111
 cgccgcagca ggactcatcg gtgccgccat ttactcggc cccatccttc gcgtogaacc 60
 acgctccgca ctcatgaacg cataagaaaa ggaacctcac atg act ctc cac gtt 115
 Met Thr Leu His Val
 1 5
 tca aat ctc aat ctg acc gtc gcc gac gga tcc acc tca cgc acc ctg 163
 Ser Asn Leu Asn Leu Thr Val Ala Asp Gly Ser Thr Ser Arg Thr Leu
 10 15 20
 ctc aac aac ata cac ttt tgg atg tcc aac cag gcg aag tcg tcg gta 211
 Leu Asn Asn Ile His Phe Trp Met Ser Asn Gln Ala Lys Ser Ser Val
 25 30 35
 tca ccg gcc cat ccg gct ccg gaa aat cca ccc tac tcg ccg tcc tcg 259
 Ser Pro Ala His Pro Ala Pro Glu Asn Pro Pro Tyr Ser Pro Ser Ser
 40 45 50

gct gcc tcc aaa gcg ccc gat tcc ggc acc gcg acg ctc ggc gac atc 307
 Ala Ala Ser Lys Ala Pro Asp Ser Gly Thr Ala Thr Leu Gly Asp Ile
 55 60 65

gac ctg ctc aac ccc caa aac cga gct gct tta cga cgc aac cac cta 355
 Asp Leu Leu Asn Pro Gln Asn Arg Ala Ala Leu Arg Arg Asn His Leu
 70 75 80 85

gga att gtc ttc caa cag cca aac ctg ctc ccc tcg ttg act gtc ctc 403
 Gly Ile Val Phe Gln Gln Pro Asn Leu Leu Pro Ser Leu Thr Val Leu
 90 95 100

gac caa ctg ctg ctc att ccc cgg ctc ggc agg atc ctc ccg ccc agc 451
 Asp Gln Leu Leu Leu Ile Pro Arg Leu Gly Arg Ile Leu Pro Pro Ser
 105 110 115

cgc agc gca cgc acc caa cac aaa gac aaa gcc ctt tca ctt ctg aac 499
 Arg Ser Ala Arg Thr Gln His Lys Asp Lys Ala Leu Ser Leu Leu Asn
 120 125 130

tcc atc gga ctc ggc gac tta gca aaa cgc aag gtc agc gaa cta tcc 547
 Ser Ile Gly Leu Gly Asp Leu Ala Lys Arg Lys Val Ser Glu Leu Ser
 135 140 145

ggt gga caa caa gcc cgc gtt aac ttg gcc cgc gcg ctg atg aac tcc 595
 Gly Gly Gln Gln Ala Arg Val Asn Leu Ala Arg Ala Leu Met Asn Ser
 150 155 160 165

ccc aag ctc ctg ctt gtc gat gaa ccc acc gcc gcc ctc gat caa cat 643
 Pro Lys Leu Leu Leu Val Asp Glu Pro Thr Ala Ala Leu Asp Gln His
 170 175 180

tcc gcc agc gaa gtc acc gaa cta atc gtc tcg atg gcc cac caa tac 691
 Ser Ala Ser Glu Val Thr Glu Leu Ile Val Ser Met Ala His Gln Tyr
 185 190 195

aac gcc ccc aca 703
 Asn Ala Pro Thr
 200

<210> 112

<211> 201

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 112

Met Thr Leu His Val Ser Asn Leu Asn Leu Thr Val Ala Asp Gly Ser
 1 5 10 15

Thr Ser Arg Thr Leu Leu Asn Asn Ile His Phe Trp Met Ser Asn Gln
 20 25 30

Ala Lys Ser Ser Val Ser Pro Ala His Pro Ala Pro Glu Asn Pro Pro
 35 40 45

Tyr Ser Pro Ser Ser Ala Ala Ser Lys Ala Pro Asp Ser Gly Thr Ala
 50 55 60

Thr Leu Gly Asp Ile Asp Leu Leu Asn Pro Gln Asn Arg Ala Ala Leu

65	70	75	80
Arg Arg Asn His Leu Gly Ile Val Phe Gln Gln Pro Asn Leu Leu Pro	85	90	95
Ser Leu Thr Val Leu Asp Gln Leu Leu Leu Ile Pro Arg Leu Gly Arg	100	105	110
Ile Leu Pro Pro Ser Arg Ser Ala Arg Thr Gln His Lys Asp Lys Ala	115	120	125
Leu Ser Leu Leu Asn Ser Ile Gly Leu Gly Asp Leu Ala Lys Arg Lys	130	135	140
Val Ser Glu Leu Ser Gly Gly Gln Gln Ala Arg Val Asn Leu Ala Arg	145	150	155
Ala Leu Met Asn Ser Pro Lys Leu Leu Leu Val Asp Glu Pro Thr Ala	165	170	175
Ala Leu Asp Gln His Ser Ala Ser Glu Val Thr Glu Leu Ile Val Ser	180	185	190
Met Ala His Gln Tyr Asn Ala Pro Thr	195	200	

<210> 113

<211> 614

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(591)

<223> RXN00726

<400> 113

aac gcg ggt cgc ttg tat gtc gat ggc gat ctc att ggc tac cga gag	48
Asn Ala Gly Arg Leu Tyr Val Asp Gly Asp Leu Ile Gly Tyr Arg Glu	
1 5 10 15	
cgc gat ggc gtg ctg tac gaa atc tct gag aag gac gcc gcc aag cag	96
Arg Asp Gly Val Leu Tyr Glu Ile Ser Glu Lys Asp Ala Ala Lys Gln	
20 25 30	
cgc tcc gat atc ggc atg gtg ttc cag aac ttc aac ctc ttc ccc cac	144
Arg Ser Asp Ile Gly Met Val Phe Gln Asn Phe Asn Leu Phe Pro His	
35 40 45	
cgc acg gtg atc gag aac atc atc gaa gct ccc atc cac gtg aag aag	192
Arg Thr Val Ile Glu Asn Ile Ile Glu Ala Pro Ile His Val Lys Lys	
50 55 60	
cag ccc gaa agc aag gcc cgc gca cgt gcc atg gag ctg ctt gag cag	240
Gln Pro Glu Ser Lys Ala Arg Ala Arg Ala Met Glu Leu Leu Glu Gln	
65 70 75 80	
gtc ggc ctc gcc cac aag gcg gac gcc tac ccc gtc caa ctg tcg ggt	288
Val Gly Leu Ala His Lys Ala Asp Ala Tyr Pro Val Gln Leu Ser Gly	
85 90 95	

ggt cag cag cag cgc gtt gca att gcc cgc gcc gtc gcc atg gag cca 336
 Gly Gln Gln Gln Arg Val Ala Ile Ala Arg Ala Val Ala Met Glu Pro
 100 105 110
 aag ctc atg ctt ttc gac gaa ccc acc agc gct ttg gac cct gaa ctc 384
 Lys Leu Met Leu Phe Asp Glu Pro Thr Ser Ala Leu Asp Pro Glu Leu
 115 120 125
 gtc ggt gaa gtc ctg cga gtg atg aaa cag ctc gcc gac gac ggc atg 432
 Val Gly Glu Val Leu Arg Val Met Lys Gln Leu Ala Asp Asp Gly Met
 130 135 140
 acc atg ctt gtt gtc acc cac gaa atg ggc ttc gcc cac gaa gtc gcc 480
 Thr Met Leu Val Val Thr His Glu Met Gly Phe Ala His Glu Val Ala
 145 150 155 160
 gac cag gtc gtg ttc atg gcc gat gga gtt gtc gtt gaa gcc gga acc 528
 Asp Gln Val Val Phe Met Ala Asp Gly Val Val Val Glu Ala Gly Thr
 165 170 175
 ccc gaa caa gtt ctg gac aat cca aag gaa cag cgc acc aaa gac ttc 576
 Pro Glu Gln Val Leu Asp Asn Pro Lys Glu Gln Arg Thr Lys Asp Phe
 180 185 190
 ctg tct tct ctg ctc taaccttttc gggtcttaaa aaa 614
 Leu Ser Ser Leu Leu
 195

<210> 114

<211> 197

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 114

Asn Ala Gly Arg Leu Tyr Val Asp Gly Asp Leu Ile Gly Tyr Arg Glu
 1 5 10 15
 Arg Asp Gly Val Leu Tyr Glu Ile Ser Glu Lys Asp Ala Ala Lys Gln
 20 25 30
 Arg Ser Asp Ile Gly Met Val Phe Gln Asn Phe Asn Leu Phe Pro His
 35 40 45
 Arg Thr Val Ile Glu Asn Ile Ile Glu Ala Pro Ile His Val Lys Lys
 50 55 60
 Gln Pro Glu Ser Lys Ala Arg Ala Arg Ala Met Glu Leu Leu Glu Gln
 65 70 75 80
 Val Gly Leu Ala His Lys Ala Asp Ala Tyr Pro Val Gln Leu Ser Gly
 85 90 95
 Gly Gln Gln Gln Arg Val Ala Ile Ala Arg Ala Val Ala Met Glu Pro
 100 105 110
 Lys Leu Met Leu Phe Asp Glu Pro Thr Ser Ala Leu Asp Pro Glu Leu
 115 120 125
 Val Gly Glu Val Leu Arg Val Met Lys Gln Leu Ala Asp Asp Gly Met

130 135 140

Thr Met Leu Val Val Thr His Glu Met Gly Phe Ala His Glu Val Ala
 145 150 155 160

Asp Gln Val Val Phe Met Ala Asp Gly Val Val Val Glu Ala Gly Thr
 165 170 175

Pro Glu Gln Val Leu Asp Asn Pro Lys Glu Gln Arg Thr Lys Asp Phe
 180 185 190

Leu Ser Ser Leu Leu
 195

<210> 115
 <211> 765
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(742)
 <223> RXN02570

<400> 115
 ccattgttat gctcattgtg tttgtggtgg tcaagtcgct acccaagcgc accactaggg 60

cattgggttcc gcagcgggtt ccggaggacg tcgcttaaacc atg aat cct ttg aca 115
 Met Asn Pro Leu Thr
 1 5

tgg atc att ggc gca ttc agc atg tgg atc gtg gtg ctg ggc gtt aat 163
 Trp Ile Ile Gly Ala Phe Ser Met Trp Ile Val Val Leu Gly Val Asn
 10 15 20

aag ctt ggt tta agc atc gca gtg atc atc atc gcg cag gtc gtg gcg 211
 Lys Leu Gly Leu Ser Ile Ala Val Ile Ile Ile Ala Gln Val Val Ala
 25 30 35

atg att cgg gtg cgc aat gta tct gtg ttg gct tca aca gca ttg tta 259
 Met Ile Arg Val Arg Asn Val Ser Val Leu Ala Ser Thr Ala Leu Leu
 40 45 50

tcg gtt cct gca ttg gcc tcg atg gcg ctg att cac atg ccg tat tct 307
 Ser Val Pro Ala Leu Ala Ser Met Ala Leu Ile His Met Pro Tyr Ser
 55 60 65

tcc gac ggc tgg ttg att gct ctt acc ttg acg gct cgt ttt agt gcg 355
 Ser Asp Gly Trp Leu Ile Ala Leu Thr Leu Thr Ala Arg Phe Ser Ala
 70 75 80 85

ttg atg tct att ttc ctc ctt gca gca aca gcg att act att cct gag 403
 Leu Met Ser Ile Phe Leu Leu Ala Ala Thr Ala Ile Thr Ile Pro Glu
 90 95 100

ctg gtg aaa tcc cta tat cgt tgg ccc aag ctg gcg tat atc gtg ggt 451
 Leu Val Lys Ser Leu Tyr Arg Trp Pro Lys Leu Ala Tyr Ile Val Gly
 105 110 115

tct gca ttg cag atg att ccg cag ggt aaa cag acc ttg gcg ttg gtt 499

Ser Ala Leu Gln Met Ile Pro Gln Gly Lys Gln Thr Leu Ala Leu Val
 120 125 130

cgt gat gcc aat gct ttg cgc ggg cgc agc gtt aaa ggt ccc gtg cgc 547
 Arg Asp Ala Asn Ala Leu Arg Gly Arg Ser Val Lys Gly Pro Val Arg
 135 140 145

gcg gtg aaa tat gtg ggt ttg ccc ctg att aca cat tta ctt agt gca 595
 Ala Val Lys Tyr Val Gly Leu Pro Leu Ile Thr His Leu Leu Ser Ala
 150 155 160 165

ggt gcc gcg cga gcg att ccc ttg gag gtc gca ggc ctg gac agg ccg 643
 Gly Ala Ala Arg Ala Ile Pro Leu Glu Val Ala Gly Leu Asp Arg Pro
 170 175 180

ggg ccg cgt acg gtg ttg gtt gag gtg gtg gag ggg cgc gtc gaa aag 691
 Gly Pro Arg Thr Val Leu Val Glu Val Val Glu Gly Arg Val Glu Lys
 185 190 195

cat tgt cgc tgg ttg ttg ccg ctt ttg gca gtc ggg atg gcg tgg tgg 739
 His Cys Arg Trp Leu Leu Pro Leu Leu Ala Val Gly Met Ala Trp Trp
 200 205 210

ctc taactcaaat cgtcggaccg tcc 765
 Leu

<210> 116

<211> 214

<212> PRT

<213> Corynebacterium glutamicum

<400> 116

Met Asn Pro Leu Thr Trp Ile Ile Gly Ala Phe Ser Met Trp Ile Val
 1 5 10 15

Val Leu Gly Val Asn Lys Leu Gly Leu Ser Ile Ala Val Ile Ile Ile
 20 25 30

Ala Gln Val Val Ala Met Ile Arg Val Arg Asn Val Ser Val Leu Ala
 35 40 45

Ser Thr Ala Leu Leu Ser Val Pro Ala Leu Ala Ser Met Ala Leu Ile
 50 55 60

His Met Pro Tyr Ser Ser Asp Gly Trp Leu Ile Ala Leu Thr Leu Thr
 65 70 75 80

Ala Arg Phe Ser Ala Leu Met Ser Ile Phe Leu Leu Ala Ala Thr Ala
 85 90 95

Ile Thr Ile Pro Glu Leu Val Lys Ser Leu Tyr Arg Trp Pro Lys Leu
 100 105 110

Ala Tyr Ile Val Gly Ser Ala Leu Gln Met Ile Pro Gln Gly Lys Gln
 115 120 125

Thr Leu Ala Leu Val Arg Asp Ala Asn Ala Leu Arg Gly Arg Ser Val
 130 135 140

Lys Gly Pro Val Arg Ala Val Lys Tyr Val Gly Leu Pro Leu Ile Thr
 145 150 155 160
 His Leu Leu Ser Ala Gly Ala Ala Arg Ala Ile Pro Leu Glu Val Ala
 165 170 175
 Gly Leu Asp Arg Pro Gly Pro Arg Thr Val Leu Val Glu Val Val Glu
 180 185 190
 Gly Arg Val Glu Lys His Cys Arg Trp Leu Leu Pro Leu Leu Ala Val
 195 200 205
 Gly Met Ala Trp Trp Leu
 210

<210> 117
 <211> 957
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(934)
 <223> RXN02354

<400> 117
 gaataaagaa aaagaaactg ggcggaacca aggatgagaa acccaccgct aaggatgctg 60
 ttgtaaaggc cgattctgct gtgaaggaag ccgctaagcc atg act aaa cga aca 115
 Met Thr Lys Arg Thr
 1 5
 aaa gga ctc atc ctc aac tac gcc gga gtg gtg ttc atc ctc ttc tgg 163
 Lys Gly Leu Ile Leu Asn Tyr Ala Gly Val Val Phe Ile Leu Phe Trp
 10 15 20
 gga cta gct ccc ttc tac tgg atg gtt atc acc gca ctg cgc gat tcc 211
 Gly Leu Ala Pro Phe Tyr Trp Met Val Ile Thr Ala Leu Arg Asp Ser
 25 30 35
 aag cac acc ttt gac acc acc cca tgg cca acg cac gtc acc ttg gat 259
 Lys His Thr Phe Asp Thr Thr Pro Trp Pro Thr His Val Thr Leu Asp
 40 45 50
 aac ttc cgg gac gca ctg gcc acc gac aaa ggc aac aac ttc ctc gca 307
 Asn Phe Arg Asp Ala Leu Ala Thr Asp Lys Gly Asn Asn Phe Leu Ala
 55 60 65
 gcc att ggc aac tca ctg gtc atc agc gtc acc aca aca gcg atc gct 355
 Ala Ile Gly Asn Ser Leu Val Ile Ser Val Thr Thr Thr Ala Ile Ala
 70 75 80 85
 gtt ctc gtg gga gtg ttc acc gcc tac gct cta gcc cga ctg gaa ttc 403
 Val Leu Val Gly Val Phe Thr Ala Tyr Ala Leu Ala Arg Leu Glu Phe
 90 95 100
 ccg ggc aaa ggc att gtc acc ggc atc atc ttg gca gcc tcc atg ttc 451
 Pro Gly Lys Gly Ile Val Thr Gly Ile Ile Leu Ala Ala Ser Met Phe
 105 110 115

ccc ggc atc gcc ctg gtc act ccg ctg ttc cag ctc ttc ggt gac ctc 499
 Pro Gly Ile Ala Leu Val Thr Pro Leu Phe Gln Leu Phe Gly Asp Leu
 120 125 130

aac tgg atc ggc acc tac caa gcg ctg att atc ccg aac att tcc ttc 547
 Asn Trp Ile Gly Thr Tyr Gln Ala Leu Ile Ile Pro Asn Ile Ser Phe
 135 140 145

gcg cta cct ctg acg atc tac acg ctc gta tcc ttc ttc agg caa ctg 595
 Ala Leu Pro Leu Thr Ile Tyr Thr Leu Val Ser Phe Phe Arg Gln Leu
 150 155 160 165

ccc tgg gaa ctc gaa gaa tca gca cgt gtc gac ggc gcc aca cgt ggc 643
 Pro Trp Glu Leu Glu Glu Ser Ala Arg Val Asp Gly Ala Thr Arg Gly
 170 175 180

caa gcc ttc cgc atg atc ctg ctt cct cta gca gcg ccc gca cta ttt 691
 Gln Ala Phe Arg Met Ile Leu Leu Pro Leu Ala Ala Pro Ala Leu Phe
 185 190 195

acc acc gcg atc ctc gca ttc att gca acg tgg aac gaa ttc atg ctg 739
 Thr Thr Ala Ile Leu Ala Phe Ile Ala Thr Trp Asn Glu Phe Met Leu
 200 205 210

gcc cgc caa cta tcc aac acc tcc aca gag cca gtg acc gtt gcg atc 787
 Ala Arg Gln Leu Ser Asn Thr Ser Thr Glu Pro Val Thr Val Ala Ile
 215 220 225

gca agg ttc acc gga cca agc tcc ttc gaa tac ccc tac gcc tct gtc 835
 Ala Arg Phe Thr Gly Pro Ser Ser Phe Glu Tyr Pro Tyr Ala Ser Val
 230 235 240 245

atg gca gcg gga gct ttg gtg acc atc cca ctg atc atc atg gtt ctc 883
 Met Ala Ala Gly Ala Leu Val Thr Ile Pro Leu Ile Ile Met Val Leu
 250 255 260

atc ttc caa cgc cgc atc gtc tcc gga ctc acc gca ggt ggc gtg aaa 931
 Ile Phe Gln Arg Arg Ile Val Ser Gly Leu Thr Ala Gly Gly Val Lys
 265 270 275

gcc tagactagat actcatgagt gct 957
 Ala

<210> 118

<211> 278

<212> PRT

<213> Corynebacterium glutamicum

<400> 118

Met Thr Lys Arg Thr Lys Gly Leu Ile Leu Asn Tyr Ala Gly Val Val
1 5 10 15

Phe Ile Leu Phe Trp Gly Leu Ala Pro Phe Tyr Trp Met Val Ile Thr
20 25 30

Ala Leu Arg Asp Ser Lys His Thr Phe Asp Thr Thr Pro Trp Pro Thr
35 40 45

His Val Thr Leu Asp Asn Phe Arg Asp Ala Leu Ala Thr Asp Lys Gly

50	55	60
Asn Asn Phe Leu Ala Ala Ile Gly Asn Ser Leu Val Ile Ser Val Thr 65 70 75 80		
Thr Thr Ala Ile Ala Val Leu Val Gly Val Phe Thr Ala Tyr Ala Leu 85 90 95		
Ala Arg Leu Glu Phe Pro Gly Lys Gly Ile Val Thr Gly Ile Ile Leu 100 105 110		
Ala Ala Ser Met Phe Pro Gly Ile Ala Leu Val Thr Pro Leu Phe Gln 115 120 125		
Leu Phe Gly Asp Leu Asn Trp Ile Gly Thr Tyr Gln Ala Leu Ile Ile 130 135 140		
Pro Asn Ile Ser Phe Ala Leu Pro Leu Thr Ile Tyr Thr Leu Val Ser 145 150 155 160		
Phe Phe Arg Gln Leu Pro Trp Glu Leu Glu Glu Ser Ala Arg Val Asp 165 170 175		
Gly Ala Thr Arg Gly Gln Ala Phe Arg Met Ile Leu Leu Pro Leu Ala 180 185 190		
Ala Pro Ala Leu Phe Thr Thr Ala Ile Leu Ala Phe Ile Ala Thr Trp 195 200 205		
Asn Glu Phe Met Leu Ala Arg Gln Leu Ser Asn Thr Ser Thr Glu Pro 210 215 220		
Val Thr Val Ala Ile Ala Arg Phe Thr Gly Pro Ser Ser Phe Glu Tyr 225 230 235 240		
Pro Tyr Ala Ser Val Met Ala Ala Gly Ala Leu Val Thr Ile Pro Leu 245 250 255		
Ile Ile Met Val Leu Ile Phe Gln Arg Arg Ile Val Ser Gly Leu Thr 260 265 270		
Ala Gly Gly Val Lys Ala 275		

<210> 119

<211> 889

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(889)

<223> FRXA02354

<400> 119

gaataaagaa aaagaaactg ggcggaacca aggatgagaa acccaccgct aaggatgctg 60

ttgtaaaggc cgattctgct gtgaaggaag cgcctaagcc atg act aaa cga aca 115
Met Thr Lys Arg Thr

1

5

aaa gga ctc atc ctc aac tac gcc gga gtg gtg ttc atc ctc ttc tgg	163
Lys Gly Leu Ile Leu Asn Tyr Ala Gly Val Val Phe Ile Leu Phe Trp	
10 15 20	
gga cta gct ccc ttc tac tgg atg gtt atc acc gca ctg cgc gat tcc	211
Gly Leu Ala Pro Phe Tyr Trp Met Val Ile Thr Ala Leu Arg Asp Ser	
25 30 35	
aag cac acc ttt gac acc acc cca tgg cca acg cac gtc acc ttg gat	259
Lys His Thr Phe Asp Thr Thr Pro Trp Pro Thr His Val Thr Leu Asp	
40 45 50	
aac ttc cgg gac gca ctg gcc acc gac aaa ggc aac aac ttc ctc gca	307
Asn Phe Arg Asp Ala Leu Ala Thr Asp Lys Gly Asn Asn Phe Leu Ala	
55 60 65	
gcc att ggc aac tca ctg gtc atc agc gtc acc aca aca gcg atc gct	355
Ala Ile Gly Asn Ser Leu Val Ile Ser Val Thr Thr Thr Ala Ile Ala	
70 75 80 85	
gtt ctc gtg gga gtg ttc acc gcc tac gct cta gcc cga ctg gaa ttc	403
Val Leu Val Gly Val Phe Thr Ala Tyr Ala Leu Ala Arg Leu Glu Phe	
90 95 100	
ccg ggc aaa ggc att gtc acc ggc atc atc ttg gca gcc tcc atg ttc	451
Pro Gly Lys Gly Ile Val Thr Gly Ile Ile Leu Ala Ala Ser Met Phe	
105 110 115	
ccc ggc atc gcc ctg gtc act ccg ctg ttc cag ctc ttc ggt gac ctc	499
Pro Gly Ile Ala Leu Val Thr Pro Leu Phe Gln Leu Phe Gly Asp Leu	
120 125 130	
aac tgg atc ggc acc tac caa gcg ctg att atc ccg aac att tcc ttc	547
Asn Trp Ile Gly Thr Tyr Gln Ala Leu Ile Ile Pro Asn Ile Ser Phe	
135 140 145	
gcg cta cct ctg acg atc tac acg ctc gta tcc ttc ttc agg caa ctg	595
Ala Leu Pro Leu Thr Ile Tyr Thr Leu Val Ser Phe Phe Arg Gln Leu	
150 155 160 165	
ccc tgg gaa ctc gaa gaa tca gca cgt gtc gac ggc gcc aca cgt ggc	643
Pro Trp Glu Leu Glu Glu Ser Ala Arg Val Asp Gly Ala Thr Arg Gly	
170 175 180	
caa gcc ttc cgc atg atc ctg ctt cct cta gca gcg ccc gca cta ttt	691
Gln Ala Phe Arg Met Ile Leu Leu Pro Leu Ala Ala Pro Ala Leu Phe	
185 190 195	
acc acc gcg atc ctc gca ttc att gca acg tgg aac gaa ttc atg ctg	739
Thr Thr Ala Ile Leu Ala Phe Ile Ala Thr Trp Asn Glu Phe Met Leu	
200 205 210	
gcc cgc caa cta tcc aac acc tcc aca gag cca gtg acc gtt gcg atc	787
Ala Arg Gln Leu Ser Asn Thr Ser Thr Glu Pro Val Thr Val Ala Ile	
215 220 225	
gca agg ttc acc gga cca agc tcc ttc gaa tac ccc tac gcc tct gtc	835
Ala Arg Phe Thr Gly Pro Ser Ser Phe Glu Tyr Pro Tyr Ala Ser Val	
230 235 240 245	

atc ttc	889
Ile Phe	

<400> 120																
Met	Thr	Lys	Arg	Thr	Lys	Gly	Leu	Ile	Leu	Asn	Tyr	Ala	Gly	Val	Val	
1				5					10					15		
Phe	Ile	Leu	Phe	Trp	Gly	Leu	Ala	Pro	Phe	Tyr	Trp	Met	Val	Ile	Thr	
			20					25					30			
Ala	Leu	Arg	Asp	Ser	Lys	His	Thr	Phe	Asp	Thr	Thr	Pro	Trp	Pro	Thr	
		35					40					45				
His	Val	Thr	Leu	Asp	Asn	Phe	Arg	Asp	Ala	Leu	Ala	Thr	Asp	Lys	Gly	
	50					55					60					
Asn	Asn	Phe	Leu	Ala	Ala	Ile	Gly	Asn	Ser	Leu	Val	Ile	Ser	Val	Thr	
65					70					75					80	
Thr	Thr	Ala	Ile	Ala	Val	Leu	Val	Gly	Val	Phe	Thr	Ala	Tyr	Ala	Leu	
				85					90					95		
Ala	Arg	Leu	Glu	Phe	Pro	Gly	Lys	Gly	Ile	Val	Thr	Gly	Ile	Ile	Leu	
			100					105					110			
Ala	Ala	Ser	Met	Phe	Pro	Gly	Ile	Ala	Leu	Val	Thr	Pro	Leu	Phe	Gln	
		115				120						125				
Leu	Phe	Gly	Asp	Leu	Asn	Trp	Ile	Gly	Thr	Tyr	Gln	Ala	Leu	Ile	Ile	
	130					135					140					
Pro	Asn	Ile	Ser	Phe	Ala	Leu	Pro	Leu	Thr	Ile	Tyr	Thr	Leu	Val	Ser	
145				150						155					160	
Phe	Phe	Arg	Gln	Leu	Pro	Trp	Glu	Leu	Glu	Glu	Ser	Ala	Arg	Val	Asp	
				165				170						175		
Gly	Ala	Thr	Arg	Gly	Gln	Ala	Phe	Arg	Met	Ile	Leu	Leu	Pro	Leu	Ala	
			180					185					190			
Ala	Pro	Ala	Leu	Phe	Thr	Thr	Ala	Ile	Leu	Ala	Phe	Ile	Ala	Thr	Trp	
		195					200					205				
Asn	Glu	Phe	Met	Leu	Ala	Arg	Gln	Leu	Ser	Asn	Thr	Ser	Thr	Glu	Pro	
	210					215					220					
Val	Thr	Val	Ala	Ile	Ala	Arg	Phe	Thr	Gly	Pro	Ser	Ser	Phe	Glu	Tyr	
225				230						235					240	
Pro	Tyr	Ala	Ser	Val	Met	Ala	Ala	Gly	Ala	Leu	Val	Thr	Ile	Pro	Leu	

245

250

255

Ile Ile Met Val Leu Ile Phe
260

<210> 121
<211> 1251
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1228)
<223> RXN00001

<400> 121
tgtcatagggc agcactctag atggcgcaca gtgactcact tcaactgtttc tcacactacg 60

gatcgttcgg cacgtacctg ccgatggagg agattctgca atg gca acc gta acg 115
Met Ala Thr Val Thr
1 5

ttc aaa gat gct tcc cta agc tac ccg gga gca aag gaa ccc acc gtc 163
Phe Lys Asp Ala Ser Leu Ser Tyr Pro Gly Ala Lys Glu Pro Thr Val
10 15 20

aag aaa ttc aac ctg gaa atc gcc gat ggc gag ttc ctc gtc ctc gtc 211
Lys Lys Phe Asn Leu Glu Ile Ala Asp Gly Glu Phe Leu Val Leu Val
25 30 35

ggc cct tcc ggc tgt ggt aaa tcc acc acg ctg cgc atg ctg gcc ggt 259
Gly Pro Ser Gly Cys Gly Lys Ser Thr Thr Leu Arg Met Leu Ala Gly
40 45 50

ttg gaa aac gtt act gac ggt gcc att ttc atc gga gac aag gac gtt 307
Leu Glu Asn Val Thr Asp Gly Ala Ile Phe Ile Gly Asp Lys Asp Val
55 60 65

acc cac gtt gca ccg cgt gac cgt gac atc gcc atg gtt ttc cag aac 355
Thr His Val Ala Pro Arg Asp Arg Asp Ile Ala Met Val Phe Gln Asn
70 75 80 85

tat gct ctc tac ccc cac atg acc gtg ggc gag aac atg ggc ttc gca 403
Tyr Ala Leu Tyr Pro His Met Thr Val Gly Glu Asn Met Gly Phe Ala
90 95 100

ctg aag atc gcc ggc aag tcc caa gac gag atc aat aag cgc gtc gac 451
Leu Lys Ile Ala Gly Lys Ser Gln Asp Glu Ile Asn Lys Arg Val Asp
105 110 115

gaa gcc gcc gcc act ttg ggc ctg acc gaa ttc ttg gag cgc aag ccg 499
Glu Ala Ala Ala Thr Leu Gly Leu Thr Glu Phe Leu Glu Arg Lys Pro
120 125 130

aag gcc ctg tcc ggt ggt cag cgt cag cgt gtg gcc atg ggc cgc gcc 547
Lys Ala Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Met Gly Arg Ala
135 140 145

att gtt cgc aac ccg cag gtc ttt ctc atg gat gag ccg ctg tct aac 595
Ile Val Arg Asn Pro Gln Val Phe Leu Met Asp Glu Pro Leu Ser Asn

150	155	160	165	
ctc gat gcc aag ctg cgt gtt cag acc cgt acc cag att gca gcc ctg Leu Asp Ala Lys Leu Arg Val Gln Thr Arg Thr Gln Ile Ala Ala Leu	170	175	180	643
cag cgc aag ctt ggg gtt acc acc gtt tac gtc acc cac gac cag acg Gln Arg Lys Leu Gly Val Thr Thr Val Tyr Val Thr His Asp Gln Thr	185	190	195	691
gag gcc ttg acc atg ggt gac cgc atc gcg gtg ctg aag gat ggc tac Glu Ala Leu Thr Met Gly Asp Arg Ile Ala Val Leu Lys Asp Gly Tyr	200	205	210	739
ctg cag cag gtt ggc gcg ccc cga gag ctt tat gac cgc ccc gcc aac Leu Gln Gln Val Gly Ala Pro Arg Glu Leu Tyr Asp Arg Pro Ala Asn	215	220	225	787
gtc ttc gtc gcc ggc ttc atc ggc tcc cca gcc atg aac ttg ggc acc Val Phe Val Ala Gly Phe Ile Gly Ser Pro Ala Met Asn Leu Gly Thr	230	235	240	835
ttc tgc gtc aag gat ggt gac gct acc tct ggt cac gct cgc atc aag Phe Ser Val Lys Asp Gly Asp Ala Thr Ser Gly His Ala Arg Ile Lys	250	255	260	883
ctt tcc ccg gaa acc ctc gcc gcc atg acg ccg gag gat aat ggc cgc Leu Ser Pro Glu Thr Leu Ala Ala Met Thr Pro Glu Asp Asn Gly Arg	265	270	275	931
atc acc att ggt ttc cgc ccg gag gca ctg gag atc att ccg gaa ggc Ile Thr Ile Gly Phe Arg Pro Glu Ala Leu Glu Ile Ile Pro Glu Gly	280	285	290	979
gag tcc acc gat ctt tcc atc cca atc aag ctc gac ttc gtg gag gaa Glu Ser Thr Asp Leu Ser Ile Pro Ile Lys Leu Asp Phe Val Glu Glu	295	300	305	1027
ctc ggt tcc gat tcc ttc ctc tac ggc aag ctg gta ggc gag ggc gac Leu Gly Ser Asp Ser Phe Leu Tyr Gly Lys Leu Val Gly Glu Gly Asp	310	315	320	1075
ctt gga tcc tcc agc gag gat gtc ccc gag tcc ggc caa atc gtc gtc Leu Gly Ser Ser Ser Glu Asp Val Pro Glu Ser Gly Gln Ile Val Val	330	335	340	1123
cgc gct gct ccg aac gcc gcg cct gct ccg ggc agt gtt ttc cac gca Arg Ala Ala Pro Asn Ala Ala Pro Ala Pro Gly Ser Val Phe His Ala	345	350	355	1171
cgc atc gtg gag ggc ggc cag cac aac ttc tgc gcg tgc act ggc aag Arg Ile Val Glu Gly Gly Gln His Asn Phe Ser Ala Ser Thr Gly Lys	360	365	370	1219
cgc ctc cct taagcccgcg taccggctac ccc Arg Leu Pro	375			1251

<210> 122

<211> 376

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 122

Met Ala Thr Val Thr Phe Lys Asp Ala Ser Leu Ser Tyr Pro Gly Ala
 1 5 10 15

Lys Glu Pro Thr Val Lys Lys Phe Asn Leu Glu Ile Ala Asp Gly Glu
 20 25 30

Phe Leu Val Leu Val Gly Pro Ser Gly Cys Gly Lys Ser Thr Thr Leu
 35 40 45

Arg Met Leu Ala Gly Leu Glu Asn Val Thr Asp Gly Ala Ile Phe Ile
 50 55 60

Gly Asp Lys Asp Val Thr His Val Ala Pro Arg Asp Arg Asp Ile Ala
 65 70 75 80

Met Val Phe Gln Asn Tyr Ala Leu Tyr Pro His Met Thr Val Gly Glu
 85 90 95

Asn Met Gly Phe Ala Leu Lys Ile Ala Gly Lys Ser Gln Asp Glu Ile
 100 105 110

Asn Lys Arg Val Asp Glu Ala Ala Ala Thr Leu Gly Leu Thr Glu Phe
 115 120 125

Leu Glu Arg Lys Pro Lys Ala Leu Ser Gly Gly Gln Arg Gln Arg Val
 130 135 140

Ala Met Gly Arg Ala Ile Val Arg Asn Pro Gln Val Phe Leu Met Asp
 145 150 155 160

Glu Pro Leu Ser Asn Leu Asp Ala Lys Leu Arg Val Gln Thr Arg Thr
 165 170 175

Gln Ile Ala Ala Leu Gln Arg Lys Leu Gly Val Thr Thr Val Tyr Val
 180 185 190

Thr His Asp Gln Thr Glu Ala Leu Thr Met Gly Asp Arg Ile Ala Val
 195 200 205

Leu Lys Asp Gly Tyr Leu Gln Gln Val Gly Ala Pro Arg Glu Leu Tyr
 210 215 220

Asp Arg Pro Ala Asn Val Phe Val Ala Gly Phe Ile Gly Ser Pro Ala
 225 230 235 240

Met Asn Leu Gly Thr Phe Ser Val Lys Asp Gly Asp Ala Thr Ser Gly
 245 250 255

His Ala Arg Ile Lys Leu Ser Pro Glu Thr Leu Ala Ala Met Thr Pro
 260 265 270

Glu Asp Asn Gly Arg Ile Thr Ile Gly Phe Arg Pro Glu Ala Leu Glu
 275 280 285

Ile Ile Pro Glu Gly Glu Ser Thr Asp Leu Ser Ile Pro Ile Lys Leu
 290 295 300

Asp Phe Val Glu Glu Leu Gly Ser Asp Ser Phe Leu Tyr Gly Lys Leu
305 310 315 320

Val Gly Glu Gly Asp Leu Gly Ser Ser Ser Glu Asp Val Pro Glu Ser
325 330 335

Gly Gln Ile Val Val Arg Ala Ala Pro Asn Ala Ala Pro Ala Pro Gly
340 345 350

Ser Val Phe His Ala Arg Ile Val Glu Gly Gly Gln His Asn Phe Ser
355 360 365

Ala Ser Thr Gly Lys Arg Leu Pro
370 375

<210> 123

<211> 1251

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1228)

<223> FRXA00001

<400> 123

tgtcataggc agcactctag atggcgacaca gtgactcact tcaactgtttc tcacactacg 60

gatcgttcgg cacgtacctg ccgatggagg agattctgca atg gca acc gta acg 115
Met Ala Thr Val Thr
1 5

ttc aaa gat gct tcc cta agc tac ccg gga gca aag gaa ccc acc gtc 163
Phe Lys Asp Ala Ser Leu Ser Tyr Pro Gly Ala Lys Glu Pro Thr Val
10 15 20

aag aaa ttc aac ctg gaa atc gcc gat ggc gag ttc ctc gtc ctc gtc 211
Lys Lys Phe Asn Leu Glu Ile Ala Asp Gly Glu Phe Leu Val Leu Val
25 30 35

ggc cct tcc ggc tgt ggt aaa tcc acc acg ctg cgc atg ctg gcc ggt 259
Gly Pro Ser Gly Cys Gly Lys Ser Thr Thr Leu Arg Met Leu Ala Gly
40 45 50

ttg gaa aac gtt act gac ggt gcc att ttc atc gga gac aag gac gtt 307
Leu Glu Asn Val Thr Asp Gly Ala Ile Phe Ile Gly Asp Lys Asp Val
55 60 65

acc cac gtt gca ccg cgt gac cgt gac atc gcc atg gtt ttc cag aac 355
Thr His Val Ala Pro Arg Asp Arg Asp Ile Ala Met Val Phe Gln Asn
70 75 80 85

tat gct ctc tac ccc cac atg acc gtg ggc gag aac atg ggc ttc gca 403
Tyr Ala Leu Tyr Pro His Met Thr Val Gly Glu Asn Met Gly Phe Ala
90 95 100

ctg aag atc gcc ggc aag tcc caa gac gag atc aat aag cgc gtc gac 451
Leu Lys Ile Ala Gly Lys Ser Gln Asp Glu Ile Asn Lys Arg Val Asp
105 110 115

gaa gcc gcc gcc act ttg ggc ctg acc gaa ttc ttg gag cgc aag ccg Glu Ala Ala Ala Thr Leu Gly Leu Thr Glu Phe Leu Glu Arg Lys Pro 120 125 130	499
aag gcc ctg tcc ggt ggt cag cgt cag cgt gtg gcc atg ggc cgc gcc Lys Ala Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Met Gly Arg Ala 135 140 145	547
att gtt cgc aac ccg cag gtc ttt ctc atg gat gag ccg ctg tct aac Ile Val Arg Asn Pro Gln Val Phe Leu Met Asp Glu Pro Leu Ser Asn 150 155 160 165	595
ctc gat gcc aag ctg cgt gtt cag acc cgt acc cag att gca gcc ctg Leu Asp Ala Lys Leu Arg Val Gln Thr Arg Thr Gln Ile Ala Ala Leu 170 175 180	643
cag cgc aag ctt ggg gtt acc acc gtt tac gtc acc cac gac cag acg Gln Arg Lys Leu Gly Val Thr Thr Val Tyr Val Thr His Asp Gln Thr 185 190 195	691
gag gcc ttg acc atg ggt gac cgc atc gcg gtg ctg aag gat ggc tac Glu Ala Leu Thr Met Gly Asp Arg Ile Ala Val Leu Lys Asp Gly Tyr 200 205 210	739
ctg cag cag gtt ggc gcg ccc cga gag ctt tat gac cgc ccc gcc aac Leu Gln Gln Val Gly Ala Pro Arg Glu Leu Tyr Asp Arg Pro Ala Asn 215 220 225	787
gtc ttc gtc gcc ggc ttc atc ggc tcc cca gcc atg aac ttg ggc acc Val Phe Val Ala Gly Phe Ile Gly Ser Pro Ala Met Asn Leu Gly Thr 230 235 240 245	835
ttc tcg gtc aag gat ggt gac gct acc tct ggt cac gct cgc atc aag Phe Ser Val Lys Asp Gly Asp Ala Thr Ser Gly His Ala Arg Ile Lys 250 255 260	883
ctt tcc ccg gaa acc ctc gcc gcc atg acg ccg gag gat aat ggc cgc Leu Ser Pro Glu Thr Leu Ala Ala Met Thr Pro Glu Asp Asn Gly Arg 265 270 275	931
atc acc att ggt ttc cgc ccg gag gca ctg gag atc att ccg gaa ggc Ile Thr Ile Gly Phe Arg Pro Glu Ala Leu Glu Ile Ile Pro Glu Gly 280 285 290	979
gag tcc acc gat ctt tcc atc cca atc aag ctc gac ttc gtg gag gaa Glu Ser Thr Asp Leu Ser Ile Pro Ile Lys Leu Asp Phe Val Glu Glu 295 300 305	1027
ctc ggt tcc gat tcc ttc ctc tac ggc aag ctg gta ggc gag ggc gac Leu Gly Ser Asp Ser Phe Leu Tyr Gly Lys Leu Val Gly Glu Gly Asp 310 315 320 325	1075
ctt gga tcc tcc agc gag gat gtc ccc gag tcc ggc caa atc gtc gtc Leu Gly Ser Ser Ser Glu Asp Val Pro Glu Ser Gly Gln Ile Val Val 330 335 340	1123
cgc gct gct ccg aac gcc gcg cct gct ccg ggc agt gtt ttc cac gca Arg Ala Ala Pro Asn Ala Ala Pro Ala Pro Gly Ser Val Phe His Ala 345 350 355	1171
cgc atc gtg gag ggc ggc cag cac aac ttc tcg gcg tcg act ggc aag	1219

Arg Ile Val Glu Gly Gly Gln His Asn Phe Ser Ala Ser Thr Gly Lys
 360 365 370

cgc ctc cct taagcccgcg taccggctac ccc
 Arg Leu Pro
 375

1251

<210> 124

<211> 376

<212> PRT

<213> Corynebacterium glutamicum

<400> 124

Met Ala Thr Val Thr Phe Lys Asp Ala Ser Leu Ser Tyr Pro Gly Ala
 1 5 10 15

Lys Glu Pro Thr Val Lys Lys Phe Asn Leu Glu Ile Ala Asp Gly Glu
 20 25 30

Phe Leu Val Leu Val Gly Pro Ser Gly Cys Gly Lys Ser Thr Thr Leu
 35 40 45

Arg Met Leu Ala Gly Leu Glu Asn Val Thr Asp Gly Ala Ile Phe Ile
 50 55 60

Gly Asp Lys Asp Val Thr His Val Ala Pro Arg Asp Arg Asp Ile Ala
 65 70 75 80

Met Val Phe Gln Asn Tyr Ala Leu Tyr Pro His Met Thr Val Gly Glu
 85 90 95

Asn Met Gly Phe Ala Leu Lys Ile Ala Gly Lys Ser Gln Asp Glu Ile
 100 105 110

Asn Lys Arg Val Asp Glu Ala Ala Ala Thr Leu Gly Leu Thr Glu Phe
 115 120 125

Leu Glu Arg Lys Pro Lys Ala Leu Ser Gly Gly Gln Arg Gln Arg Val
 130 135 140

Ala Met Gly Arg Ala Ile Val Arg Asn Pro Gln Val Phe Leu Met Asp
 145 150 155 160

Glu Pro Leu Ser Asn Leu Asp Ala Lys Leu Arg Val Gln Thr Arg Thr
 165 170 175

Gln Ile Ala Ala Leu Gln Arg Lys Leu Gly Val Thr Thr Val Tyr Val
 180 185 190

Thr His Asp Gln Thr Glu Ala Leu Thr Met Gly Asp Arg Ile Ala Val
 195 200 205

Leu Lys Asp Gly Tyr Leu Gln Gln Val Gly Ala Pro Arg Glu Leu Tyr
 210 215 220

Asp Arg Pro Ala Asn Val Phe Val Ala Gly Phe Ile Gly Ser Pro Ala
 225 230 235 240

Met Asn Leu Gly Thr Phe Ser Val Lys Asp Gly Asp Ala Thr Ser Gly
 245 250 255

His Ala Arg Ile Lys Leu Ser Pro Glu Thr Leu Ala Ala Met Thr Pro
 260 265 270

Glu Asp Asn Gly Arg Ile Thr Ile Gly Phe Arg Pro Glu Ala Leu Glu
 275 280 285

Ile Ile Pro Glu Gly Glu Ser Thr Asp Leu Ser Ile Pro Ile Lys Leu
 290 295 300

Asp Phe Val Glu Glu Leu Gly Ser Asp Ser Phe Leu Tyr Gly Lys Leu
 305 310 315 320

Val Gly Glu Gly Asp Leu Gly Ser Ser Ser Glu Asp Val Pro Glu Ser
 325 330 335

Gly Gln Ile Val Val Arg Ala Ala Pro Asn Ala Ala Pro Ala Pro Gly
 340 345 350

Ser Val Phe His Ala Arg Ile Val Glu Gly Gly Gln His Asn Phe Ser
 355 360 365

Ala Ser Thr Gly Lys Arg Leu Pro
 370 375

<210> 125
 <211> 1119
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1096)
 <223> RXN02356

<400> 125
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aaaccacaaa tgtgtactgg tgctggtaat ttagtagaac atg gca acg gtc aca 115
 Met Ala Thr Val Thr
 1 5

ttc gac aag gtc aca atc cgg tac ccc ggc gcg gag cgc gca aca gtt 163
 Phe Asp Lys Val Thr Ile Arg Tyr Pro Gly Ala Glu Arg Ala Thr Val
 10 15 20

cat gag ctt gat tta gat atc gct gat ggc gag ttt ttg gtg ctc gtc 211
 His Glu Leu Asp Leu Asp Ile Ala Asp Gly Glu Phe Leu Val Leu Val
 25 30 35

ggc cct tcg ggt tgt ggt aaa tcc act acg ctg cgt gct ttg gcg ggg 259
 Gly Pro Ser Gly Cys Gly Lys Ser Thr Thr Leu Arg Ala Leu Ala Gly
 40 45 50

ctt gag ggc gtg gag tcg ggt gtg atc aaa att gat ggc aag gat gtc 307
 Leu Glu Gly Val Glu Ser Gly Val Ile Lys Ile Asp Gly Lys Asp Val
 55 60 65

act ggt cag gag ccg gcg gat cgc gat atc gcg atg gtg ttc cag aat 355
 Thr Gly Gln Glu Pro Ala Asp Arg Asp Ile Ala Met Val Phe Gln Asn

70	75	80	85	
tat gct ctg tac cct cac atg acg gtg gcg aag aat atg ggt ttt gcg Tyr Ala Leu Tyr Pro His Met Thr Val Ala Lys Asn Met Gly Phe Ala 90 95 100				403
ctg aag ttg gct aag ctg ccg cag gcg cag atc gat gcg aag gtc aat Leu Lys Leu Ala Lys Leu Pro Gln Ala Gln Ile Asp Ala Lys Val Asn 105 110 115				451
gag gct gcg gaa att ctt ggg ttg acg gag ttt ttg gat cgc aag cct Glu Ala Ala Glu Ile Leu Gly Leu Thr Glu Phe Leu Asp Arg Lys Pro 120 125 130				499
aag gat tta tgc ggt ggt cag cgt cag cgt gtg gcg atg ggt cgc gcg Lys Asp Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Met Gly Arg Ala 135 140 145				547
ttg gtg cgt gat ccg aag gtg ttc ctc atg gat gag ccg ctg tcc aac Leu Val Arg Asp Pro Lys Val Phe Leu Met Asp Glu Pro Leu Ser Asn 150 155 160 165				595
ctg gat gcg aaa ttg cgc gtg caa acc cgc gcg gag gtc gct gct ttg Leu Asp Ala Lys Leu Arg Val Gln Thr Arg Ala Glu Val Ala Ala Leu 170 175 180				643
cag cgt cgc ctg ggc acc acc acg gtg tat gtc acc cac gat cag gtt Gln Arg Arg Leu Gly Thr Thr Thr Val Tyr Val Thr His Asp Gln Val 185 190 195				691
gag gca atg acg atg ggc gat cgg gtt gcg gtg ctc aag gac ggg ttg Glu Ala Met Thr Met Gly Asp Arg Val Ala Val Leu Lys Asp Gly Leu 200 205 210				739
ctg cag cag gtc gca ccg ccc agg gag ctt tac gac gcc ccg gtc aac Leu Gln Gln Val Ala Pro Pro Arg Glu Leu Tyr Asp Ala Pro Val Asn 215 220 225				787
gaa ttc gtt gcg ggc ttc atc ggc tgc ccg tcc atg aac ctc ttc cct Glu Phe Val Ala Gly Phe Ile Gly Ser Pro Ser Met Asn Leu Phe Pro 230 235 240 245				835
gcc aac ggg cac aag atg ggt gtg cgc ccg gag aag atg ctg gtc aat Ala Asn Gly His Lys Met Gly Val Arg Pro Glu Lys Met Leu Val Asn 250 255 260				883
gag acc cct gag ggt ttc aca agc att gat gct gtg gtg gat atc gtc Glu Thr Pro Glu Gly Phe Thr Ser Ile Asp Ala Val Val Asp Ile Val 265 270 275				931
gag gag ctt ggc tcc gaa tgc tat gtt tat gcc act tgg gag ggc cac Glu Glu Leu Gly Ser Glu Ser Tyr Val Tyr Ala Thr Trp Glu Gly His 280 285 290				979
cgc ctg gtg gcc cgt tgg gtg gaa ggc ccc gtg cca gcc cct ggc acg Arg Leu Val Ala Arg Trp Val Glu Gly Pro Val Pro Ala Pro Gly Thr 295 300 305				1027
cct gtg act ttt tcc tat gat gcg gcg cag gcg cat cat ttc gat ctg Pro Val Thr Phe Ser Tyr Asp Ala Ala Gln Ala His His Phe Asp Leu 310 315 320 325				1075

gag tcg ggc gag cgt atc gct tagtttcgga cgtggggagg cgt
 Glu Ser Gly Glu Arg Ile Ala
 330

1119

<210> 126

<211> 332

<212> PRT

<213> Corynebacterium glutamicum

<400> 126

Met Ala Thr Val Thr Phe Asp Lys Val Thr Ile Arg Tyr Pro Gly Ala
 1 5 10 15

Glu Arg Ala Thr Val His Glu Leu Asp Leu Asp Ile Ala Asp Gly Glu
 20 25 30

Phe Leu Val Leu Val Gly Pro Ser Gly Cys Gly Lys Ser Thr Thr Leu
 35 40 45

Arg Ala Leu Ala Gly Leu Glu Gly Val Glu Ser Gly Val Ile Lys Ile
 50 55 60

Asp Gly Lys Asp Val Thr Gly Gln Glu Pro Ala Asp Arg Asp Ile Ala
 65 70 75 80

Met Val Phe Gln Asn Tyr Ala Leu Tyr Pro His Met Thr Val Ala Lys
 85 90 95

Asn Met Gly Phe Ala Leu Lys Leu Ala Lys Leu Pro Gln Ala Gln Ile
 100 105 110

Asp Ala Lys Val Asn Glu Ala Ala Glu Ile Leu Gly Leu Thr Glu Phe
 115 120 125

Leu Asp Arg Lys Pro Lys Asp Leu Ser Gly Gly Gln Arg Gln Arg Val
 130 135 140

Ala Met Gly Arg Ala Leu Val Arg Asp Pro Lys Val Phe Leu Met Asp
 145 150 155 160

Glu Pro Leu Ser Asn Leu Asp Ala Lys Leu Arg Val Gln Thr Arg Ala
 165 170 175

Glu Val Ala Ala Leu Gln Arg Arg Leu Gly Thr Thr Thr Val Tyr Val
 180 185 190

Thr His Asp Gln Val Glu Ala Met Thr Met Gly Asp Arg Val Ala Val
 195 200 205

Leu Lys Asp Gly Leu Leu Gln Gln Val Ala Pro Pro Arg Glu Leu Tyr
 210 215 220

Asp Ala Pro Val Asn Glu Phe Val Ala Gly Phe Ile Gly Ser Pro Ser
 225 230 235 240

Met Asn Leu Phe Pro Ala Asn Gly His Lys Met Gly Val Arg Pro Glu
 245 250 255

Lys Met Leu Val Asn Glu Thr Pro Glu Gly Phe Thr Ser Ile Asp Ala

260 265 270

Val Val Asp Ile Val Glu Glu Leu Gly Ser Glu Ser Tyr Val Tyr Ala
275 280 285

Thr Trp Glu Gly His Arg Leu Val Ala Arg Trp Val Glu Gly Pro Val
290 295 300

Pro Ala Pro Gly Thr Pro Val Thr Phe Ser Tyr Asp Ala Ala Gln Ala
305 310 315 320

His His Phe Asp Leu Glu Ser Gly Glu Arg Ile Ala
325 330

<210> 127
<211> 1369
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1369)
<223> RXN02455

<400> 127
aagccttcgt tatgggaggt ctcccagaca caatcgaata cgggccggat atccatctcg 60

gctcatcacc ccgcttttta tcaagaaaga tgaggacctc ttg aag cgt ctt act 115
Leu Lys Arg Leu Thr
1 5

cgc atc gca tcc atc agc atg gcc tcc atg ctc gcc gcc gca agt ctc 163
Arg Ile Ala Ser Ile Ser Met Ala Ser Met Leu Ala Ala Ala Ser Leu
10 15 20

gtc gcg tgc tcc ggc tcc acc gac gag gaa ggc gat gtt tac ttc ctg 211
Val Ala Cys Ser Gly Ser Thr Asp Glu Glu Gly Asp Val Tyr Phe Leu
25 30 35

aac ttc aag cct gaa cag gac gtg gca tac cag gaa atc gca aag gcc 259
Asn Phe Lys Pro Glu Gln Asp Val Ala Tyr Gln Glu Ile Ala Lys Ala
40 45 50

tac act gaa gag acc ggc gtt aag gtc aag gtc gtt act gcc gcc tcc 307
Tyr Thr Glu Glu Thr Gly Val Lys Val Lys Val Val Thr Ala Ala Ser
55 60 65

ggc tcc tat gag cag acc ctc aag gcc gag att ggc aag gac gaa gcc 355
Gly Ser Tyr Glu Gln Thr Leu Lys Ala Glu Ile Gly Lys Asp Glu Ala
70 75 80 85

ccg act ctc ttc cag gtc aat ggc cca gcc ggc ttc atc act tgg cag 403
Pro Thr Leu Phe Gln Val Asn Gly Pro Ala Gly Phe Ile Thr Trp Gln
90 95 100

gac tac atg gca gat atg tcg gac acc gag gta gct aag cag ctg acc 451
Asp Tyr Met Ala Asp Met Ser Asp Thr Glu Val Ala Lys Gln Leu Thr
105 110 115

gac gac att ccg ccg ctg acc acc gag gat ggc gag gta cgt ggc gtt 499

Asp	Asp	Ile	Pro	Pro	Leu	Thr	Thr	Glu	Asp	Gly	Glu	Val	Arg	Gly	Val	
		120						125				130				
ccg	ttc	gcc	gtc	gag	ggc	ttc	ggc	atc	atc	tac	aac	gac	gag	atc	ttc	547
Pro	Phe	Ala	Val	Glu	Gly	Phe	Gly	Ile	Ile	Tyr	Asn	Asp	Glu	Ile	Phe	
	135					140					145					
gac	aag	tac	atc	gcc	acg	tcc	ggc	gca	aag	atc	aag	tcc	acg	gat	gag	595
Asp	Lys	Tyr	Ile	Ala	Thr	Ser	Gly	Ala	Lys	Ile	Lys	Ser	Thr	Asp	Glu	
150					155					160					165	
atc	acg	agc	tac	cag	aag	ctc	aag	gaa	gtc	gcc	gag	gat	atg	cag	gca	643
Ile	Thr	Ser	Tyr	Gln	Lys	Leu	Lys	Glu	Val	Ala	Glu	Asp	Met	Gln	Ala	
				170					175					180		
aag	aag	gac	gag	ctc	ggt	atc	gaa	ggc	gcc	ttc	gcc	tcc	acc	tcg	ctg	691
Lys	Lys	Asp	Glu	Leu	Gly	Ile	Glu	Gly	Ala	Phe	Ala	Ser	Thr	Ser	Leu	
			185					190					195			
aca	tcc	agt	gag	gac	tgg	cgt	tgg	cag	acc	cac	ctg	gcc	aac	gct	ccg	739
Thr	Ser	Ser	Glu	Asp	Trp	Arg	Trp	Gln	Thr	His	Leu	Ala	Asn	Ala	Pro	
		200					205					210				
atc	tgg	cag	gag	tac	cag	gac	aag	gga	gtc	gag	gac	acc	aac	gag	atc	787
Ile	Trp	Gln	Glu	Tyr	Gln	Asp	Lys	Gly	Val	Glu	Asp	Thr	Asn	Glu	Ile	
	215					220					225					
gag	ttc	tcc	tac	aac	aag	gag	tac	aag	aac	ctt	ttc	gat	ctc	tac	ctt	835
Glu	Phe	Ser	Tyr	Asn	Lys	Glu	Tyr	Lys	Asn	Leu	Phe	Asp	Leu	Tyr	Leu	
230					235					240					245	
gag	aac	tcc	acc	gta	gaa	aag	tct	ctt	gcg	ccg	tct	aag	acg	gtg	tct	883
Glu	Asn	Ser	Thr	Val	Glu	Lys	Ser	Leu	Ala	Pro	Ser	Lys	Thr	Val	Ser	
				250					255					260		
gat	tcc	atg	gct	gag	ttc	gca	cag	ggc	aag	gcc	gct	atg	ggt	cag	aac	931
Asp	Ser	Met	Ala	Glu	Phe	Ala	Gln	Gly	Lys	Ala	Ala	Met	Val	Gln	Asn	
			265					270					275			
ggt	aac	tgg	gca	tgg	tcc	cag	att	tcc	gag	act	tct	ggc	aac	gtg	gtc	979
Gly	Asn	Trp	Ala	Trp	Ser	Gln	Ile	Ser	Glu	Thr	Ser	Gly	Asn	Val	Val	
		280					285					290				
aag	gaa	gac	aag	atc	aag	ttc	ctg	ccc	atg	tac	atg	ggt	ctg	cca	gat	1027
Lys	Glu	Asp	Lys	Ile	Lys	Phe	Leu	Pro	Met	Tyr	Met	Gly	Leu	Pro	Asp	
	295					300					305					
gaa	gaa	aag	cac	ggc	atc	aac	gtc	ggt	acc	gag	aac	tat	ttg	ggc	gtg	1075
Glu	Glu	Lys	His	Gly	Ile	Asn	Val	Gly	Thr	Glu	Asn	Tyr	Leu	Gly	Val	
310					315					320					325	
aac	tct	gag	gcc	tcc	gag	gtc	gac	cag	cag	gcc	acc	aag	gac	ttc	gtg	1123
Asn	Ser	Glu	Ala	Ser	Glu	Val	Asp	Gln	Gln	Ala	Thr	Lys	Asp	Phe	Val	
				330					335					340		
gat	tgg	ctg	ttt	acc	tct	gaa	gct	ggc	aag	gag	cac	gtg	gtg	aag	gac	1171
Asp	Trp	Leu	Phe	Thr	Ser	Glu	Ala	Gly	Lys	Glu	His	Val	Val	Lys	Asp	
			345					350					355			
ctt	ggc	ttc	atc	gca	ccg	ttc	gaa	agc	tac	acc	gct	gag	aac	acc	ccg	1219
Leu	Gly	Phe	Ile	Ala	Pro	Phe	Glu	Ser	Tyr	Thr	Ala	Glu	Asn	Thr	Pro	

360	365	370	
aat gac ccc ott tct gag	caa gtc gcg gaa gct	atc gct aac aag gat	1267
Asn Asp Pro Leu Ser Glu	Gln Val Ala Glu Ala	Ile Ala Asn Lys Asp	
375	380	385	
ctg acc acc tac ccg tgg	aac ttc cag tac ttc	ccg tcc cag cag ttc	1315
Leu Thr Thr Tyr Pro Trp	Asn Phe Gln Tyr Phe	Pro Ser Gln Gln Phe	
390	395	400	405
aag gat gac ttc ggc cag	gat ctg tcg cag tac	gcc tcc gga aag ctg	1363
Lys Asp Asp Phe Gly	Gln Asp Leu Ser Gln	Tyr Ala Ser Gly Lys	Leu
	410	415	420
aag tgg			1369
Lys Trp			

<210> 128

<211> 423

<212> PRT

<213> Corynebacterium glutamicum

<400> 128

Leu Lys Arg Leu Thr Arg	Ile Ala Ser Ile Ser Met	Ala Ser Met Leu
1	5	10
Ala Ala Ala Ser Leu Val	Ala Cys Ser Gly Ser Thr	Asp Glu Gly
20	25	30
Asp Val Tyr Phe Leu Asn	Phe Lys Pro Glu Gln Asp	Val Ala Tyr Gln
35	40	45
Glu Ile Ala Lys Ala Tyr	Thr Glu Glu Thr Gly Val	Lys Val Lys Val
50	55	60
Val Thr Ala Ala Ser Gly	Ser Tyr Glu Gln Thr Leu	Lys Ala Glu Ile
65	70	75
Gly Lys Asp Glu Ala Pro	Thr Leu Phe Gln Val Asn	Gly Pro Ala Gly
85	90	95
Phe Ile Thr Trp Gln Asp	Tyr Met Ala Asp Met Ser	Asp Thr Glu Val
100	105	110
Ala Lys Gln Leu Thr Asp	Asp Ile Pro Pro Leu Thr	Thr Glu Asp Gly
115	120	125
Glu Val Arg Gly Val Pro	Phe Ala Val Glu Gly Phe	Gly Ile Ile Tyr
130	135	140
Asn Asp Glu Ile Phe Asp	Lys Tyr Ile Ala Thr Ser	Gly Ala Lys Ile
145	150	155
Lys Ser Thr Asp Glu Ile	Thr Ser Tyr Gln Lys Leu	Lys Glu Val Ala
165	170	175
Glu Asp Met Gln Ala Lys	Lys Asp Glu Leu Gly Ile	Glu Gly Ala Phe
180	185	190

Ala Ser Thr Ser Leu Thr Ser Ser Glu Asp Trp Arg Trp Gln Thr His
 195 200 205

Leu Ala Asn Ala Pro Ile Trp Gln Glu Tyr Gln Asp Lys Gly Val Glu
 210 215 220

Asp Thr Asn Glu Ile Glu Phe Ser Tyr Asn Lys Glu Tyr Lys Asn Leu
 225 230 235 240

Phe Asp Leu Tyr Leu Glu Asn Ser Thr Val Glu Lys Ser Leu Ala Pro
 245 250 255

Ser Lys Thr Val Ser Asp Ser Met Ala Glu Phe Ala Gln Gly Lys Ala
 260 265 270

Ala Met Val Gln Asn Gly Asn Trp Ala Trp Ser Gln Ile Ser Glu Thr
 275 280 285

Ser Gly Asn Val Val Lys Glu Asp Lys Ile Lys Phe Leu Pro Met Tyr
 290 295 300

Met Gly Leu Pro Asp Glu Glu Lys His Gly Ile Asn Val Gly Thr Glu
 305 310 315 320

Asn Tyr Leu Gly Val Asn Ser Glu Ala Ser Glu Val Asp Gln Gln Ala
 325 330 335

Thr Lys Asp Phe Val Asp Trp Leu Phe Thr Ser Glu Ala Gly Lys Glu
 340 345 350

His Val Val Lys Asp Leu Gly Phe Ile Ala Pro Phe Glu Ser Tyr Thr
 355 360 365

Ala Glu Asn Thr Pro Asn Asp Pro Leu Ser Glu Gln Val Ala Glu Ala
 370 375 380

Ile Ala Asn Lys Asp Leu Thr Thr Tyr Pro Trp Asn Phe Gln Tyr Phe
 385 390 395 400

Pro Ser Gln Gln Phe Lys Asp Asp Phe Gly Gln Asp Leu Ser Gln Tyr
 405 410 415

Ala Ser Gly Lys Leu Lys Trp
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<210> 129

<211> 1560

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1537)

<223> RXN02795

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ggtttacgcg atgccatcga tccaaagcgg gaggtcggcc gtg ctt aaa gtt tct 115
 Val Leu Lys Val Ser

	1	5	
gat tta acg gtt ggc aac aat ttt gtc cac aac gtc tcc ttc gag gtc			163
Asp Leu Thr Val Gly Asn Asn Phe Val His Asn Val Ser Phe Glu Val	10	20	
aac ccc ggc gaa cgc gtc ggc atc atc ggc gag tcc ggc tca ggc aaa			211
Asn Pro Gly Glu Arg Val Gly Ile Ile Gly Glu Ser Gly Ser Gly Lys	25	30	35
tca ctc acc gcg cta tcc atc atg ggt tta act gac ctg ccg acc acc			259
Ser Leu Thr Ala Leu Ser Ile Met Gly Leu Thr Asp Leu Pro Thr Thr	40	45	50
ggc cag atc acc ttc aac ggc aaa ccc tcc gct aca ttc cgt ggc acc			307
Gly Gln Ile Thr Phe Asn Gly Lys Pro Ser Ala Thr Phe Arg Gly Thr	55	60	65
cgc atc gcc atg gtt ttc caa gaa cca atg agc gca ctc aac ccg ctc			355
Arg Ile Ala Met Val Phe Gln Glu Pro Met Ser Ala Leu Asn Pro Leu	70	75	80
atg cgc atc ggc cgc caa atc gaa gaa atg atg acc ctg cac ggg gca			403
Met Arg Ile Gly Arg Gln Ile Glu Glu Met Met Thr Leu His Gly Ala	90	95	100
agc aaa aaa gac gcg cgg gcg cgc tta aaa agc ttg ctt atc gac gtc			451
Ser Lys Lys Asp Ala Arg Ala Arg Leu Lys Ser Leu Leu Ile Asp Val	105	110	115
tcc ctc ccc gaa cgc acc gct tcc gcc tac cca cac gaa ctt tca ggc			499
Ser Leu Pro Glu Arg Thr Ala Ser Ala Tyr Pro His Glu Leu Ser Gly	120	125	130
ggg caa cgc caa cgc gca cta atc gca atg gcg ctg gcc aat gat cct			547
Gly Gln Arg Gln Arg Ala Leu Ile Ala Met Ala Leu Ala Asn Asp Pro	135	140	145
gac ctg ttg atc tgc gat gaa ccc acc acg gct ttg gat gtg gtt gtg			595
Asp Leu Leu Ile Cys Asp Glu Pro Thr Thr Ala Leu Asp Val Val Val	150	155	160
caa aaa caa atc gtc gat ctg ctg ctg cgt ctc acc aaa gaa cgt ggc			643
Gln Lys Gln Ile Val Asp Leu Leu Leu Arg Leu Thr Lys Glu Arg Gly	170	175	180
acc gct tta ttg ttc atc acc cac gat ctt gga ctc atc gcg cgc acc			691
Thr Ala Leu Leu Phe Ile Thr His Asp Leu Gly Leu Ile Ala Arg Thr	185	190	195
tgc gaa cgc tta ttg gtg atg aaa tcc ggc gaa acc gta gaa cgc ggc			739
Cys Glu Arg Leu Leu Val Met Lys Ser Gly Glu Thr Val Glu Arg Gly	200	205	210
gac acc gag gca att ctt cgc tcc ccc gcc cat tcc tat acc caa cag			787
Asp Thr Glu Ala Ile Leu Arg Ser Pro Ala His Ser Tyr Thr Gln Gln	215	220	225
ctc ctt gat gct tca atc ctt gac cag cca gaa atc gcc tca gat tct			835
Leu Leu Asp Ala Ser Ile Leu Asp Gln Pro Glu Ile Ala Ser Asp Ser	230	235	240
			245

ggc gcg ccg gta gtg att gat gtg gag gag gcg tcg aaa agc ttt aaa	883
Gly Ala Pro Val Val Ile Asp Val Glu Glu Ala Ser Lys Ser Phe Lys	
250 255 260	
gaa acc acc gcc ctc cac aag gtt tca ttg gcg gtg cgc aaa ggt gac	931
Glu Thr Thr Ala Leu His Lys Val Ser Leu Ala Val Arg Lys Gly Asp	
265 270 275	
ctg ctt gga ata gtc ggc gga tca ggt tcc ggc aaa acg act ctg ctg	979
Leu Leu Gly Ile Val Gly Gly Ser Gly Ser Gly Lys Thr Thr Leu Leu	
280 285 290	
aag ctc atc gcc ggt ttg gat aag ccc aca acc ggt acc gtt gcg gta	1027
Lys Leu Ile Ala Gly Leu Asp Lys Pro Thr Thr Gly Thr Val Ala Val	
295 300 305	
acc ggt ggt gtg cag atg gtg ttt cag gat ccc caa tca agc ctc aac	1075
Thr Gly Gly Val Gln Met Val Phe Gln Asp Pro Gln Ser Ser Leu Asn	
310 315 320 325	
cca cgg atg aaa atc aaa gac att gtc gcc gaa cca ctg ctt ggt tgg	1123
Pro Arg Met Lys Ile Lys Asp Ile Val Ala Glu Pro Leu Leu Gly Trp	
330 335 340	
aac gcg gcg gag aaa acc aca cgg gtt gcg gaa gtc atc acc caa gtg	1171
Asn Ala Ala Glu Lys Thr Thr Arg Val Ala Glu Val Ile Thr Gln Val	
345 350 355	
gga ctg agc ccc gat gtc tta gat cgc tac ccc cac gaa ttc tcc gga	1219
Gly Leu Ser Pro Asp Val Leu Asp Arg Tyr Pro His Glu Phe Ser Gly	
360 365 370	
gga cag cgc caa cga atc tcc atc gcc aga gcc ctc gcc atc aaa cca	1267
Gly Gln Arg Gln Arg Ile Ser Ile Ala Arg Ala Leu Ala Ile Lys Pro	
375 380 385	
gcg atc ctg ctt gcc gac gaa cct gtc tcc gcc ctc gat gtg tcc gta	1315
Ala Ile Leu Leu Ala Asp Glu Pro Val Ser Ala Leu Asp Val Ser Val	
390 395 400 405	
cgt aaa caa gta ctg gat ctt ctc caa caa ctc gtc gaa gaa tac ggc	1363
Arg Lys Gln Val Leu Asp Leu Leu Gln Gln Leu Val Glu Glu Tyr Gly	
410 415 420	
atc acc ttg gtg ttc gtc tcc cac gat ctg gca gtg gtg aga cac ctg	1411
Ile Thr Leu Val Phe Val Ser His Asp Leu Ala Val Val Arg His Leu	
425 430 435	
tgc aca acc gtg tgg gtg atg gaa cag gga cga gtc ctt gag caa ggg	1459
Cys Thr Thr Val Trp Val Met Glu Gln Gly Arg Val Leu Glu Gln Gly	
440 445 450	
ccc atc gat tcg gtt tat gat cac cca cag acc gaa tac acc aag gag	1507
Pro Ile Asp Ser Val Tyr Asp His Pro Gln Thr Glu Tyr Thr Lys Glu	
455 460 465	
ctg ctt gat gcc gtt ccg cgg ttg agc ctt taaaccagcg cagatgacaa cgc	1560
Leu Leu Asp Ala Val Pro Arg Leu Ser Leu	
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<210> 130

<211> 479

<212> PRT

<213> Corynebacterium glutamicum

<400> 130

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			20					25					30		

Ser	Gly	Ser	Gly	Lys	Ser	Leu	Thr	Ala	Leu	Ser	Ile	Met	Gly	Leu	Thr
		35					40					45			

Asp	Leu	Pro	Thr	Thr	Gly	Gln	Ile	Thr	Phe	Asn	Gly	Lys	Pro	Ser	Ala
	50					55					60				

Thr	Phe	Arg	Gly	Thr	Arg	Ile	Ala	Met	Val	Phe	Gln	Glu	Pro	Met	Ser
65					70					75					80

Ala	Leu	Asn	Pro	Leu	Met	Arg	Ile	Gly	Arg	Gln	Ile	Glu	Glu	Met	Met
				85					90					95	

Thr	Leu	His	Gly	Ala	Ser	Lys	Lys	Asp	Ala	Arg	Ala	Arg	Leu	Lys	Ser
			100					105					110		

Leu	Leu	Ile	Asp	Val	Ser	Leu	Pro	Glu	Arg	Thr	Ala	Ser	Ala	Tyr	Pro
		115					120					125			

His	Glu	Leu	Ser	Gly	Gly	Gln	Arg	Gln	Arg	Ala	Leu	Ile	Ala	Met	Ala
	130					135					140				

Leu	Ala	Asn	Asp	Pro	Asp	Leu	Leu	Ile	Cys	Asp	Glu	Pro	Thr	Thr	Ala
145					150					155					160

Leu	Asp	Val	Val	Val	Gln	Lys	Gln	Ile	Val	Asp	Leu	Leu	Leu	Arg	Leu
			165						170					175	

Thr	Lys	Glu	Arg	Gly	Thr	Ala	Leu	Leu	Phe	Ile	Thr	His	Asp	Leu	Gly
			180				185						190		

Leu	Ile	Ala	Arg	Thr	Cys	Glu	Arg	Leu	Leu	Val	Met	Lys	Ser	Gly	Glu
		195					200					205			

Thr	Val	Glu	Arg	Gly	Asp	Thr	Glu	Ala	Ile	Leu	Arg	Ser	Pro	Ala	His
	210					215					220				

Ser	Tyr	Thr	Gln	Gln	Leu	Leu	Asp	Ala	Ser	Ile	Leu	Asp	Gln	Pro	Glu
225					230					235					240

Ile	Ala	Ser	Asp	Ser	Gly	Ala	Pro	Val	Val	Ile	Asp	Val	Glu	Glu	Ala
				245					250					255	

Ser	Lys	Ser	Phe	Lys	Glu	Thr	Thr	Ala	Leu	His	Lys	Val	Ser	Leu	Ala
			260					265					270		

Val	Arg	Lys	Gly	Asp	Leu	Leu	Gly	Ile	Val	Gly	Gly	Ser	Gly	Ser	Gly
		275					280					285			

Lys Thr Thr Leu Leu Lys Leu Ile Ala Gly Leu Asp Lys Pro Thr Thr
 290 295 300
 Gly Thr Val Ala Val Thr Gly Gly Val Gln Met Val Phe Gln Asp Pro
 305 310 315 320
 Gln Ser Ser Leu Asn Pro Arg Met Lys Ile Lys Asp Ile Val Ala Glu
 325 330 335
 Pro Leu Leu Gly Trp Asn Ala Ala Glu Lys Thr Thr Arg Val Ala Glu
 340 345 350
 Val Ile Thr Gln Val Gly Leu Ser Pro Asp Val Leu Asp Arg Tyr Pro
 355 360 365
 His Glu Phe Ser Gly Gly Gln Arg Gln Arg Ile Ser Ile Ala Arg Ala
 370 375 380
 Leu Ala Ile Lys Pro Ala Ile Leu Leu Ala Asp Glu Pro Val Ser Ala
 385 390 395 400
 Leu Asp Val Ser Val Arg Lys Gln Val Leu Asp Leu Leu Gln Gln Leu
 405 410 415
 Val Glu Glu Tyr Gly Ile Thr Leu Val Phe Val Ser His Asp Leu Ala
 420 425 430
 Val Val Arg His Leu Cys Thr Thr Val Trp Val Met Glu Gln Gly Arg
 435 440 445
 Val Leu Glu Gln Gly Pro Ile Asp Ser Val Tyr Asp His Pro Gln Thr
 450 455 460
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<211> 1118

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(1095)

<223> FRXA02795

<400> 131

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 Leu Ser Gly Gly Gln Arg Gln Arg Ala Leu Ile Ala Met Ala Leu Ala
 20 25 30
 aat gat cct gac ctg ttg atc tgc gat gaa ccc acc acg gct ttg gat 144
 Asn Asp Pro Asp Leu Leu Ile Cys Asp Glu Pro Thr Thr Ala Leu Asp
 35 40 45
 gtg gtt gtg caa aaa caa atc gtc gat ctg ctg ctg cgt ctc acc aaa 192

Val	Val	Val	Gln	Lys	Gln	Ile	Val	Asp	Leu	Leu	Leu	Arg	Leu	Thr	Lys	
	50					55					60					
gaa	cgt	ggc	acc	gct	tta	ttg	ttc	atc	acc	cac	gat	ctt	gga	ctc	atc	240
Glu	Arg	Gly	Thr	Ala	Leu	Leu	Phe	Ile	Thr	His	Asp	Leu	Gly	Leu	Ile	
.65					70				75						80	
gcg	cgc	acc	tgc	gaa	cgc	tta	ttg	gtg	atg	aaa	tcc	ggc	gaa	acc	gta	288
Ala	Arg	Thr	Cys	Glu	Arg	Leu	Leu	Val	Met	Lys	Ser	Gly	Glu	Thr	Val	
				85					90						95	
gaa	cgc	ggc	gac	acc	gag	gca	att	ctt	cgc	tcc	ccc	gcc	cat	tcg	tat	336
Glu	Arg	Gly	Asp	Thr	Glu	Ala	Ile	Leu	Arg	Ser	Pro	Ala	His	Ser	Tyr	
			100					105					110			
acc	caa	cag	ctc	ctt	gat	gct	tca	atc	ctt	gac	cag	cca	gaa	atc	gcc	384
Thr	Gln	Gln	Leu	Leu	Asp	Ala	Ser	Ile	Leu	Asp	Gln	Pro	Glu	Ile	Ala	
		115						120				125				
tca	gat	tct	ggc	gcg	ccg	gta	gtg	att	gat	gtg	gag	gag	gcg	tcg	aaa	432
Ser	Asp	Ser	Gly	Ala	Pro	Val	Val	Ile	Asp	Val	Glu	Glu	Ala	Ser	Lys	
	130					135					140					
agc	ttt	aaa	gaa	acc	acc	gcc	ctc	cac	aag	gtt	tca	ttg	gcg	gtg	cgc	480
Ser	Phe	Lys	Glu	Thr	Thr	Ala	Leu	His	Lys	Val	Ser	Leu	Ala	Val	Arg	
145					150					155					160	
aaa	ggt	gac	ctg	ctt	gga	ata	gtc	ggc	gga	tca	ggt	tcc	ggc	aaa	acg	528
Lys	Gly	Asp	Leu	Leu	Gly	Ile	Val	Gly	Gly	Ser	Gly	Ser	Gly	Lys	Thr	
				165					170						175	
act	ctg	ctg	aag	ctc	atc	gcc	ggt	ttg	gat	aag	ccc	aca	acc	ggt	acc	576
Thr	Leu	Leu	Lys	Leu	Ile	Ala	Gly	Leu	Asp	Lys	Pro	Thr	Thr	Gly	Thr	
			180					185						190		
gtt	gcg	gta	acc	ggt	ggt	gtg	cag	atg	gtg	ttt	cag	gat	ccc	caa	tca	624
Val	Ala	Val	Thr	Gly	Gly	Val	Gln	Met	Val	Phe	Gln	Asp	Pro	Gln	Ser	
		195					200					205				
agc	ctc	aac	cca	cgg	atg	aaa	atc	aaa	gac	att	gtc	gcc	gaa	cca	ctg	672
Ser	Leu	Asn	Pro	Arg	Met	Lys	Ile	Lys	Asp	Ile	Val	Ala	Glu	Pro	Leu	
	210					215					220					
ctt	ggt	tgg	aac	gcg	gcg	gag	aaa	acc	aca	cgg	gtt	gcg	gaa	gtc	atc	720
Leu	Gly	Trp	Asn	Ala	Ala	Glu	Lys	Thr	Thr	Arg	Val	Ala	Glu	Val	Ile	
225					230					235					240	
acc	caa	gtg	gga	ctg	agc	ccc	gat	gtc	tta	gat	cgc	tac	ccc	cac	gaa	768
Thr	Gln	Val	Gly	Leu	Ser	Pro	Asp	Val	Leu	Asp	Arg	Tyr	Pro	His	Glu	
				245					250						255	
ttc	tcc	gga	gga	cag	cgc	caa	cga	atc	tcc	atc	gcc	aga	gcc	ctc	gcc	816
Phe	Ser	Gly	Gly	Gln	Arg	Gln	Arg	Ile	Ser	Ile	Ala	Arg	Ala	Leu	Ala	
			260					265					270			
atc	aaa	cca	gcg	atc	ctg	ctt	gcc	gac	gaa	cct	gtc	tcc	gcc	ctc	gat	864
Ile	Lys	Pro	Ala	Ile	Leu	Leu	Ala	Asp	Glu	Pro	Val	Ser	Ala	Leu	Asp	
		275					280					285				
gtg	tcc	gta	cgt	aaa	caa	gta	ctg	gat	ctt	ctc	caa	caa	ctc	gtc	gaa	912
Val	Ser	Val	Arg	Lys	Gln	Val	Leu	Asp	Leu	Leu	Gln	Gln	Leu	Val	Glu	

290 295 300
 gaa tac ggc atc acc ttg gtg ttc gtc tcc cac gat ctg gca gtg gtg 960
 Glu Tyr Gly Ile Thr Leu Val Phe Val Ser His Asp Leu Ala Val Val
 305 310 315 320
 aga cac ctg tgc aca acc gtg tgg gtg atg gaa cag gga cga gtc ctt 1008
 Arg His Leu Cys Thr Thr Val Trp Val Met Glu Gln Gly Arg Val Leu
 325 330 335
 gag caa ggg ccc atc gat tgc gtt tat gat cac cca cag acc gaa tac 1056
 Glu Gln Gly Pro Ile Asp Ser Val Tyr Asp His Pro Gln Thr Glu Tyr
 340 345 350
 acc aag gag ctg ctt gat gcc gtt ccg cgg ttg agc ctt taaaccagcg 1105
 Thr Lys Glu Leu Leu Asp Ala Val Pro Arg Leu Ser Leu
 355 360 365
 cagatgacaa cgc 1118

 <210> 132
 <211> 365
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 <213> Corynebacterium glutamicum

 <400> 132
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 Asn Asp Pro Asp Leu Leu Ile Cys Asp Glu Pro Thr Thr Ala Leu Asp
 35 40 45
 Val Val Val Gln Lys Gln Ile Val Asp Leu Leu Leu Arg Leu Thr Lys
 50 55 60
 Glu Arg Gly Thr Ala Leu Leu Phe Ile Thr His Asp Leu Gly Leu Ile
 65 70 75 80
 Ala Arg Thr Cys Glu Arg Leu Leu Val Met Lys Ser Gly Glu Thr Val
 85 90 95
 Glu Arg Gly Asp Thr Glu Ala Ile Leu Arg Ser Pro Ala His Ser Tyr
 100 105 110
 Thr Gln Gln Leu Leu Asp Ala Ser Ile Leu Asp Gln Pro Glu Ile Ala
 115 120 125
 Ser Asp Ser Gly Ala Pro Val Val Ile Asp Val Glu Glu Ala Ser Lys
 130 135 140
 Ser Phe Lys Glu Thr Thr Ala Leu His Lys Val Ser Leu Ala Val Arg
 145 150 155 160
 Lys Gly Asp Leu Leu Gly Ile Val Gly Gly Ser Gly Ser Gly Lys Thr
 165 170 175
 Thr Leu Leu Lys Leu Ile Ala Gly Leu Asp Lys Pro Thr Thr Gly Thr

180					185					190					
Val	Ala	Val	Thr	Gly	Gly	Val	Gln	Met	Val	Phe	Gln	Asp	Pro	Gln	Ser
	195					200						205			
Ser	Leu	Asn	Pro	Arg	Met	Lys	Ile	Lys	Asp	Ile	Val	Ala	Glu	Pro	Leu
	210					215					220				
Leu	Gly	Trp	Asn	Ala	Ala	Glu	Lys	Thr	Thr	Arg	Val	Ala	Glu	Val	Ile
	225					230					235				240
Thr	Gln	Val	Gly	Leu	Ser	Pro	Asp	Val	Leu	Asp	Arg	Tyr	Pro	His	Glu
				245					250					255	
Phe	Ser	Gly	Gly	Gln	Arg	Gln	Arg	Ile	Ser	Ile	Ala	Arg	Ala	Leu	Ala
				260					265					270	
Ile	Lys	Pro	Ala	Ile	Leu	Leu	Ala	Asp	Glu	Pro	Val	Ser	Ala	Leu	Asp
		275					280						285		
Val	Ser	Val	Arg	Lys	Gln	Val	Leu	Asp	Leu	Leu	Gln	Gln	Leu	Val	Glu
		290					295					300			
Glu	Tyr	Gly	Ile	Thr	Leu	Val	Phe	Val	Ser	His	Asp	Leu	Ala	Val	Val
	305					310					315				320
Arg	His	Leu	Cys	Thr	Thr	Val	Trp	Val	Met	Glu	Gln	Gly	Arg	Val	Leu
				325					330					335	
Glu	Gln	Gly	Pro	Ile	Asp	Ser	Val	Tyr	Asp	His	Pro	Gln	Thr	Glu	Tyr
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Thr	Lys	Glu	Leu	Leu	Asp	Ala	Val	Pro	Arg	Leu	Ser	Leu			
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<210> 133
 <211> 1854
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1831)
 <223> RXN01939

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 Met Thr Thr Asn Ile
 1 5
 cca caa acc ccc aac cac gag ggt gaa cag cca ctg ctc gag ctg aag 163
 Pro Gln Thr Pro Asn His Glu Gly Glu Gln Pro Leu Leu Glu Leu Lys
 10 15 20
 gat cta aag att tcc ttc acc tcc tcc acc ggt gtt gtc gac gct gtc 211
 Asp Leu Lys Ile Ser Phe Thr Ser Thr Gly Val Val Asp Ala Val
 25 30 35

cgt ggc gca aac ctc acc att tat cct ggc caa tct gtt gcc atc gtg	259
Arg Gly Ala Asn Leu Thr Ile Tyr Pro Gly Gln Ser Val Ala Ile Val	
40 45 50	
ggt gaa tcc ggt tca ggt aaa tcg acc acg gca atg tcg atc atc ggt	307
Gly Glu Ser Gly Ser Gly Lys Ser Thr Thr Ala Met Ser Ile Ile Gly	
55 60 65	
ctg ctt cca ggc acc ggc aaa gtg acc gaa ggt tcc atc atg ttt gat	355
Leu Leu Pro Gly Thr Gly Lys Val Thr Glu Gly Ser Ile Met Phe Asp	
70 75 80 85	
ggc caa gac atc aca ggc ttg agt aac aag cag atg gaa aag tac cgc	403
Gly Gln Asp Ile Thr Gly Leu Ser Asn Lys Gln Met Glu Lys Tyr Arg	
90 95 100	
ggt tca gaa atc gga ctg gtc ccc cag gat ccg atg acc aac ttg aac	451
Gly Ser Glu Ile Gly Leu Val Pro Gln Asp Pro Met Thr Asn Leu Asn	
105 110 115	
ccg gtg tgg cgc atc ggc acc cag gtc aag gaa tcc ctc cga gcc aac	499
Pro Val Trp Arg Ile Gly Thr Gln Val Lys Glu Ser Leu Arg Ala Asn	
120 125 130	
cac gtg gtt cca ggc tca gag atg gac aag cgc gtg gca gaa gtt ctg	547
His Val Val Pro Gly Ser Glu Met Asp Lys Arg Val Ala Glu Val Leu	
135 140 145	
gcc gag gca ggt ctt cct gat gct gag cgt cgc gca aag cag tac cca	595
Ala Glu Ala Gly Leu Pro Asp Ala Glu Arg Arg Ala Lys Gln Tyr Pro	
150 155 160 165	
cat gag ttc tct ggc ggt atg cgc cag cgc gca ctg atc gcc att ggt	643
His Glu Phe Ser Gly Gly Met Arg Gln Arg Ala Leu Ile Ala Ile Gly	
170 175 180	
ttg gcg gca cgc ccg aag ctc ttg atc gcc gac gag ccc acc tct gcg	691
Leu Ala Ala Arg Pro Lys Leu Leu Ile Ala Asp Glu Pro Thr Ser Ala	
185 190 195	
ctg gat gtc acc gtg cag cgc caa atc ctt gat cac ctt gaa aca ctg	739
Leu Asp Val Thr Val Gln Arg Gln Ile Leu Asp His Leu Glu Thr Leu	
200 205 210	
acc aag gat ctc ggc acc gca gtg cta ttt att acc cac gac ttg ggc	787
Thr Lys Asp Leu Gly Thr Ala Val Leu Phe Ile Thr His Asp Leu Gly	
215 220 225	
ctt gcc gct gag cgc gcg gag cac ctc gtg gtg atg cac cgc gga cgc	835
Leu Ala Ala Glu Arg Ala Glu His Leu Val Val Met His Arg Gly Arg	
230 235 240 245	
atc gtg gag tcc ggg cca tca ttg aag att ctg cgc aat cca cag cac	883
Ile Val Glu Ser Gly Pro Ser Leu Lys Ile Leu Arg Asn Pro Gln His	
250 255 260	
cca tat acc caa cgc ttg gtt aag gct gcg ccg tct ctg gct tct gca	931
Pro Tyr Thr Gln Arg Leu Val Lys Ala Ala Pro Ser Leu Ala Ser Ala	
265 270 275	
cgt att caa agt gcg cag gaa caa ggc att gaa tct gca gaa ctg ctc	979

Arg	Ile	Gln	Ser	Ala	Gln	Glu	Gln	Gly	Ile	Glu	Ser	Ala	Glu	Leu	Leu		
	280						285					290					
tct	gca	acg	gcc	gtt	gct	gag	ggc	act	att	cca	gag	atg	gaa	gaa	aaa	1027	
Ser	Ala	Thr	Ala	Val	Ala	Glu	Gly	Thr	Ile	Pro	Glu	Met	Glu	Glu	Lys		
	295					300					305						
gtt	atc	gag	gtg	aaa	aac	ctc	acc	cgc	gaa	ttt	gat	atc	cgc	ggg	gcc	1075	
Val	Ile	Glu	Val	Lys	Asn	Leu	Thr	Arg	Glu	Phe	Asp	Ile	Arg	Gly	Ala		
310					315				320					325			
cgt	ggc	gat	aag	aag	aag	ctg	aag	gcc	gtt	gat	gat	gtg	tcc	ttc	ttc	1123	
Arg	Gly	Asp	Lys	Lys	Lys	Leu	Lys	Ala	Val	Asp	Asp	Val	Ser	Phe	Phe		
			330					335					340				
gta	cgt	aaa	ggc	acc	acc	acc	gca	ctt	gtg	ggg	gaa	tcc	ggg	tcg	ggg	1171	
Val	Arg	Lys	Gly	Thr	Thr	Thr	Ala	Leu	Val	Gly	Glu	Ser	Gly	Ser	Gly		
		345					350					355					
aaa	tcc	acc	gtg	gcc	aac	atg	gtg	ctc	aac	ctt	ctc	gag	cca	acc	agc	1219	
Lys	Ser	Thr	Val	Ala	Asn	Met	Val	Leu	Asn	Leu	Leu	Glu	Pro	Thr	Ser		
	360					365					370						
gga	gag	gtg	ctc	tac	aac	ggc	acc	gat	ctt	acg	tcc	ttg	agc	cac	aag	1267	
Gly	Glu	Val	Leu	Tyr	Asn	Gly	Thr	Asp	Leu	Thr	Ser	Leu	Ser	His	Lys		
	375				380				385								
gaa	atc	ttc	caa	atg	cga	cgc	aaa	ctg	cag	gtg	gtg	ttc	cag	aac	ccc	1315	
Glu	Ile	Phe	Gln	Met	Arg	Arg	Lys	Leu	Gln	Val	Val	Phe	Gln	Asn	Pro		
390				395			400							405			
tac	ggc	tcg	ctt	gat	ccg	atg	tac	tcc	atc	tac	cgg	tgt	att	gag	gaa	1363	
Tyr	Gly	Ser	Leu	Asp	Pro	Met	Tyr	Ser	Ile	Tyr	Arg	Cys	Ile	Glu	Glu		
			410				415						420				
ccg	ctg	acc	atc	cac	aag	gtt	ggg	gga	gac	cgc	aag	gca	cgc	gaa	gct	1411	
Pro	Leu	Thr	Ile	His	Lys	Val	Gly	Gly	Asp	Arg	Lys	Ala	Arg	Glu	Ala		
		425				430			435								
cgc	gtc	gct	gaa	ctt	ctc	gat	atg	gtg	tcc	atg	ccc	agg	tcc	acc	atg	1459	
Arg	Val	Ala	Glu	Leu	Leu	Asp	Met	Val	Ser	Met	Pro	Arg	Ser	Thr	Met		
	440					445					450						
cgc	cgc	tac	ccc	aac	gag	ctt	tcc	ggg	ggc	caa	cgt	cag	cgc	atc	gcc	1507	
Arg	Arg	Tyr	Pro	Asn	Glu	Leu	Ser	Gly	Gly	Gln	Arg	Gln	Arg	Ile	Ala		
	455				460					465							
atc	gcc	cgt	gca	ttg	gca	ctg	aat	cca	gaa	gtg	atc	gtg	ttg	gat	gaa	1555	
Ile	Ala	Arg	Ala	Leu	Ala	Leu	Asn	Pro	Glu	Val	Ile	Val	Leu	Asp	Glu		
470				475				480						485			
gcg	gtt	tcc	gct	ttg	gac	gtg	ttg	gtt	cag	aac	cag	atc	ctc	acc	ctg	1603	
Ala	Val	Ser	Ala	Leu	Asp	Val	Leu	Val	Gln	Asn	Gln	Ile	Leu	Thr	Leu		
			490				495						500				
ctt	gca	gaa	ctt	cag	cag	gaa	ctg	aag	ctc	acc	tat	ttg	ttc	atc	acc	1651	
Leu	Ala	Glu	Leu	Gln	Gln	Glu	Leu	Lys	Leu	Thr	Tyr	Leu	Phe	Ile	Thr		
		505					510					515					
cac	gac	ttg	gcc	gtt	gtt	cga	caa	acc	gcc	gac	gat	gtt	gtg	gtg	atg	1699	
His	Asp	Leu	Ala	Val	Val	Arg	Gln	Thr	Ala	Asp	Asp	Val	Val	Val	Met		

520 525 530
 caa aag gga cga atc gtt gaa aag ggt cgt acc gac gac atc ttc aac 1747
 Gln Lys Gly Arg Ile Val Glu Lys Gly Arg Thr Asp Asp Ile Phe Asn
 535 540 545

 gat cct cag cag cac tac acc cgc gat ttg atc aat gcg gta cct ggt 1795
 Asp Pro Gln Gln His Tyr Thr Arg Asp Leu Ile Asn Ala Val Pro Gly
 550 555 560 565

 ctg gga atc gag ttg ggt act gga gaa aac ctg gtt taaccgcac 1841
 Leu Gly Ile Glu Leu Gly Thr Gly Glu Asn Leu Val
 570 575

 agcctcacta aac 1854

 <210> 134
 <211> 577
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 134
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 20 25 30

 Val Val Asp Ala Val Arg Gly Ala Asn Leu Thr Ile Tyr Pro Gly Gln
 35 40 45

 Ser Val Ala Ile Val Gly Glu Ser Gly Ser Gly Lys Ser Thr Thr Ala
 50 55 60

 Met Ser Ile Ile Gly Leu Leu Pro Gly Thr Gly Lys Val Thr Glu Gly
 65 70 75 80

 Ser Ile Met Phe Asp Gly Gln Asp Ile Thr Gly Leu Ser Asn Lys Gln
 85 90 95

 Met Glu Lys Tyr Arg Gly Ser Glu Ile Gly Leu Val Pro Gln Asp Pro
 100 105 110

 Met Thr Asn Leu Asn Pro Val Trp Arg Ile Gly Thr Gln Val Lys Glu
 115 120 125

 Ser Leu Arg Ala Asn His Val Val Pro Gly Ser Glu Met Asp Lys Arg
 130 135 140

 Val Ala Glu Val Leu Ala Glu Ala Gly Leu Pro Asp Ala Glu Arg Arg
 145 150 155 160

 Ala Lys Gln Tyr Pro His Glu Phe Ser Gly Gly Met Arg Gln Arg Ala
 165 170 175

 Leu Ile Ala Ile Gly Leu Ala Ala Arg Pro Lys Leu Leu Ile Ala Asp
 180 185 190

 Glu Pro Thr Ser Ala Leu Asp Val Thr Val Gln Arg Gln Ile Leu Asp
 195 200 205

His Leu Glu Thr Leu Thr Lys Asp Leu Gly Thr Ala Val Leu Phe Ile
 210 215 220
 Thr His Asp Leu Gly Leu Ala Ala Glu Arg Ala Glu His Leu Val Val
 225 230 235 240
 Met His Arg Gly Arg Ile Val Glu Ser Gly Pro Ser Leu Lys Ile Leu
 245 250 255
 Arg Asn Pro Gln His Pro Tyr Thr Gln Arg Leu Val Lys Ala Ala Pro
 260 265 270
 Ser Leu Ala Ser Ala Arg Ile Gln Ser Ala Gln Glu Gln Gly Ile Glu
 275 280 285
 Ser Ala Glu Leu Leu Ser Ala Thr Ala Val Ala Glu Gly Thr Ile Pro
 290 295 300
 Glu Met Glu Glu Lys Val Ile Glu Val Lys Asn Leu Thr Arg Glu Phe
 305 310 315 320
 Asp Ile Arg Gly Ala Arg Gly Asp Lys Lys Lys Leu Lys Ala Val Asp
 325 330 335
 Asp Val Ser Phe Phe Val Arg Lys Gly Thr Thr Thr Ala Leu Val Gly
 340 345 350
 Glu Ser Gly Ser Gly Lys Ser Thr Val Ala Asn Met Val Leu Asn Leu
 355 360 365
 Leu Glu Pro Thr Ser Gly Glu Val Leu Tyr Asn Gly Thr Asp Leu Thr
 370 375 380
 Ser Leu Ser His Lys Glu Ile Phe Gln Met Arg Arg Lys Leu Gln Val
 385 390 395 400
 Val Phe Gln Asn Pro Tyr Gly Ser Leu Asp Pro Met Tyr Ser Ile Tyr
 405 410 415
 Arg Cys Ile Glu Glu Pro Leu Thr Ile His Lys Val Gly Gly Asp Arg
 420 425 430
 Lys Ala Arg Glu Ala Arg Val Ala Glu Leu Leu Asp Met Val Ser Met
 435 440 445
 Pro Arg Ser Thr Met Arg Arg Tyr Pro Asn Glu Leu Ser Gly Gly Gln
 450 455 460
 Arg Gln Arg Ile Ala Ile Ala Arg Ala Leu Ala Leu Asn Pro Glu Val
 465 470 475 480
 Ile Val Leu Asp Glu Ala Val Ser Ala Leu Asp Val Leu Val Gln Asn
 485 490 495
 Gln Ile Leu Thr Leu Leu Ala Glu Leu Gln Gln Glu Leu Lys Leu Thr
 500 505 510
 Tyr Leu Phe Ile Thr His Asp Leu Ala Val Val Arg Gln Thr Ala Asp
 515 520 525

Asp Val Val Val Met Gln Lys Gly Arg Ile Val Glu Lys Gly Arg Thr
530 535 540

Asp Asp Ile Phe Asn Asp Pro Gln Gln His Tyr Thr Arg Asp Leu Ile
545 550 555 560

Asn Ala Val Pro Gly Leu Gly Ile Glu Leu Gly Thr Gly Glu Asn Leu
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Val

<210> 135

<211> 691

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(691)

<223> FRXA00761

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atgtcgtccg cgacgctctg gatcctaagt cgaggaagcg atg acc acc aac atc 115
Met Thr Thr Asn Ile
1 5

cca caa acc ccc aac cac gag ggt gaa cag cca ctg ctc gag ctg aag 163
Pro Gln Thr Pro Asn His Glu Gly Glu Gln Pro Leu Leu Glu Leu Lys
10 15 20

gat cta aag att tcc ttc acc tcc tcc acc ggt gtt gtc gac gct gtc 211
Asp Leu Lys Ile Ser Phe Thr Ser Ser Thr Gly Val Val Asp Ala Val
25 30 35

cgt ggc gca aac ctc acc att tat cct ggc caa tct gtt gcc atc gtg 259
Arg Gly Ala Asn Leu Thr Ile Tyr Pro Gly Gln Ser Val Ala Ile Val
40 45 50

ggt gaa tcc ggt tca ggt aaa tcg acc acg gca atg tcg atc atc ggt 307
Gly Glu Ser Gly Ser Gly Lys Ser Thr Thr Ala Met Ser Ile Ile Gly
55 60 65

ctg ctt cca ggc acc ggc aaa gtg acc gaa ggt tcc atc atg ttt gat 355
Leu Leu Pro Gly Thr Gly Lys Val Thr Glu Gly Ser Ile Met Phe Asp
70 75 80 85

ggc caa gac atc aca ggc ttg agt aac aag cag atg gaa aag tac cgc 403
Gly Gln Asp Ile Thr Gly Leu Ser Asn Lys Gln Met Glu Lys Tyr Arg
90 95 100

ggt tca gaa atc gga ctg gtc ccc cag gat ccg atg acc aac ttg aac 451
Gly Ser Glu Ile Gly Leu Val Pro Gln Asp Pro Met Thr Asn Leu Asn
105 110 115

ccg gtg tgg cgc atc ggc acc cag gtc aag gaa tcc ctc cga gcc aac 499
Pro Val Trp Arg Ile Gly Thr Gln Val Lys Glu Ser Leu Arg Ala Asn
120 125 130

cac gtg gtt cca ggc tca gag atg gac aag cgc gtg gca gaa gtt ctg 547
 His Val Val Pro Gly Ser Glu Met Asp Lys Arg Val Ala Glu Val Leu
 135 140 145

gcc gag gca ggt ctt cct gat gct gag cgt cgc gca aag cag tac cca 595
 Ala Glu Ala Gly Leu Pro Asp Ala Glu Arg Arg Ala Lys Gln Tyr Pro
 150 155 160 165

cat gag ttc tct ggc ggt atg cgc cac cgc gca ctg atc gcc att ggt 643
 His Glu Phe Ser Gly Gly Met Arg His Arg Ala Leu Ile Ala Ile Gly
 170 175 180

ttg gcg gca cgc ccg aag ctc ttg atc gcc gac gag ccc acc tct gcg 691
 Leu Ala Ala Arg Pro Lys Leu Leu Ile Ala Asp Glu Pro Thr Ser Ala
 185 190 195

<210> 136

<211> 197

<212> PRT

<213> Corynebacterium glutamicum

<400> 136

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Leu Leu Glu Leu Lys Asp Leu Lys Ile Ser Phe Thr Ser Ser Thr Gly
 20 25 30

Val Val Asp Ala Val Arg Gly Ala Asn Leu Thr Ile Tyr Pro Gly Gln
 35 40 45

Ser Val Ala Ile Val Gly Glu Ser Gly Ser Gly Lys Ser Thr Thr Ala
 50 55 60

Met Ser Ile Ile Gly Leu Leu Pro Gly Thr Gly Lys Val Thr Glu Gly
 65 70 75 80

Ser Ile Met Phe Asp Gly Gln Asp Ile Thr Gly Leu Ser Asn Lys Gln
 85 90 95

Met Glu Lys Tyr Arg Gly Ser Glu Ile Gly Leu Val Pro Gln Asp Pro
 100 105 110

Met Thr Asn Leu Asn Pro Val Trp Arg Ile Gly Thr Gln Val Lys Glu
 115 120 125

Ser Leu Arg Ala Asn His Val Val Pro Gly Ser Glu Met Asp Lys Arg
 130 135 140

Val Ala Glu Val Leu Ala Glu Ala Gly Leu Pro Asp Ala Glu Arg Arg
 145 150 155 160

Ala Lys Gln Tyr Pro His Glu Phe Ser Gly Gly Met Arg His Arg Ala
 165 170 175

Leu Ile Ala Ile Gly Leu Ala Ala Arg Pro Lys Leu Leu Ile Ala Asp
 180 185 190

Glu Pro Thr Ser Ala

195

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 <211> 626
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(603)
 <223> FRXA01939

<400> 137

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1 5 10 15	
caa atg cga cgc aaa ctg cag gtg gtg ttc cag aac ccc tac ggc tcg	96
Gln Met Arg Arg Lys Leu Gln Val Val Phe Gln Asn Pro Tyr Gly Ser	
20 25 30	
ctt gat ccg atg tac tcc atc tac cgg tgt att gag gaa ccg ctg acc	144
Leu Asp Pro Met Tyr Ser Ile Tyr Arg Cys Ile Glu Glu Pro Leu Thr	
35 40 45	
atc cac aag gtt ggt gga gac cgc aag gca cgc gaa gct cgc gtc gtt	192
Ile His Lys Val Gly Gly Asp Arg Lys Ala Arg Glu Ala Arg Val Val	
50 55 60	
gaa ctt ctc gat atg gtg tcc atg ccc agg tcc acc atg cgc cgc tac	240
Glu Leu Leu Asp Met Val Ser Met Pro Arg Ser Thr Met Arg Arg Tyr	
65 70 75 80	
ccc aac gag ctt tcc ggt ggc caa cgt cag cgc atc gcc atc gcc cgt	288
Pro Asn Glu Leu Ser Gly Gly Gln Arg Gln Arg Ile Ala Ile Ala Arg	
85 90 95	
gca ttg gca ctg aat cca gaa gtg atc gtg ttg gat gaa gcg gtt tcc	336
Ala Leu Ala Leu Asn Pro Glu Val Ile Val Leu Asp Glu Ala Val Ser	
100 105 110	
gct ttg gac gtg ttg gtt cag aac cag atc ctc acc ctg ctt gca gaa	384
Ala Leu Asp Val Leu Val Gln Asn Gln Ile Leu Thr Leu Leu Ala Glu	
115 120 125	
ctt cag cag gaa ctg aag ctc acc tat ttg ttc atc acc cac gac ttg	432
Leu Gln Gln Glu Leu Lys Leu Thr Tyr Leu Phe Ile Thr His Asp Leu	
130 135 140	
gcc gtt gtt cga caa acc gcc gac gat gtt gtg gtg atg caa aag gga	480
Ala Val Val Arg Gln Thr Ala Asp Asp Val Val Val Met Gln Lys Gly	
145 150 155 160	
cga atc gtt gaa aag ggt cgt acc gac gac atc ttc aac gat cct cag	528
Arg Ile Val Glu Lys Gly Arg Thr Asp Asp Ile Phe Asn Asp Pro Gln	
165 170 175	
cag cac tac acc cgc gat ttg atc aat gcg gta cct ggt ctg gga atc	576
Gln His Tyr Thr Arg Asp Leu Ile Asn Ala Val Pro Gly Leu Gly Ile	
180 185 190	

gag ttg ggt act gga gaa aac ctg gtt taaccgcac agcctcacta aac 626
 Glu Leu Gly Thr Gly Glu Asn Leu Val
 195 200

<210> 138

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 138

Ser Thr Ser Gly Thr Asp Leu Thr Ser Leu Ser His Lys Glu Ile Phe
 1 5 10 15

Gln Met Arg Arg Lys Leu Gln Val Val Phe Gln Asn Pro Tyr Gly Ser
 20 25 30

Leu Asp Pro Met Tyr Ser Ile Tyr Arg Cys Ile Glu Glu Pro Leu Thr
 35 40 45

Ile His Lys Val Gly Gly Asp Arg Lys Ala Arg Glu Ala Arg Val Val
 50 55 60

Glu Leu Leu Asp Met Val Ser Met Pro Arg Ser Thr Met Arg Arg Tyr
 65 70 75 80

Pro Asn Glu Leu Ser Gly Gly Gln Arg Gln Arg Ile Ala Ile Ala Arg
 85 90 95

Ala Leu Ala Leu Asn Pro Glu Val Ile Val Leu Asp Glu Ala Val Ser
 100 105 110

Ala Leu Asp Val Leu Val Gln Asn Gln Ile Leu Thr Leu Leu Ala Glu
 115 120 125

Leu Gln Gln Glu Leu Lys Leu Thr Tyr Leu Phe Ile Thr His Asp Leu
 130 135 140

Ala Val Val Arg Gln Thr Ala Asp Asp Val Val Val Met Gln Lys Gly
 145 150 155 160

Arg Ile Val Glu Lys Gly Arg Thr Asp Asp Ile Phe Asn Asp Pro Gln
 165 170 175

Gln His Tyr Thr Arg Asp Leu Ile Asn Ala Val Pro Gly Leu Gly Ile
 180 185 190

Glu Leu Gly Thr Gly Glu Asn Leu Val
 195 200

<210> 139

<211> 1047

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1024)

<223> RXN00759

<400> 139

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accataatcc attccccagc aagcaaggac acccacgctc atg ctt cgt tac gtc 115
Met Leu Arg Tyr Val
1 5

ggg cga cgt ttg ctc caa atg att ccg gtc ttt ttc gga gcg acc tta 163
Gly Arg Arg Leu Leu Gln Met Ile Pro Val Phe Phe Gly Ala Thr Leu
10 15 20

ctg att tac gcc ctc gtg ttc ctc atg cct ggt gac cca gtc cag gca 211
Leu Ile Tyr Ala Leu Val Phe Leu Met Pro Gly Asp Pro Val Gln Ala
25 30 35

ttg gga ggt gac cgc ggc cta acc gag gct gcg gcc gag aaa atc cgt 259
Leu Gly Gly Asp Arg Gly Leu Thr Glu Ala Ala Ala Glu Lys Ile Arg
40 45 50

caa gaa tac aat ctt gat aaa ccc ttc atc gtt caa tac ctc ctg tac 307
Gln Glu Tyr Asn Leu Asp Lys Pro Phe Ile Val Gln Tyr Leu Leu Tyr
55 60 65

atc aag ggc atc ttc gtc tta gat ttt gga aca acc ttc tct ggt cag 355
Ile Lys Gly Ile Phe Val Leu Asp Phe Gly Thr Thr Phe Ser Gly Gln
70 75 80 85

cca gtt att gat gtg atg gcc agg gcc ttc ccc gtc acc atc aaa ctc 403
Pro Val Ile Asp Val Met Ala Arg Ala Phe Pro Val Thr Ile Lys Leu
90 95 100

gcc atc atg gcc ctg ctg ttt gaa tca atc ctc ggc att atc ttt ggt 451
Ala Ile Met Ala Leu Leu Phe Glu Ser Ile Leu Gly Ile Ile Phe Gly
105 110 115

gtc atc gca ggt att cgc cgc gga gga atc ttc gac tcc acc gtg ctg 499
Val Ile Ala Gly Ile Arg Arg Gly Gly Ile Phe Asp Ser Thr Val Leu
120 125 130

gtc ctt tct ctg ata gtc atc gca gtc ccc acc ttc gtc att ggt ttc 547
Val Leu Ser Leu Ile Val Ile Ala Val Pro Thr Phe Val Ile Gly Phe
135 140 145

gtg ctg cag ttc tta gtc ggc gtg aaa tgg ggc tta ctg ccc gtc acc 595
Val Leu Gln Phe Leu Val Gly Val Lys Trp Gly Leu Leu Pro Val Thr
150 155 160 165

gta ggt tcc aac aca tca ata acg gcg ctg atc atg ccg gct gtc gta 643
Val Gly Ser Asn Thr Ser Ile Thr Ala Leu Ile Met Pro Ala Val Val
170 175 180

ctg ggt gca gta tgc ttc gcc tac gtt ctt cgc ctc acc aga caa tcc 691
Leu Gly Ala Val Ser Phe Ala Tyr Val Leu Arg Leu Thr Arg Gln Ser
185 190 195

gtg agc gaa aac ctc cgc gct gat tac gtt cga acc gct cga gca aaa 739
Val Ser Glu Asn Leu Arg Ala Asp Tyr Val Arg Thr Ala Arg Ala Lys
200 205 210

ggc atg tcc gga ttc aac gtg atg aac cgc cat gtg ctt cga aac tca 787

Gly Met Ser Gly Phe Asn Val Met Asn Arg His Val Leu Arg Asn Ser
 215 220 225
 ctg att ccc gtt gcc acc ttc ctg ggc gcc gat ctc ggt gca ctg atg 835
 Leu Ile Pro Val Ala Thr Phe Leu Gly Ala Asp Leu Gly Ala Leu Met
 230 235 240 245
 ggt gga gcg att gtc acc gaa ggt atc ttc ggc atc aac ggt gtc ggt 883
 Gly Gly Ala Ile Val Thr Glu Gly Ile Phe Gly Ile Asn Gly Val Gly
 250 255 260
 gga acg ctc tac cag gcc att ttg aaa ggt gaa ccc acc acg gtt gtc 931
 Gly Thr Leu Tyr Gln Ala Ile Leu Lys Gly Glu Pro Thr Thr Val Val
 265 270 275
 tcc att gtc act gtg ctg gtc atc gtc tac atc atc gcc aac ctt ctc 979
 Ser Ile Val Thr Val Leu Val Ile Val Tyr Ile Ile Ala Asn Leu Leu
 280 285 290
 gtg gac ttg atc tac gcc gtt ctc gat ccg agg atc cgc tat gcc 1024
 Val Asp Leu Ile Tyr Ala Val Leu Asp Pro Arg Ile Arg Tyr Ala
 295 300 305
 taataatgaa ttccacacaa acc 1047

<210> 140

<211> 308

<212> PRT

<213> Corynebacterium glutamicum

<400> 140

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 Asp Pro Val Gln Ala Leu Gly Gly Asp Arg Gly Leu Thr Glu Ala Ala
 35 40 45
 Ala Glu Lys Ile Arg Gln Glu Tyr Asn Leu Asp Lys Pro Phe Ile Val
 50 55 60
 Gln Tyr Leu Leu Tyr Ile Lys Gly Ile Phe Val Leu Asp Phe Gly Thr
 65 70 75 80
 Thr Phe Ser Gly Gln Pro Val Ile Asp Val Met Ala Arg Ala Phe Pro
 85 90 95
 Val Thr Ile Lys Leu Ala Ile Met Ala Leu Leu Phe Glu Ser Ile Leu
 100 105 110
 Gly Ile Ile Phe Gly Val Ile Ala Gly Ile Arg Arg Gly Gly Ile Phe
 115 120 125
 Asp Ser Thr Val Leu Val Leu Ser Leu Ile Val Ile Ala Val Pro Thr
 130 135 140
 Phe Val Ile Gly Phe Val Leu Gln Phe Leu Val Gly Val Lys Trp Gly
 145 150 155 160

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<210> 141
<211> 1047
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(1024)
<223> FRXA00759
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<220>
<223> All occurrences of n = any nucleotide

<220>
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tcaccttgaa cacttaaaac ataacttcat ccggcgcttt attagcttga agcgccccgc 60
accataatcc attccccagc aagcaaggac acccacgctc atg ctt cgt tac gtc 115
Met Leu Arg Tyr Val
1 5
ggg cga cgt ttg ctc caa atg att ccg gtc ttt ttc gga gcg acc tta 163
Gly Arg Arg Leu Leu Gln Met Ile Pro Val Phe Phe Gly Ala Thr Leu
10 15 20
ctg att tac gcc ctc gtg ttc ctc atg cct ggt gac cca gtc cag gca 211
Leu Ile Tyr Ala Leu Val Phe Leu Met Pro Gly Asp Pro Val Gln Ala

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25	30	35	
ttg gga ggt gac cgc ggc cta acc gag gct gcg gcc gag aaa atc cgt Leu Gly Gly Asp Arg Gly Leu Thr Glu Ala Ala Ala Glu Lys Ile Arg 40 45 50			259
caa gaa tac aat ctt gat aaa ccc ttc atc gtt caa tac ctc ctg tac Gln Glu Tyr Asn Leu Asp Lys Pro Phe Ile Val Gln Tyr Leu Leu Tyr 55 60 65			307
atc aag ggc atc ttc gtc tta gat ttt gga aca acc ttc tct ggt cag Ile Lys Gly Ile Phe Val Leu Asp Phe Gly Thr Thr Phe Ser Gly Gln 70 75 80 85			355
cca gtt att gat gtg atg gcc agg gcc ttc ccc gtc acc atc aaa ctc Pro Val Ile Asp Val Met Ala Arg Ala Phe Pro Val Thr Ile Lys Leu 90 95 100			403
gcc atc atg gcc ctg ctg ttt gaa tca atc ctc ggc att atc ttt ggt Ala Ile Met Ala Leu Leu Phe Glu Ser Ile Leu Gly Ile Ile Phe Gly 105 110 115			451
gtc atc gca ggt att cgc cgc gga gga atc ttc gac tcc acc gtg ctg Val Ile Ala Gly Ile Arg Arg Gly Gly Ile Phe Asp Ser Thr Val Leu 120 125 130			499
gtc ctt tct ctg ata gtc atc gca gtc ccc acc ttc gtc att ggt ttc Val Leu Ser Leu Ile Val Ile Ala Val Pro Thr Phe Val Ile Gly Phe 135 140 145			547
gtg ctg cag ttc tta ntc ggc gtg aaa tgg ggc tta ctg ccc gtc acc Val Leu Gln Phe Leu Xaa Gly Val Lys Trp Gly Leu Leu Pro Val Thr 150 155 160 165			595
gta ggt tcc aac aca tca ata acg gcg ctg atc atg ccg gct gtc gta Val Gly Ser Asn Thr Ser Ile Thr Ala Leu Ile Met Pro Ala Val Val 170 175 180			643
ctg ggt gca gta tct ttc gcc tac gtt ctt cgc ctc acc aga caa tcc Leu Gly Ala Val Ser Phe Ala Tyr Val Leu Arg Leu Thr Arg Gln Ser 185 190 195			691
gtg agc gaa aac ctc cgc gct gat tac gtt cga acc gct cga gca aaa Val Ser Glu Asn Leu Arg Ala Asp Tyr Val Arg Thr Ala Arg Ala Lys 200 205 210			739
ggc atg tcc gga ttc aac gtg atg aac cgc cat gtg ctt cga aac tca Gly Met Ser Gly Phe Asn Val Met Asn Arg His Val Leu Arg Asn Ser 215 220 225			787
ctg att ccc gtt gcc acc ttc ctg ggc gcc gat ctc ggt gca ctg atg Leu Ile Pro Val Ala Thr Phe Leu Gly Ala Asp Leu Gly Ala Leu Met 230 235 240 245			835
ggt gga gcg att gtc acc gaa ggt atc ttc ggc atc aac ggt gtc ggt Gly Gly Ala Ile Val Thr Glu Gly Ile Phe Gly Ile Asn Gly Val Gly 250 255 260			883
gga acg ctc tac cag gcc att ttg aaa ggt gaa ccc acc acg gtt gtc Gly Thr Leu Tyr Gln Ala Ile Leu Lys Gly Glu Pro Thr Thr Val Val 265 270 275			931

tcc att gtc act gtg ctg gtc atc gtc tac atc atc gcc aac ott ctc 979
 Ser Ile Val Thr Val Leu Val Ile Val Tyr Ile Ile Ala Asn Leu Leu
 280 285 290

gtg gac ttg atc tac gcc gtt ctc gat ccg agg atc cgc tat gcc 1024
 Val Asp Leu Ile Tyr Ala Val Leu Asp Pro Arg Ile Arg Tyr Ala
 295 300 305

taataatgaa ttccacacaa acc 1047

<210> 142

<211> 308

<212> PRT

<213> Corynebacterium glutamicum

<220>

<223> All occurrences of Xaa = any amino acid

<400> 142

Met Leu Arg Tyr Val Gly Arg Arg Leu Leu Gln Met Ile Pro Val Phe
 1 5 10 15

Phe Gly Ala Thr Leu Leu Ile Tyr Ala Leu Val Phe Leu Met Pro Gly
 20 25 30

Asp Pro Val Gln Ala Leu Gly Gly Asp Arg Gly Leu Thr Glu Ala Ala
 35 40 45

Ala Glu Lys Ile Arg Gln Glu Tyr Asn Leu Asp Lys Pro Phe Ile Val
 50 55 60

Gln Tyr Leu Leu Tyr Ile Lys Gly Ile Phe Val Leu Asp Phe Gly Thr
 65 70 75 80

Thr Phe Ser Gly Gln Pro Val Ile Asp Val Met Ala Arg Ala Phe Pro
 85 90 95

Val Thr Ile Lys Leu Ala Ile Met Ala Leu Leu Phe Glu Ser Ile Leu
 100 105 110

Gly Ile Ile Phe Gly Val Ile Ala Gly Ile Arg Arg Gly Gly Ile Phe
 115 120 125

Asp Ser Thr Val Leu Val Leu Ser Leu Ile Val Ile Ala Val Pro Thr
 130 135 140

Phe Val Ile Gly Phe Val Leu Gln Phe Leu Xaa Gly Val Lys Trp Gly
 145 150 155 160

Leu Leu Pro Val Thr Val Gly Ser Asn Thr Ser Ile Thr Ala Leu Ile
 165 170 175

Met Pro Ala Val Val Leu Gly Ala Val Ser Phe Ala Tyr Val Leu Arg
 180 185 190

Leu Thr Arg Gln Ser Val Ser Glu Asn Leu Arg Ala Asp Tyr Val Arg
 195 200 205

Thr Ala Arg Ala Lys Gly Met Ser Gly Phe Asn Val Met Asn Arg His

210 215 220

Val Leu Arg Asn Ser Leu Ile Pro Val Ala Thr Phe Leu Gly Ala Asp
 225 230 235 240

Leu Gly Ala Leu Met Gly Gly Ala Ile Val Thr Glu Gly Ile Phe Gly
 245 250 255

Ile Asn Gly Val Gly Gly Thr Leu Tyr Gln Ala Ile Leu Lys Gly Glu
 260 265 270

Pro Thr Thr Val Val Ser Ile Val Thr Val Leu Val Ile Val Tyr Ile
 275 280 285

Ile Ala Asn Leu Leu Val Asp Leu Ile Tyr Ala Val Leu Asp Pro Arg
 290 295 300

Ile Arg Tyr Ala
 305

<210> 143
 <211> 912
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(889)
 <223> RXN00431

<400> 143
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 tggcgattcc gcgtcagcta ctgggtataa ggagcaccac atg gta tcc atc gat 115
 Met Val Ser Ile Asp
 1 5

aca tac aac gcc tgc gtc gac ttc ccc atc ttc gac gcc aaa tcc cgc 163
 Thr Tyr Asn Ala Cys Val Asp Phe Pro Ile Phe Asp Ala Lys Ser Arg
 10 15 20

tcc atg aag aaa gcc ttc ctc ggc gca gcc ggc gga gca atc ggg cgc 211
 Ser Met Lys Lys Ala Phe Leu Gly Ala Ala Gly Gly Ala Ile Gly Arg
 25 30 35

aat caa gac aac gtc gta gtc gtc gaa gcg ctg aag aac gtc aac ctg 259
 Asn Gln Asp Asn Val Val Val Val Glu Ala Leu Lys Asn Val Asn Leu
 40 45 50

cac ttg cgc gaa ggt gac cgg gtc gga ctc gtc ggc cac aac ggc gcc 307
 His Leu Arg Glu Gly Asp Arg Val Gly Leu Val Gly His Asn Gly Ala
 55 60 65

ggc aaa tcc acc ctc ctg cga ctc ctc tcc ggc atc tac gaa ccc acc 355
 Gly Lys Ser Thr Leu Leu Arg Leu Leu Ser Gly Ile Tyr Glu Pro Thr
 70 75 80 85

cgc gga agc gct gac atc cgt gga cgc gtc gcc ccc gtc ttc gac ctc 403
 Arg Gly Ser Ala Asp Ile Arg Gly Arg Val Ala Pro Val Phe Asp Leu
 90 95 100

ggc gtc ggc atg gat cca gaa atc tcc ggc tac gaa aat atc atc atc 451
 Gly Val Gly Met Asp Pro Glu Ile Ser Gly Tyr Glu Asn Ile Ile Ile
 105 110 115

cgc ggc ctc ttc ctc ggt caa acc cgc aaa cag atg aaa gcc aaa atg 499
 Arg Gly Leu Phe Leu Gly Gln Thr Arg Lys Gln Met Lys Ala Lys Met
 120 125 130

gaa gaa atc gcc gac ttc acc gaa ctc ggc gaa tac ctc tcc atg cct 547
 Glu Glu Ile Ala Asp Phe Thr Glu Leu Gly Glu Tyr Leu Ser Met Pro
 135 140 145

ctc cga acc tac tcc acc ggc atg cgc atc cgc cta gcc ctc ggc gtg 595
 Leu Arg Thr Tyr Ser Thr Gly Met Arg Ile Arg Leu Ala Leu Gly Val
 150 155 160 165

gtc acc tcc atc gag ccc gaa att ctg ctt ctt gat gaa ggc atc ggc 643
 Val Thr Ser Ile Glu Pro Glu Ile Leu Leu Leu Asp Glu Gly Ile Gly
 170 175 180

gcc gtc gac gcc gcc ttc atg gcc aaa gcc cgc gac cgc ctc caa gcc 691
 Ala Val Asp Ala Ala Phe Met Ala Lys Ala Arg Asp Arg Leu Gln Ala
 185 190 195

ctc gtc gaa cga tcc ggc atc ctc gtc ttc gcc tcc cac tcc aac gac 739
 Leu Val Glu Arg Ser Gly Ile Leu Val Phe Ala Ser His Ser Asn Asp
 200 205 210

ttc ctc gcc caa ctc tgc aac acc gca ctc tgg gtc gac cac gga caa 787
 Phe Leu Ala Gln Leu Cys Asn Thr Ala Leu Trp Val Asp His Gly Gln
 215 220 225

atc cgc gaa gcg gga cta gtt cca gac gtg gtg gaa gcc tac gaa ggc 835
 Ile Arg Glu Ala Gly Leu Val Pro Asp Val Val Glu Ala Tyr Glu Gly
 230 235 240 245

aag ggc gcc ggc gac cac gtc cgc aga ctc ctc acc cgc atg gaa gaa 883
 Lys Gly Ala Gly Asp His Val Arg Arg Leu Leu Thr Arg Met Glu Glu
 250 255 260

gaa aag tagctcctgc gtttcgggtt tgc 912
 Glu Lys

<210> 144

<211> 263

<212> PRT

<213> Corynebacterium glutamicum

<400> 144

Met Val Ser Ile Asp Thr Tyr Asn Ala Cys Val Asp Phe Pro Ile Phe
 1 5 10 15

Asp Ala Lys Ser Arg Ser Met Lys Lys Ala Phe Leu Gly Ala Ala Gly
 20 25 30

Gly Ala Ile Gly Arg Asn Gln Asp Asn Val Val Val Val Glu Ala Leu
 35 40 45

Lys Asn Val Asn Leu His Leu Arg Glu Gly Asp Arg Val Gly Leu Val
 50 55 60
 Gly His Asn Gly Ala Gly Lys Ser Thr Leu Leu Arg Leu Leu Ser Gly
 65 70 75 80
 Ile Tyr Glu Pro Thr Arg Gly Ser Ala Asp Ile Arg Gly Arg Val Ala
 85 90 95
 Pro Val Phe Asp Leu Gly Val Gly Met Asp Pro Glu Ile Ser Gly Tyr
 100 105 110
 Glu Asn Ile Ile Ile Arg Gly Leu Phe Leu Gly Gln Thr Arg Lys Gln
 115 120 125
 Met Lys Ala Lys Met Glu Glu Ile Ala Asp Phe Thr Glu Leu Gly Glu
 130 135 140
 Tyr Leu Ser Met Pro Leu Arg Thr Tyr Ser Thr Gly Met Arg Ile Arg
 145 150 155 160
 Leu Ala Leu Gly Val Val Thr Ser Ile Glu Pro Glu Ile Leu Leu Leu
 165 170 175
 Asp Glu Gly Ile Gly Ala Val Asp Ala Ala Phe Met Ala Lys Ala Arg
 180 185 190
 Asp Arg Leu Gln Ala Leu Val Glu Arg Ser Gly Ile Leu Val Phe Ala
 195 200 205
 Ser His Ser Asn Asp Phe Leu Ala Gln Leu Cys Asn Thr Ala Leu Trp
 210 215 220
 Val Asp His Gly Gln Ile Arg Glu Ala Gly Leu Val Pro Asp Val Val
 225 230 235 240
 Glu Ala Tyr Glu Gly Lys Gly Ala Gly Asp His Val Arg Arg Leu Leu
 245 250 255
 Thr Arg Met Glu Glu Glu Lys
 260

<210> 145

<211> 775

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(775)

<223> FRXA00431

<400> 145

tggatcgtcc tcgccttcac attcgtcggc ctggccttg ctctcctcgc gatgaagcaa 60

tggcgattcc gcgtcagcta ctgggtataa ggagcaccac atg gta tcc atc gat 115

Met Val Ser Ile Asp

1

5

aca tac aac gcc tgc gtc gac ttc ccc atc ttc gac gcc aaa tcc cgc 163

Thr	Tyr	Asn	Ala	Cys	Val	Asp	Phe	Pro	Ile	Phe	Asp	Ala	Lys	Ser	Arg		
				10					15					20			
tcc	atg	aag	aaa	gcc	ttc	ctc	ggc	gca	gcc	ggc	gga	gca	atc	ggg	cgc	211	
Ser	Met	Lys	Lys	Ala	Phe	Leu	Gly	Ala	Ala	Gly	Gly	Ala	Ile	Gly	Arg		
			25					30					35				
aat	caa	gac	aac	gtc	gta	gtc	gtc	gaa	gcg	ctg	aag	aac	gtc	aac	ctg	259	
Asn	Gln	Asp	Asn	Val	Val	Val	Val	Glu	Ala	Leu	Lys	Asn	Val	Asn	Leu		
			40				45					50					
cac	ttg	cgc	gaa	ggc	gac	cgg	gtc	gga	ctc	gtc	ggc	cac	aac	ggc	gcc	307	
His	Leu	Arg	Glu	Gly	Asp	Arg	Val	Gly	Leu	Val	Gly	His	Asn	Gly	Ala		
	55					60					65						
ggc	aaa	tcc	acc	ctc	ctg	cga	ctc	ctc	tcc	ggc	atc	tac	gaa	ccc	acc	355	
Gly	Lys	Ser	Thr	Leu	Leu	Arg	Leu	Leu	Ser	Gly	Ile	Tyr	Glu	Pro	Thr		
	70				75				80						85		
cgc	gga	agc	gct	gac	atc	cgt	gga	cgc	gtc	gcc	ccc	gtc	ttc	gac	ctc	403	
Arg	Gly	Ser	Ala	Asp	Ile	Arg	Gly	Arg	Val	Ala	Pro	Val	Phe	Asp	Leu		
				90				95						100			
ggc	gtc	ggc	atg	gat	cca	gaa	atc	tcc	ggc	tac	gaa	aac	atc	atc	atc	451	
Gly	Val	Gly	Met	Asp	Pro	Glu	Ile	Ser	Gly	Tyr	Glu	Asn	Ile	Ile	Ile		
			105					110					115				
cgc	ggc	ctc	ttc	ctc	ggc	caa	acc	cgc	aaa	cag	atg	aaa	gcc	aaa	atg	499	
Arg	Gly	Leu	Phe	Leu	Gly	Gln	Thr	Arg	Lys	Gln	Met	Lys	Ala	Lys	Met		
		120					125					130					
gaa	gaa	atc	gcc	gac	ttc	acc	gaa	ctc	ggc	gaa	tac	ctc	tcc	atg	cct	547	
Glu	Glu	Ile	Ala	Asp	Phe	Thr	Glu	Leu	Gly	Glu	Tyr	Leu	Ser	Met	Pro		
	135					140					145						
ctc	cga	acc	tac	tcc	acc	ggc	atg	cgc	atc	cgc	cta	gcc	ctc	ggc	gtg	595	
Leu	Arg	Thr	Tyr	Ser	Thr	Gly	Met	Arg	Ile	Arg	Leu	Ala	Leu	Gly	Val		
	150				155				160					165			
gtc	acc	tcc	atc	gag	ccc	gaa	att	ctg	ctt	ctt	gat	gaa	ggc	atc	ggc	643	
Val	Thr	Ser	Ile	Glu	Pro	Glu	Ile	Leu	Leu	Leu	Asp	Glu	Gly	Ile	Gly		
				170				175						180			
gcc	gtc	gac	gcc	gcc	ttc	atg	gcc	aaa	gcc	cgc	gac	cgg	ctc	caa	gcc	691	
Ala	Val	Asp	Ala	Ala	Phe	Met	Ala	Lys	Ala	Arg	Asp	Arg	Leu	Gln	Ala		
			185					190					195				
ctc	gtc	gaa	cga	tcc	ggc	atc	ctc	gtc	ttc	gcc	tcc	act	caa	cga	ctt	739	
Leu	Val	Glu	Arg	Ser	Gly	Ile	Leu	Val	Phe	Ala	Ser	Thr	Gln	Arg	Leu		
		200				205						210					
tct	tgc	caa	ctc	tgc	aac	acc	gca	ctc	tgg	gtc	gac					775	
Ser	Cys	Gln	Leu	Cys	Asn	Thr	Ala	Leu	Trp	Val	Asp						
	215				220						225						

<210> 146

<211> 225

<212> PRT

<213> Corynebacterium glutamicum

<400> 146

Met Val Ser Ile Asp Thr Tyr Asn Ala Cys Val Asp Phe Pro Ile Phe
 1 5 10 15

Asp Ala Lys Ser Arg Ser Met Lys Lys Ala Phe Leu Gly Ala Ala Gly
 20 25 30

Gly Ala Ile Gly Arg Asn Gln Asp Asn Val Val Val Glu Ala Leu
 35 40 45

Lys Asn Val Asn Leu His Leu Arg Glu Gly Asp Arg Val Gly Leu Val
 50 55 60

Gly His Asn Gly Ala Gly Lys Ser Thr Leu Leu Arg Leu Leu Ser Gly
 65 70 75 80

Ile Tyr Glu Pro Thr Arg Gly Ser Ala Asp Ile Arg Gly Arg Val Ala
 85 90 95

Pro Val Phe Asp Leu Gly Val Gly Met Asp Pro Glu Ile Ser Gly Tyr
 100 105 110

Glu Asn Ile Ile Ile Arg Gly Leu Phe Leu Gly Gln Thr Arg Lys Gln
 115 120 125

Met Lys Ala Lys Met Glu Glu Ile Ala Asp Phe Thr Glu Leu Gly Glu
 130 135 140

Tyr Leu Ser Met Pro Leu Arg Thr Tyr Ser Thr Gly Met Arg Ile Arg
 145 150 155 160

Leu Ala Leu Gly Val Val Thr Ser Ile Glu Pro Glu Ile Leu Leu Leu
 165 170 175

Asp Glu Gly Ile Gly Ala Val Asp Ala Ala Phe Met Ala Lys Ala Arg
 180 185 190

Asp Arg Leu Gln Ala Leu Val Glu Arg Ser Gly Ile Leu Val Phe Ala
 195 200 205

Ser Thr Gln Arg Leu Ser Cys Gln Leu Cys Asn Thr Ala Leu Trp Val
 210 215 220

Asp
 225

<210> 147

<211> 1670

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1647)

<223> RXN00732

<400> 147

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 Asn His Leu Leu Leu Leu Pro Thr Val Lys Ala Asp Ile Ile Asp Asn
 1 5 10 15

ggt gtg gtc aca ggt gac atc ggc tat att tgg cac acc ggt gga atc	96
Gly Val Val Thr Gly Asp Ile Gly Tyr Ile Trp His Thr Gly Gly Ile	
20 25 30	
atg ctg gcc ctg aca tta gtc cag gtt gcc tgc gct atc gcc ggt gtt	144
Met Leu Ala Leu Thr Leu Val Gln Val Ala Cys Ala Ile Ala Gly Val	
35 40 45	
tat ttc ggt tcc aaa cta tcc atg aga gtg ggc cgc gat ctg cgt tcg	192
Tyr Phe Gly Ser Lys Leu Ser Met Arg Val Gly Arg Asp Leu Arg Ser	
50 55 60	
gcg atc ttt ggc aag gta gtg aac ttc tct gag cgt gag atg ggt cag	240
Ala Ile Phe Gly Lys Val Val Asn Phe Ser Glu Arg Glu Met Gly Gln	
65 70 75 80	
ttt ggc gca ccg tcg ctg atc acc cga aac acc aac gat gtg cag cag	288
Phe Gly Ala Pro Ser Leu Ile Thr Arg Asn Thr Asn Asp Val Gln Gln	
85 90 95	
gtt cag atg ctg gtg cag atg acc tcc act ttg atg att tcc gcc ccg	336
Val Gln Met Leu Val Gln Met Thr Ser Thr Leu Met Ile Ser Ala Pro	
100 105 110	
atg ctg gcc att ggt ggc atc atc atg gcg gtg cgt cag gat ctt ggt	384
Met Leu Ala Ile Gly Gly Ile Ile Met Ala Val Arg Gln Asp Leu Gly	
115 120 125	
ttg tct tgg ctg atg gtg gtc agt att ccg gtg ctc atc atc gtg gtg	432
Leu Ser Trp Leu Met Val Val Ser Ile Pro Val Leu Ile Ile Val Val	
130 135 140	
gcg ctg atc att gtg cgc atg gtt ccg ttg ttc caa acc atg caa aag	480
Ala Leu Ile Ile Val Arg Met Val Pro Leu Phe Gln Thr Met Gln Lys	
145 150 155 160	
cgc att gac cgc atc aat cag att ata cgc gag cag ctc acc ggt atc	528
Arg Ile Asp Arg Ile Asn Gln Ile Ile Arg Glu Gln Leu Thr Gly Ile	
165 170 175	
cgc gtg atc cgc gcg ttc gtg cgt gaa gat gtg gaa cgc gaa cga ttc	576
Arg Val Ile Arg Ala Phe Val Arg Glu Asp Val Glu Arg Glu Arg Phe	
180 185 190	
acc act gct agt aaa gat gtc gct gat atc ggc gtg cgc acc ggt aac	624
Thr Thr Ala Ser Lys Asp Val Ala Asp Ile Gly Val Arg Thr Gly Asn	
195 200 205	
ctg atg gcg ttg atg ttc cct gcc gtg atg ctg atc atg aac ctt tct	672
Leu Met Ala Leu Met Phe Pro Ala Val Met Leu Ile Met Asn Leu Ser	
210 215 220	
gcc gtt gct gtg att tgg ttt ggt gct ttc cag gtg gaa tcc gcc gag	720
Ala Val Ala Val Ile Trp Phe Gly Ala Phe Gln Val Glu Ser Gly Glu	
225 230 235 240	
acg cag atc ggt acg ctc ttt gca ttc ttg cag tac atc atg cag atc	768
Thr Gln Ile Gly Thr Leu Phe Ala Phe Leu Gln Tyr Ile Met Gln Ile	
245 250 255	

ctc atg ggc gtc atg atg gca gcg ttc atg ttt gtc atg gtt ccg cgc	816
Leu Met Gly Val Met Met Ala Ala Phe Met Phe Val Met Val Pro Arg	
260 265 270	
gct gcc gtt tcc gct gat cgc atc ggt gag gtt ctg gaa acc aca ccg	864
Ala Ala Val Ser Ala Asp Arg Ile Gly Glu Val Leu Glu Thr Thr Pro	
275 280 285	
tct gtg cag gcg cca gaa aca ccg gcg cag ccg tcg aca agc gct ggc	912
Ser Val Gln Ala Pro Glu Thr Pro Ala Gln Pro Ser Thr Ser Ala Gly	
290 295 300	
gaa atc gtg ttc aac aac gcg act ttt gcc tac ccc ggc gcg gat gac	960
Glu Ile Val Phe Asn Asn Ala Thr Phe Ala Tyr Pro Gly Ala Asp Asp	
305 310 315 320	
ccc gtg tta aat aat gtg agc ttc cgc gtt gcg cct ggt agc acg acg	1008
Pro Val Leu Asn Asn Val Ser Phe Arg Val Ala Pro Gly Ser Thr Thr	
325 330 335	
gcg atc atc ggc tcg acg ggt tcg ggt aag acg acg ttg atc ggg ctg	1056
Ala Ile Ile Gly Ser Thr Gly Ser Gly Lys Thr Thr Leu Ile Gly Leu	
340 345 350	
gtt cct agg ctt ttc gac gtc acc gaa ggc gac gtt acc gtc gat ggc	1104
Val Pro Arg Leu Phe Asp Val Thr Glu Gly Asp Val Thr Val Asp Gly	
355 360 365	
acc gat gtt cgt gaa ttt gag ccg ctg aag ctg tgg gat cgg atc ggt	1152
Thr Asp Val Arg Glu Phe Glu Pro Leu Lys Leu Trp Asp Arg Ile Gly	
370 375 380	
ctt gtt ccg cag aag tcg ttc ctg ttt tct gga acg atc gcc agc aac	1200
Leu Val Pro Gln Lys Ser Phe Leu Phe Ser Gly Thr Ile Ala Ser Asn	
385 390 395 400	
ctg cgt tat ggc aat gaa gat gcc acg gaa acg cag ctg tgg cag gcg	1248
Leu Arg Tyr Gly Asn Glu Asp Ala Thr Glu Thr Gln Leu Trp Gln Ala	
405 410 415	
ctt gca att gct cag gcg gcg gac ttt gtg cgt gag atg cca gag ggt	1296
Leu Ala Ile Ala Gln Ala Ala Asp Phe Val Arg Glu Met Pro Glu Gly	
420 425 430	
ctt gat tct gag att gct cag ggt gga acc aat gtt tct ggt ggt cag	1344
Leu Asp Ser Glu Ile Ala Gln Gly Gly Thr Asn Val Ser Gly Gly Gln	
435 440 445	
cgc cag cga cta gcc att gcc agg gcg ttg ttg aag caa cct gag atc	1392
Arg Gln Arg Leu Ala Ile Ala Arg Ala Leu Leu Lys Gln Pro Glu Ile	
450 455 460	
tat att ttc gac gat tct ttc tcc gcc ctc gat gtg agc aca gac gcc	1440
Tyr Ile Phe Asp Asp Ser Phe Ser Ala Leu Asp Val Ser Thr Asp Ala	
465 470 475 480	
gct ctt cgc cga gcg ctg agc acc aac ctg ccg gat gca acc aag ttg	1488
Ala Leu Arg Arg Ala Leu Ser Thr Asn Leu Pro Asp Ala Thr Lys Leu	
485 490 495	
att gtc gcc cag cgt gtc agc acg att cga gat gcc gat cag att gtg	1536

Ile Val Ala Gln Arg Val Ser Thr Ile Arg Asp Ala Asp Gln Ile Val
 500 505 510
 gtg ctt gat aac ggc gag gtt gtc ggt att gga acg cac acg aat ttg 1584
 Val Leu Asp Asn Gly Glu Val Val Gly Ile Gly Thr His Thr Asn Leu
 515 520 525
 ctg aac acg tgc ggt acc tac cgt gaa att gtt gaa tcc caa gag act 1632
 Leu Asn Thr Cys Gly Thr Tyr Arg Glu Ile Val Glu Ser Gln Glu Thr
 530 535 540
 gcg cag gcg caa tca tgagtaatac tgcaggcccc cgc 1670
 Ala Gln Ala Gln Ser
 545
 <210> 148
 <211> 549
 <212> PRT
 <213> *Corynebacterium glutamicum*
 <400> 148
 Asn His Leu Leu Leu Leu Pro Thr Val Lys Ala Asp Ile Ile Asp Asn
 1 5 10 15
 Gly Val Val Thr Gly Asp Ile Gly Tyr Ile Trp His Thr Gly Gly Ile
 20 25 30
 Met Leu Ala Leu Thr Leu Val Gln Val Ala Cys Ala Ile Ala Gly Val
 35 40 45
 Tyr Phe Gly Ser Lys Leu Ser Met Arg Val Gly Arg Asp Leu Arg Ser
 50 55 60
 Ala Ile Phe Gly Lys Val Val Asn Phe Ser Glu Arg Glu Met Gly Gln
 65 70 75 80
 Phe Gly Ala Pro Ser Leu Ile Thr Arg Asn Thr Asn Asp Val Gln Gln
 85 90 95
 Val Gln Met Leu Val Gln Met Thr Ser Thr Leu Met Ile Ser Ala Pro
 100 105 110
 Met Leu Ala Ile Gly Gly Ile Ile Met Ala Val Arg Gln Asp Leu Gly
 115 120 125
 Leu Ser Trp Leu Met Val Val Ser Ile Pro Val Leu Ile Ile Val Val
 130 135 140
 Ala Leu Ile Ile Val Arg Met Val Pro Leu Phe Gln Thr Met Gln Lys
 145 150 155 160
 Arg Ile Asp Arg Ile Asn Gln Ile Ile Arg Glu Gln Leu Thr Gly Ile
 165 170 175
 Arg Val Ile Arg Ala Phe Val Arg Glu Asp Val Glu Arg Glu Arg Phe
 180 185 190
 Thr Thr Ala Ser Lys Asp Val Ala Asp Ile Gly Val Arg Thr Gly Asn
 195 200 205

Leu Met Ala Leu Met Phe Pro Ala Val Met Leu Ile Met Asn Leu Ser
 210 215 220
 Ala Val Ala Val Ile Trp Phe Gly Ala Phe Gln Val Glu Ser Gly Glu
 225 230 235 240
 Thr Gln Ile Gly Thr Leu Phe Ala Phe Leu Gln Tyr Ile Met Gln Ile
 245 250 255
 Leu Met Gly Val Met Met Ala Ala Phe Met Phe Val Met Val Pro Arg
 260 265 270
 Ala Ala Val Ser Ala Asp Arg Ile Gly Glu Val Leu Glu Thr Thr Pro
 275 280 285
 Ser Val Gln Ala Pro Glu Thr Pro Ala Gln Pro Ser Thr Ser Ala Gly
 290 295 300
 Glu Ile Val Phe Asn Asn Ala Thr Phe Ala Tyr Pro Gly Ala Asp Asp
 305 310 315 320
 Pro Val Leu Asn Asn Val Ser Phe Arg Val Ala Pro Gly Ser Thr Thr
 325 330 335
 Ala Ile Ile Gly Ser Thr Gly Ser Gly Lys Thr Thr Leu Ile Gly Leu
 340 345 350
 Val Pro Arg Leu Phe Asp Val Thr Glu Gly Asp Val Thr Val Asp Gly
 355 360 365
 Thr Asp Val Arg Glu Phe Glu Pro Leu Lys Leu Trp Asp Arg Ile Gly
 370 375 380
 Leu Val Pro Gln Lys Ser Phe Leu Phe Ser Gly Thr Ile Ala Ser Asn
 385 390 395 400
 Leu Arg Tyr Gly Asn Glu Asp Ala Thr Glu Thr Gln Leu Trp Gln Ala
 405 410 415
 Leu Ala Ile Ala Gln Ala Ala Asp Phe Val Arg Glu Met Pro Glu Gly
 420 425 430
 Leu Asp Ser Glu Ile Ala Gln Gly Gly Thr Asn Val Ser Gly Gly Gln
 435 440 445
 Arg Gln Arg Leu Ala Ile Ala Arg Ala Leu Leu Lys Gln Pro Glu Ile
 450 455 460
 Tyr Ile Phe Asp Asp Ser Phe Ser Ala Leu Asp Val Ser Thr Asp Ala
 465 470 475 480
 Ala Leu Arg Arg Ala Leu Ser Thr Asn Leu Pro Asp Ala Thr Lys Leu
 485 490 495
 Ile Val Ala Gln Arg Val Ser Thr Ile Arg Asp Ala Asp Gln Ile Val
 500 505 510
 Val Leu Asp Asn Gly Glu Val Val Gly Ile Gly Thr His Thr Asn Leu
 515 520 525
 Leu Asn Thr Cys Gly Thr Tyr Arg Glu Ile Val Glu Ser Gln Glu Thr

530

535

540

Ala Gln Ala Gln Ser
545

<210> 149

<211> 922

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(922)

<223> FRXA00732

<400> 149

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ctgatcaccc cgaaacacca acgatgtgca gcaggttcag atg ctg gtg cag atg 115
Met Leu Val Gln Met
1 5

acc tcc act ttg atg att tcc gcc ccg atg ctg gcc att ggt ggc atc 163
Thr Ser Thr Leu Met Ile Ser Ala Pro Met Leu Ala Ile Gly Gly Ile
10 15 20

atc atg gcg gtg cgt cag gat ctt ggt ttg tct tgg ctg atg gtg gtc 211
Ile Met Ala Val Arg Gln Asp Leu Gly Leu Ser Trp Leu Met Val Val
25 30 35

agt att ccg gtg ctc atc atc gtg gtg gcg ctg atc att gtg cgc atg 259
Ser Ile Pro Val Leu Ile Ile Val Val Ala Leu Ile Ile Val Arg Met
40 45 50

gtt ccg ttg ttc caa acc atg caa aag cgc att gac cgc atc aat cag 307
Val Pro Leu Phe Gln Thr Met Gln Lys Arg Ile Asp Arg Ile Asn Gln
55 60 65

att ata cgc gag cag ctc acc ggt atc cgc gtg atc cgc gcg ttc gtg 355
Ile Ile Arg Glu Gln Leu Thr Gly Ile Arg Val Ile Arg Ala Phe Val
70 75 80 85

cgt gaa gat gtg gaa cgc gaa cga ttc acc act gct agt aaa gat gtc 403
Arg Glu Asp Val Glu Arg Glu Arg Phe Thr Thr Ala Ser Lys Asp Val
90 95 100

gct gat atc ggc gtg cgc acc ggt aac ctg atg gcg ttg atg ttc cct 451
Ala Asp Ile Gly Val Arg Thr Gly Asn Leu Met Ala Leu Met Phe Pro
105 110 115

gcc gtg atg ctg atc atg aac ctt tct gcc gtt gct gtg att tgg ttt 499
Ala Val Met Leu Ile Met Asn Leu Ser Ala Val Ala Val Ile Trp Phe
120 125 130

ggg gct ttc cag gtg gaa tcc ggc gag acg cag atc ggt acg ctc ttt 547
Gly Ala Phe Gln Val Glu Ser Gly Glu Thr Gln Ile Gly Thr Leu Phe
135 140 145

gca ttc ttg cag tac atc atg cag atc ctc atg ggc gtc atg atg gca 595
Ala Phe Leu Gln Tyr Ile Met Gln Ile Leu Met Gly Val Met Met Ala

150	155	160	165	
gcg ttc atg ttt gtc atg gtt ccg cgc gct gcc gtt tcc gct gat cgc				643
Ala Phe Met Phe Val Met Val Pro Arg Ala Ala Val Ser Ala Asp Arg				
170		175	180	
atc ggt gag gtt ctg gaa acc aca ccg tct gtg cag gcg cca gaa aca				691
Ile Gly Glu Val Leu Glu Thr Thr Pro Ser Val Gln Ala Pro Glu Thr				
185		190	195	
ccg gcg cag ccg tcg aca agc gct ggc gaa atc gtg ttc aac aac gcg				739
Pro Ala Gln Pro Ser Thr Ser Ala Gly Glu Ile Val Phe Asn Asn Ala				
200		205	210	
act ttt gcc tac ccc ggc gcg gat gac ccc gtg tta aat aat gtg agc				787
Thr Phe Ala Tyr Pro Gly Ala Asp Asp Pro Val Leu Asn Asn Val Ser				
215		220	225	
ttc cgc gtt gcg cct ggt agc acg acg gcg atc atc ggc tcg acg ggt				835
Phe Arg Val Ala Pro Gly Ser Thr Thr Ala Ile Ile Gly Ser Thr Gly				
230		235	240	245
tcg ggt aag acg acg ttg atc ggg ctg gtt cct agg ctt ttc gac gtc				883
Ser Gly Lys Thr Thr Leu Ile Gly Leu Val Pro Arg Leu Phe Asp Val				
250		255	260	
acc gaa ggc gac gtt acc gtc gat ggc acc gat gtt cgt				922
Thr Glu Gly Asp Val Thr Val Asp Gly Thr Asp Val Arg				
265		270		

<210> 150

<211> 274

<212> PRT

<213> Corynebacterium glutamicum

<400> 150

Met Leu Val Gln Met Thr Ser Thr Leu Met Ile Ser Ala Pro Met Leu				
1	5	10	15	
Ala Ile Gly Gly Ile Ile Met Ala Val Arg Gln Asp Leu Gly Leu Ser				
20		25	30	
Trp Leu Met Val Val Ser Ile Pro Val Leu Ile Ile Val Val Ala Leu				
35		40	45	
Ile Ile Val Arg Met Val Pro Leu Phe Gln Thr Met Gln Lys Arg Ile				
50		55	60	
Asp Arg Ile Asn Gln Ile Ile Arg Glu Gln Leu Thr Gly Ile Arg Val				
65		70	75	80
Ile Arg Ala Phe Val Arg Glu Asp Val Glu Arg Glu Arg Phe Thr Thr				
85		90	95	
Ala Ser Lys Asp Val Ala Asp Ile Gly Val Arg Thr Gly Asn Leu Met				
100		105	110	
Ala Leu Met Phe Pro Ala Val Met Leu Ile Met Asn Leu Ser Ala Val				
115		120	125	

Ala Val Ile Trp Phe Gly Ala Phe Gln Val Glu Ser Gly Glu Thr Gln
 130 135 140

Ile Gly Thr Leu Phe Ala Phe Leu Gln Tyr Ile Met Gln Ile Leu Met
 145 150 155 160

Gly Val Met Met Ala Ala Phe Met Phe Val Met Val Pro Arg Ala Ala
 165 170 175

Val Ser Ala Asp Arg Ile Gly Glu Val Leu Glu Thr Thr Pro Ser Val
 180 185 190

Gln Ala Pro Glu Thr Pro Ala Gln Pro Ser Thr Ser Ala Gly Glu Ile
 195 200 205

Val Phe Asn Asn Ala Thr Phe Ala Tyr Pro Gly Ala Asp Asp Pro Val
 210 215 220

Leu Asn Asn Val Ser Phe Arg Val Ala Pro Gly Ser Thr Thr Ala Ile
 225 230 235 240

Ile Gly Ser Thr Gly Ser Gly Lys Thr Thr Leu Ile Gly Leu Val Pro
 245 250 255

Arg Leu Phe Asp Val Thr Glu Gly Asp Val Thr Val Asp Gly Thr Asp
 260 265 270

Val Arg

<210> 151
 <211> 476
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(453)
 <223> FRXA00734

<400> 151
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 Arg His Leu Arg Tyr Gly Asn Glu Asp Ala Thr Glu Thr Gln Leu Trp
 1 5 10 15

cag gcg ctt gca att gct cag gcg gcg gac ttt gtg cgt gag atg cca 96
 Gln Ala Leu Ala Ile Ala Gln Ala Ala Asp Phe Val Arg Glu Met Pro
 20 25 30

gag ggt ctt gat tct gag att gct cag ggt gga acc aat gtt tct ggt 144
 Glu Gly Leu Asp Ser Glu Ile Ala Gln Gly Gly Thr Asn Val Ser Gly
 35 40 45

ggt cag cgc cag cga cta gcc att gcc agg gcg ttg ttg aag caa cct 192
 Gly Gln Arg Gln Arg Leu Ala Ile Ala Arg Ala Leu Leu Lys Gln Pro
 50 55 60

gag atc tat att ttc gac gat tct ttc tcc gcc ctc gat gtg agc aca 240
 Glu Ile Tyr Ile Phe Asp Asp Ser Phe Ser Ala Leu Asp Val Ser Thr
 65 70 75 80

gac gcc gct ctt cgc cga gcg ctg agc acc aac ctg ccg gat gca acc 288
 Asp Ala Ala Leu Arg Arg Ala Leu Ser Thr Asn Leu Pro Asp Ala Thr
 85 90 95

aag ttg att gtc gcc cag cgt gtc agc acg att cga gat gcc gat cag 336
 Lys Leu Ile Val Ala Gln Arg Val Ser Thr Ile Arg Asp Ala Asp Gln
 100 105 110

att gtg gtg ctt gat aac ggc gag gtt gtc ggt att gga acg cac acg 384
 Ile Val Val Leu Asp Asn Gly Glu Val Val Gly Ile Gly Thr His Thr
 115 120 125

aat ttg ctg aac acg tgc ggt acc tac cgt gaa att gtt gaa tcc caa 432
 Asn Leu Leu Asn Thr Cys Gly Thr Tyr Arg Glu Ile Val Glu Ser Gln
 130 135 140

gag act gcg cag gcg caa tca tgagtaatac tgcaggcccc cgc 476
 Glu Thr Ala Gln Ala Gln Ser
 145 150

<210> 152

<211> 151

<212> PRT

<213> Corynebacterium glutamicum

<400> 152

Arg His Leu Arg Tyr Gly Asn Glu Asp Ala Thr Glu Thr Gln Leu Trp
 1 5 10 15

Gln Ala Leu Ala Ile Ala Gln Ala Ala Asp Phe Val Arg Glu Met Pro
 20 25 30

Glu Gly Leu Asp Ser Glu Ile Ala Gln Gly Gly Thr Asn Val Ser Gly
 35 40 45

Gly Gln Arg Gln Arg Leu Ala Ile Ala Arg Ala Leu Leu Lys Gln Pro
 50 55 60

Glu Ile Tyr Ile Phe Asp Asp Ser Phe Ser Ala Leu Asp Val Ser Thr
 65 70 75 80

Asp Ala Ala Leu Arg Arg Ala Leu Ser Thr Asn Leu Pro Asp Ala Thr
 85 90 95

Lys Leu Ile Val Ala Gln Arg Val Ser Thr Ile Arg Asp Ala Asp Gln
 100 105 110

Ile Val Val Leu Asp Asn Gly Glu Val Val Gly Ile Gly Thr His Thr
 115 120 125

Asn Leu Leu Asn Thr Cys Gly Thr Tyr Arg Glu Ile Val Glu Ser Gln
 130 135 140

Glu Thr Ala Gln Ala Gln Ser
 145 150

<210> 153

<211> 1172

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1149)

<223> RXN01808

<400> 153

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Gln Ser Leu Ala Cys Lys Glu Leu Ala Trp Met Arg Gly Gly Ala Pro	
1 5 10 15	
gcg cga acc tca aag cct gga ttc cgc ctt gaa gcc gcg gaa gct ttg	96
Ala Arg Thr Ser Lys Pro Gly Phe Arg Leu Glu Ala Ala Glu Ala Leu	
20 25 30	
atc gca gaa gtg cca gcg cca cgc gac aaa gtc gag ctc atg gca ttt	144
Ile Ala Glu Val Pro Ala Pro Arg Asp Lys Val Glu Leu Met Ala Phe	
35 40 45	
tcc aag tcc agg caa ggc cgc gtt gtc att gaa ctt gaa gac gcc aca	192
Ser Lys Ser Ser Arg Gln Gly Arg Val Val Ile Glu Leu Glu Asp Ala Thr	
50 55 60	
gta gcc acc cct gat gat cgc atc ctg gta gaa gac ctc acc tgg cgt	240
Val Ala Thr Pro Asp Asp Arg Ile Leu Val Glu Asp Leu Thr Trp Arg	
65 70 75 80	
ttg gct cca gga gag cgc atc ggt ctt gtc ggc gtc aac ggc tcc ggc	288
Leu Ala Pro Gly Glu Arg Ile Gly Leu Val Gly Val Asn Gly Ser Gly	
85 90 95	
aaa acc acc ctg ctg cgc acc ctt gcc ggc gag cag cca ctt cag gca	336
Lys Thr Thr Leu Leu Arg Thr Leu Ala Gly Glu Gln Pro Leu Gln Ala	
100 105 110	
ggc aaa cgc atc gaa ggc caa acc gtc aaa ctg gga tgg ctc cgc cag	384
Gly Lys Arg Ile Glu Gly Gln Thr Val Lys Leu Gly Trp Leu Arg Gln	
115 120 125	
gaa ctc gat gac cta gac ctc agc cgc cga ctc atc gac tgc gtt gaa	432
Glu Leu Asp Asp Leu Asp Leu Ser Arg Arg Leu Ile Asp Cys Val Glu	
130 135 140	
gat gtc gct tcc tac gtg atg atg ggc gac aag cag gtc tcc gct tcc	480
Asp Val Ala Ser Tyr Val Met Met Gly Asp Lys Gln Val Ser Ala Ser	
145 150 155 160	
caa ttg gca gaa cgc ctc gga ttc tca ccc aag agg caa cgc acc cca	528
Gln Leu Ala Glu Arg Leu Gly Phe Ser Pro Lys Arg Gln Arg Thr Pro	
165 170 175	
gtt ggt gac ctg tcc ggt ggt gaa cgc cgc cga ctc caa ctc acc cgc	576
Val Gly Asp Leu Ser Gly Gly Glu Arg Arg Arg Leu Gln Leu Thr Arg	
180 185 190	
gtg ctc atg gcc gaa cca aac gtg ctg ctc ctc gac gag ccc acc aac	624
Val Leu Met Ala Glu Pro Asn Val Leu Leu Leu Asp Glu Pro Thr Asn	
195 200 205	

gac ctg gac att gac acc ctc caa gag ctg gaa tcc ctt ctc gac gga 672
 Asp Leu Asp Ile Asp Thr Leu Gln Glu Leu Glu Ser Leu Leu Asp Gly
 210 215 220
 tgg cca ggc acc atg gtg gtt atc tcc cac gac cgt tac ctc atc gaa 720
 Trp Pro Gly Thr Met Val Val Ile Ser His Asp Arg Tyr Leu Ile Glu
 225 230 235 240
 cgc gtc acc gac tcc acc tgg gca ctc ttc ggc gat ggc aag ctc acc 768
 Arg Val Thr Asp Ser Thr Trp Ala Leu Phe Gly Asp Gly Lys Leu Thr
 245 250 255
 aac ctg cca ggc gga att gaa gag tac ctg cag cga cga gca gcg atg 816
 Asn Leu Pro Gly Gly Ile Glu Glu Tyr Leu Gln Arg Arg Ala Ala Met
 260 265 270
 gcc gcg gcc gaa gac agt gga gtg ctg aac ttg ggt gcg gcc acg cag 864
 Ala Ala Ala Glu Asp Ser Gly Val Leu Asn Leu Gly Ala Ala Thr Gln
 275 280 285
 gct gga acc ttt tct gct gca aca gag cag gct gcc act tct gtg gaa 912
 Ala Gly Thr Phe Ser Ala Ala Thr Glu Gln Ala Ala Thr Ser Val Glu
 290 295 300
 agt tcc gga att tct tcc caa gaa cgc cac cgc atc acc aag gaa atg 960
 Ser Ser Gly Ile Ser Ser Gln Glu Arg His Arg Ile Thr Lys Glu Met
 305 310 315 320
 aac gcc ctg gag cgc aaa atg ggc aag ctt gac cag caa atg gac aag 1008
 Asn Ala Leu Glu Arg Lys Met Gly Lys Leu Asp Gln Gln Met Asp Lys
 325 330 335
 ctt aat cag cag ctc gct gat gca gcg gag gcc atg gac acc ata aag 1056
 Leu Asn Gln Gln Leu Ala Asp Ala Ala Glu Ala Met Asp Thr Ile Lys
 340 345 350
 ctc acc gag ctg gac acc aag ctc cgc gca gtg cag gaa gaa cac ggc 1104
 Leu Thr Glu Leu Asp Thr Lys Leu Arg Ala Val Gln Glu Glu His Gly
 355 360 365
 gag ctg gaa atg cag tgg ctg gaa ctc ggc gag gaa atc gag ggc 1149
 Glu Leu Glu Met Gln Trp Leu Glu Leu Gly Glu Glu Ile Glu Gly
 370 375 380
 tagttcatgc cgtcggcagg cga 1172

<210> 154

<211> 383

<212> PRT

<213> Corynebacterium glutamicum

<400> 154

Gln Ser Leu Ala Cys Lys Glu Leu Ala Trp Met Arg Gly Gly Ala Pro
 1 5 10 15

Ala Arg Thr Ser Lys Pro Gly Phe Arg Leu Glu Ala Ala Glu Ala Leu
 20 25 30

Ile Ala Glu Val Pro Ala Pro Arg Asp Lys Val Glu Leu Met Ala Phe
 35 40 45

Ser Lys Ser Arg Gln Gly Arg Val Val Ile Glu Leu Glu Asp Ala Thr
 50 55 60
 Val Ala Thr Pro Asp Asp Arg Ile Leu Val Glu Asp Leu Thr Trp Arg
 65 70 75 80
 Leu Ala Pro Gly Glu Arg Ile Gly Leu Val Gly Val Asn Gly Ser Gly
 85 90 95
 Lys Thr Thr Leu Leu Arg Thr Leu Ala Gly Glu Gln Pro Leu Gln Ala
 100 105 110
 Gly Lys Arg Ile Glu Gly Gln Thr Val Lys Leu Gly Trp Leu Arg Gln
 115 120 125
 Glu Leu Asp Asp Leu Asp Leu Ser Arg Arg Leu Ile Asp Cys Val Glu
 130 135 140
 Asp Val Ala Ser Tyr Val Met Met Gly Asp Lys Gln Val Ser Ala Ser
 145 150 155 160
 Gln Leu Ala Glu Arg Leu Gly Phe Ser Pro Lys Arg Gln Arg Thr Pro
 165 170 175
 Val Gly Asp Leu Ser Gly Gly Glu Arg Arg Arg Leu Gln Leu Thr Arg
 180 185 190
 Val Leu Met Ala Glu Pro Asn Val Leu Leu Leu Asp Glu Pro Thr Asn
 195 200 205
 Asp Leu Asp Ile Asp Thr Leu Gln Glu Leu Glu Ser Leu Leu Asp Gly
 210 215 220
 Trp Pro Gly Thr Met Val Val Ile Ser His Asp Arg Tyr Leu Ile Glu
 225 230 235 240
 Arg Val Thr Asp Ser Thr Trp Ala Leu Phe Gly Asp Gly Lys Leu Thr
 245 250 255
 Asn Leu Pro Gly Gly Ile Glu Glu Tyr Leu Gln Arg Arg Ala Ala Met
 260 265 270
 Ala Ala Ala Glu Asp Ser Gly Val Leu Asn Leu Gly Ala Ala Thr Gln
 275 280 285
 Ala Gly Thr Phe Ser Ala Ala Thr Glu Gln Ala Ala Thr Ser Val Glu
 290 295 300
 Ser Ser Gly Ile Ser Ser Gln Glu Arg His Arg Ile Thr Lys Glu Met
 305 310 315 320
 Asn Ala Leu Glu Arg Lys Met Gly Lys Leu Asp Gln Gln Met Asp Lys
 325 330 335
 Leu Asn Gln Gln Leu Ala Asp Ala Ala Glu Ala Met Asp Thr Ile Lys
 340 345 350
 Leu Thr Glu Leu Asp Thr Lys Leu Arg Ala Val Gln Glu Glu His Gly
 355 360 365

Glu Leu Glu Met Gln Trp Leu Glu Leu Gly Glu Glu Ile Glu Gly
 370 375 380

<210> 155

<211> 1142

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1119)

<223> FRXA01808

<400> 155

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Met Arg Gly Gly Ala Pro Ala Arg Thr Ser Lys Pro Gly Phe Arg Leu	
1 5 10 15	
 gaa gcc gcg gaa gct ttg atc gca gaa gtg cca gcg cca cgc gac aaa	96
Glu Ala Ala Glu Ala Leu Ile Ala Glu Val Pro Ala Pro Arg Asp Lys	
20 25 30	
 gtc gag ctc atg gca ttt tcc aag tcc agg caa ggc cgc gtt gtc att	144
Val Glu Leu Met Ala Phe Ser Lys Ser Arg Gln Gly Arg Val Val Ile	
35 40 45	
 gaa ctt gaa gac gcc aca gta gcc acc cct gat gat cgc atc ctg gta	192
Glu Leu Glu Asp Ala Thr Val Ala Thr Pro Asp Asp Arg Ile Leu Val	
50 55 60	
 gaa gac ctc acc tgg cgt ttg gct cca gga gag cgc atc ggt ctt gtc	240
Glu Asp Leu Thr Trp Arg Leu Ala Pro Gly Glu Arg Ile Gly Leu Val	
65 70 75 80	
 ggc gtc aac ggc tcc ggc aaa acc acc ctg ctg cgc acc ctt gcc ggc	288
Gly Val Asn Gly Ser Gly Lys Thr Thr Leu Leu Arg Thr Leu Ala Gly	
85 90 95	
 gag cag cca ctt cag gca ggc aaa cgc atc gaa ggc caa acc gtc aaa	336
Glu Gln Pro Leu Gln Ala Gly Lys Arg Ile Glu Gly Gln Thr Val Lys	
100 105 110	
 ctg gga tgg ctc cgc cag gaa ctc gat gac cta gac ctc agc cgc cga	384
Leu Gly Trp Leu Arg Gln Glu Leu Asp Asp Leu Asp Leu Ser Arg Arg	
115 120 125	
 ctc atc gac tgc gtt gaa gat gtc gct tcc tac gtg atg atg ggc gac	432
Leu Ile Asp Cys Val Glu Asp Val Ala Ser Tyr Val Met Met Gly Asp	
130 135 140	
 aag cag gtc tcc gct tcc caa ttg gca gaa cgc ctc gga ttc tca ccc	480
Lys Gln Val Ser Ala Ser Gln Leu Ala Glu Arg Leu Gly Phe Ser Pro	
145 150 155 160	
 aag agg caa cgc acc cca gtt ggt gac ctg tcc ggt ggt gaa cgc cgc	528
Lys Arg Gln Arg Thr Pro Val Gly Asp Leu Ser Gly Gly Glu Arg Arg	
165 170 175	
 cga ctc caa ctc acc cgc gtg ctc atg gcc gaa cca aac gtg ctg ctc	576
Arg Leu Gln Leu Thr Arg Val Leu Met Ala Glu Pro Asn Val Leu Leu	

180	185	190	
ctc gac gag ccc acc aac gac ctg gac att gac acc ctc caa gag ctg			624
Leu Asp Glu Pro Thr Asn Asp Leu Asp Ile Asp Thr Leu Gln Glu Leu			
195	200	205	
gaa tcc ctt ctc gac gga tgg cca ggc acc atg gtg gtt atc tcc cac			672
Glu Ser Leu Leu Asp Gly Trp Pro Gly Thr Met Val Val Ile Ser His			
210	215	220	
gac cgt tac ctc atc gaa cgc gtc acc gac tcc acc tgg gca ctc ttc			720
Asp Arg Tyr Leu Ile Glu Arg Val Thr Asp Ser Thr Trp Ala Leu Phe			
225	230	235	240
ggc gat ggc aag ctc acc aac ctg cca ggc gga att gaa gag tac ctg			768
Gly Asp Gly Lys Leu Thr Asn Leu Pro Gly Gly Ile Glu Glu Tyr Leu			
	245	250	255
cag cga cga gca gcg atg gcc gcg gcc gaa gac agt gga gtg ctg aac			816
Gln Arg Arg Ala Ala Met Ala Ala Ala Glu Asp Ser Gly Val Leu Asn			
	260	265	270
ttg ggt gcg gcc acg cag gct gga acc ttt tct gct gca aca gag cag			864
Leu Gly Ala Ala Thr Gln Ala Gly Thr Phe Ser Ala Ala Thr Glu Gln			
	275	280	285
gct gcc act tct gtg gaa agt tcc gga att tct tcc caa gaa cgc cac			912
Ala Ala Thr Ser Val Glu Ser Ser Gly Ile Ser Ser Gln Glu Arg His			
	290	295	300
cgc atc acc aag gaa atg aac gcc ctg gag cgc aaa atg ggc aag ctt			960
Arg Ile Thr Lys Glu Met Asn Ala Leu Glu Arg Lys Met Gly Lys Leu			
305	310	315	320
gac cag caa atg gac aag ctt aat cag cag ctc gct gat gca gcg gag			1008
Asp Gln Gln Met Asp Lys Leu Asn Gln Gln Leu Ala Asp Ala Ala Glu			
	325	330	335
gcc atg gac acc ata aag ctc acc gag ctg gac acc aag ctc cgc gca			1056
Ala Met Asp Thr Ile Lys Leu Thr Glu Leu Asp Thr Lys Leu Arg Ala			
	340	345	350
gtg cag gaa gaa cac ggc gag ctg gaa atg cag tgg ctg gaa ctc ggc			1104
Val Gln Glu Glu His Gly Glu Leu Glu Met Gln Trp Leu Glu Leu Gly			
	355	360	365
gag gaa atc gag ggc tagttcatgc cgtcggcagg cga			1142
Glu Glu Ile Glu Gly			
370			

<210> 156

<211> 373

<212> PRT

<213> Corynebacterium glutamicum

<400> 156

Met Arg Gly Gly Ala Pro Ala Arg Thr Ser Lys Pro Gly Phe Arg Leu
1 5 10 15

Glu Ala Ala Glu Ala Leu Ile Ala Glu Val Pro Ala Pro Arg Asp Lys

20					25					30					
Val	Glu	Leu	Met	Ala	Phe	Ser	Lys	Ser	Arg	Gln	Gly	Arg	Val	Val	Ile
		35					40					45			
Glu	Leu	Glu	Asp	Ala	Thr	Val	Ala	Thr	Pro	Asp	Asp	Arg	Ile	Leu	Val
	50					55					60				
Glu	Asp	Leu	Thr	Trp	Arg	Leu	Ala	Pro	Gly	Glu	Arg	Ile	Gly	Leu	Val
	65					70					75				80
Gly	Val	Asn	Gly	Ser	Gly	Lys	Thr	Thr	Leu	Leu	Arg	Thr	Leu	Ala	Gly
				85					90					95	
Glu	Gln	Pro	Leu	Gln	Ala	Gly	Lys	Arg	Ile	Glu	Gly	Gln	Thr	Val	Lys
			100					105					110		
Leu	Gly	Trp	Leu	Arg	Gln	Glu	Leu	Asp	Asp	Leu	Asp	Leu	Ser	Arg	Arg
		115					120					125			
Leu	Ile	Asp	Cys	Val	Glu	Asp	Val	Ala	Ser	Tyr	Val	Met	Met	Gly	Asp
	130					135					140				
Lys	Gln	Val	Ser	Ala	Ser	Gln	Leu	Ala	Glu	Arg	Leu	Gly	Phe	Ser	Pro
	145					150					155				160
Lys	Arg	Gln	Arg	Thr	Pro	Val	Gly	Asp	Leu	Ser	Gly	Gly	Glu	Arg	Arg
				165					170					175	
Arg	Leu	Gln	Leu	Thr	Arg	Val	Leu	Met	Ala	Glu	Pro	Asn	Val	Leu	Leu
		180						185					190		
Leu	Asp	Glu	Pro	Thr	Asn	Asp	Leu	Asp	Ile	Asp	Thr	Leu	Gln	Glu	Leu
		195					200					205			
Glu	Ser	Leu	Leu	Asp	Gly	Trp	Pro	Gly	Thr	Met	Val	Val	Ile	Ser	His
	210					215					220				
Asp	Arg	Tyr	Leu	Ile	Glu	Arg	Val	Thr	Asp	Ser	Thr	Trp	Ala	Leu	Phe
	225					230					235				240
Gly	Asp	Gly	Lys	Leu	Thr	Asn	Leu	Pro	Gly	Gly	Ile	Glu	Glu	Tyr	Leu
			245						250					255	
Gln	Arg	Arg	Ala	Ala	Met	Ala	Ala	Ala	Glu	Asp	Ser	Gly	Val	Leu	Asn
			260					265					270		
Leu	Gly	Ala	Ala	Thr	Gln	Ala	Gly	Thr	Phe	Ser	Ala	Ala	Thr	Glu	Gln
		275					280					285			
Ala	Ala	Thr	Ser	Val	Glu	Ser	Ser	Gly	Ile	Ser	Ser	Gln	Glu	Arg	His
	290					295					300				
Arg	Ile	Thr	Lys	Glu	Met	Asn	Ala	Leu	Glu	Arg	Lys	Met	Gly	Lys	Leu
	305					310					315				320
Asp	Gln	Gln	Met	Asp	Lys	Leu	Asn	Gln	Gln	Leu	Ala	Asp	Ala	Ala	Glu
			325						330				335		
Ala	Met	Asp	Thr	Ile	Lys	Leu	Thr	Glu	Leu	Asp	Thr	Lys	Leu	Arg	Ala
			340					345					350		

Val Gln Glu Glu His Gly Glu Leu Glu Met Gln Trp Leu Glu Leu Gly
 355 360 365

Glu Glu Ile Glu Gly
 370

<210> 157
 <211> 349
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(349)
 <223> RXN02975

<400> 157
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tttattgacc tggcaacttc aattgataga ctgtagggtt gtg att gtc acc aat 115
 Val Ile Val Thr Asn
 1 5

gat tta gag gtg cgc gtt ggc gca cgt acc ctt ctc gat gcc cca ggt 163
 Asp Leu Glu Val Arg Val Gly Ala Arg Thr Leu Leu Asp Ala Pro Gly
 10 15 20

cag ctc ctt cgg gtg cag cca ggc gac cgt att ggt ctg gtt ggt aga 211
 Gln Leu Leu Arg Val Gln Pro Gly Asp Arg Ile Gly Leu Val Gly Arg
 25 30 35

aat ggt gcg ggc aaa acc acc acc atg cga atc ctc tcg ggc gaa acc 259
 Asn Gly Ala Gly Lys Thr Thr Met Arg Ile Leu Ser Gly Glu Thr
 40 45 50

aag ccc tac gga gga tcc gta acc aca tct ggt gaa atc ggt tac ctg 307
 Lys Pro Tyr Gly Gly Ser Val Thr Thr Ser Gly Glu Ile Gly Tyr Leu
 55 60 65

ccc cag gac tcc cgc gaa ggc aac atc gaa caa acc gcc cgc 349
 Pro Gln Asp Ser Arg Glu Gly Asn Ile Glu Gln Thr Ala Arg
 70 75 80

<210> 158
 <211> 83
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 158
 Val Ile Val Thr Asn Asp Leu Glu Val Arg Val Gly Ala Arg Thr Leu
 1 5 10 15

Leu Asp Ala Pro Gly Gln Leu Leu Arg Val Gln Pro Gly Asp Arg Ile
 20 25 30

Gly Leu Val Gly Arg Asn Gly Ala Gly Lys Thr Thr Thr Met Arg Ile
 35 40 45

Leu Ser Gly Glu Thr Lys Pro Tyr Gly Gly Ser Val Thr Thr Ser Gly
50 55 60

Glu Ile Gly Tyr Leu Pro Gln Asp Ser Arg Glu Gly Asn Ile Glu Gln
65 70 75 80

Thr Ala Arg

<210> 159

<211> 732

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(709)

<223> RXN03116

<400> 159

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ttttgctcag gtactgtcac tggaatcggg aaggctgaaa atg ggg gag ggg gac 115
Met Gly Glu Gly Asp
1 5

gtc gaa aag cat ttt gct ttt ggt ctt aaa gct gcg aag cag cgt cgc 163
Val Glu Lys His Phe Ala Phe Gly Leu Lys Ala Ala Lys Gln Arg Arg
10 15 20

ttt ttc gcg cgt acc gtg gcc ctc atg cca cag aat cct act att cct 211
Phe Phe Ala Arg Thr Val Ala Leu Met Pro Gln Asn Pro Thr Ile Pro
25 30 35

gca ggt ctg agc gtt ttt gat tat gtg ctg ctg ggg cgt cat ccg cac 259
Ala Gly Leu Ser Val Phe Asp Tyr Val Leu Leu Gly Arg His Pro His
40 45 50

agt tac gcg ccg ggg cgt gct gat gat gag atc gtg aag cgg tgc ctc 307
Ser Tyr Ala Pro Gly Arg Ala Asp Asp Glu Ile Val Lys Arg Cys Leu
55 60 65

gct gat ctg aaa ttg gag cat ttc agc gac cgc ggc tta gac gaa ttg 355
Ala Asp Leu Lys Leu Glu His Phe Ser Asp Arg Gly Leu Asp Glu Leu
70 75 80 85

tcc ggc ggc gag cgt caa cgc gtc agc ctt gcc cgc gcg ctc gcc caa 403
Ser Gly Gly Glu Arg Gln Arg Val Ser Leu Ala Arg Ala Leu Ala Gln
90 95 100

gaa ccg cgc atc gtg ctt ctc gac gag ccg acc tcc gcg ctt gac atc 451
Glu Pro Arg Ile Val Leu Leu Asp Glu Pro Thr Ser Ala Leu Asp Ile
105 110 115

ggc cat gcg cag gaa acg ctt gag ctt atc gac gcc atc cgg cac cga 499
Gly His Ala Gln Glu Thr Leu Glu Leu Ile Asp Ala Ile Arg His Arg
120 125 130

ctc ggc ctc acc gtg atc gcg gcg atg cat gac ctc acc ctg act gcg 547
Leu Gly Leu Thr Val Ile Ala Ala Met His Asp Leu Thr Leu Thr Ala

135 140 145
 caa tac ggc gat cgg gtg ctc atg atg aat ggt ggc cgc aaa gtt ttc 595
 Gln Tyr Gly Asp Arg Val Leu Met Met Asn Gly Gly Arg Lys Val Phe
 150 155 160 165

 gag ggc act gca gcc gaa gtg ctc acc gcg cag cgg att tcg gag att 643
 Glu Gly Thr Ala Ala Glu Val Leu Thr Ala Gln Arg Ile Ser Glu Ile
 170 175 180

 tat gat gcc act gtg att gtt gag gtt att gat ggg cgt ccc gtg gtg 691
 Tyr Asp Ala Thr Val Ile Val Glu Val Ile Asp Gly Arg Pro Val Val
 185 190 195

 att ccg caa cgg tcg cac tgacctgttg tggcagacca gac 732
 Ile Pro Gln Arg Ser His
 200

 <210> 160
 <211> 203
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 160
 Met Gly Glu Gly Asp Val Glu Lys His Phe Ala Phe Gly Leu Lys Ala
 1 5 10 15

 Ala Lys Gln Arg Arg Phe Phe Ala Arg Thr Val Ala Leu Met Pro Gln
 20 25 30

 Asn Pro Thr Ile Pro Ala Gly Leu Ser Val Phe Asp Tyr Val Leu Leu
 35 40 45

 Gly Arg His Pro His Ser Tyr Ala Pro Gly Arg Ala Asp Asp Glu Ile
 50 55 60

 Val Lys Arg Cys Leu Ala Asp Leu Lys Leu Glu His Phe Ser Asp Arg
 65 70 75 80

 Gly Leu Asp Glu Leu Ser Gly Gly Glu Arg Gln Arg Val Ser Leu Ala
 85 90 95

 Arg Ala Leu Ala Gln Glu Pro Arg Ile Val Leu Leu Asp Glu Pro Thr
 100 105 110

 Ser Ala Leu Asp Ile Gly His Ala Gln Glu Thr Leu Glu Leu Ile Asp
 115 120 125

 Ala Ile Arg His Arg Leu Gly Leu Thr Val Ile Ala Ala Met His Asp
 130 135 140

 Leu Thr Leu Thr Ala Gln Tyr Gly Asp Arg Val Leu Met Met Asn Gly
 145 150 155 160

 Gly Arg Lys Val Phe Glu Gly Thr Ala Ala Glu Val Leu Thr Ala Gln
 165 170 175

 Arg Ile Ser Glu Ile Tyr Asp Ala Thr Val Ile Val Glu Val Ile Asp
 180 185 190

Gly Arg Pro Val Val Ile Pro Gln Arg Ser His
195 200

<210> 161
<211> 390
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(367)
<223> RXN03108

<400> 161
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cttgaccacc tcacgggtga gttgcagaaa gtagttcgct atg act aaa cca aac 115
Met Thr Lys Pro Asn
1 5
gct tcc gtc gag ctg aat acg atc acc aag tcc tac ggc tcc acc act 163
Ala Ser Val Glu Leu Asn Thr Ile Thr Lys Ser Tyr Gly Ser Thr Thr
10 15 20
atc att ggc gat acg agc atc acc atc aac gac ggt gaa ttc gtc tcc 211
Ile Ile Gly Asp Thr Ser Ile Thr Ile Asn Asp Gly Glu Phe Val Ser
25 30 35
ctc ctc gac cct tcc ggc tgc gga aaa tca aca att ctc aaa atg atc 259
Leu Leu Asp Pro Ser Gly Cys Gly Lys Ser Thr Ile Leu Lys Met Ile
40 45 50
gcc gga ctg gcc tcc cca tcc acc ggc aca gtc agc gca ggc aac gaa 307
Ala Gly Leu Ala Ser Pro Ser Thr Gly Thr Val Ser Ala Gly Asn Glu
55 60 65
gaa att aaa gga cca gga cct gac cga ggc atg gtt ttc caa gac cac 355
Glu Ile Lys Gly Pro Gly Pro Asp Arg Gly Met Val Phe Gln Asp His
70 75 80 85
gcc ctc ctg ccc tgattgaccg cagcggcaa cat 390
Ala Leu Leu Pro

<210> 162
<211> 89
<212> PRT
<213> Corynebacterium glutamicum

<400> 162
Met Thr Lys Pro Asn Ala Ser Val Glu Leu Asn Thr Ile Thr Lys Ser
1 5 10 15
Tyr Gly Ser Thr Thr Ile Ile Gly Asp Thr Ser Ile Thr Ile Asn Asp
20 25 30
Gly Glu Phe Val Ser Leu Leu Asp Pro Ser Gly Cys Gly Lys Ser Thr
35 40 45

Ile Leu Lys Met Ile Ala Gly Leu Ala Ser Pro Ser Thr Gly Thr Val
 50 55 60

Ser Ala Gly Asn Glu Glu Ile Lys Gly Pro Gly Pro Asp Arg Gly Met
 65 70 75 80

Val Phe Gln Asp His Ala Leu Leu Pro
 85

<210> 163

<211> 1347

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1324)

<223> RXN03129

<400> 163

gctgaggttg agaccaagct gaacaccatc tacaccgcg acatcgaacc acttatttaa 60

tccgagcact tcagctacac ctatttaagg aggctgtgac atg gcg tca atc gtc 115
 Met Ala Ser Ile Val
 1 5

ttt gaa aac gtc aca cgc aaa tac tct ccg ggc gca cgc ccg gcc gtc 163
 Phe Glu Asn Val Thr Arg Lys Tyr Ser Pro Gly Ala Arg Pro Ala Val
 10 15 20

gac aag ctt aat ttg gaa atc gcc gac ggc gag ttc cta gtt ctc gtt 211
 Asp Lys Leu Asn Leu Glu Ile Ala Asp Gly Glu Phe Leu Val Leu Val
 25 30 35

gga ccc tca ggc tgt gga aag tcc act tct ttg cgc atg ctg gct ggt 259
 Gly Pro Ser Gly Cys Gly Lys Ser Thr Ser Leu Arg Met Leu Ala Gly
 40 45 50

ctt gag cct atc gac gag gga cgt cta ctc att gat ggt aaa gac gcc 307
 Leu Glu Pro Ile Asp Glu Gly Arg Leu Leu Ile Asp Gly Lys Asp Ala
 55 60 65

acg gaa ctg cgt ccg cag gat cgt gac atc gct atg gtc ttc cag agc 355
 Thr Glu Leu Arg Pro Gln Asp Arg Asp Ile Ala Met Val Phe Gln Ser
 70 75 80 85

tac gcg ctg tac ccg aat atg act gtt cgg gac aac atg ggc ttt gcg 403
 Tyr Ala Leu Tyr Pro Asn Met Thr Val Arg Asp Asn Met Gly Phe Ala
 90 95 100

ctg aag aat cag aag gtg gct aag gct gag atc gaa aag cgt gtt gct 451
 Leu Lys Asn Gln Lys Val Ala Lys Ala Glu Ile Glu Lys Arg Val Ala
 105 110 115

gaa gcc tca cgc att ctg cag ctg gat ccg tat ctt gat cgt aag cct 499
 Glu Ala Ser Arg Ile Leu Gln Leu Asp Pro Tyr Leu Asp Arg Lys Pro
 120 125 130

gca gct ttg tct ggt ggt cag cgc cag cgc gtg gcc atg ggc cgt gca 547
 Ala Ala Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Met Gly Arg Ala

135	140	145	
att gtg cgt gag cca tcg gtg ttc tgc atg gat gag cca ctg tcc aac			595
Ile Val Arg Glu Pro Ser Val Phe Cys Met Asp Glu Pro Leu Ser Asn			
150	155	160	165
cta gat gcg aag ctg cgt gtg tct acg cgt gcg gag atc tct ggt ttg			643
Leu Asp Ala Lys Leu Arg Val Ser Thr Arg Ala Glu Ile Ser Gly Leu			
	170	175	180
cag cgt cgc atg ggc gtg acc acg gtg tat gtg act cac gat cag gtc			691
Gln Arg Arg Met Gly Val Thr Thr Val Tyr Val Thr His Asp Gln Val			
	185	190	195
gag gcc atg acc atg ggt gat cgc gtc gct gtg ctt ttg ctc ggt gtg			739
Glu Ala Met Thr Met Gly Asp Arg Val Ala Val Leu Leu Leu Gly Val			
	200	205	210
ctg cag caa gta gac acc ccg cag aac ctg tac gac tac cca gca aat			787
Leu Gln Gln Val Asp Thr Pro Gln Asn Leu Tyr Asp Tyr Pro Ala Asn			
	215	220	225
gcg ttc gtc gcc agc ttc att ggt tcc cct tcc atg aac ttg att gag			835
Ala Phe Val Ala Ser Phe Ile Gly Ser Pro Ser Met Asn Leu Ile Glu			
	230	235	240
ggc acc atc cgt ggc gat aag gtc act ttg ggt act gga att cag att			883
Gly Thr Ile Arg Gly Asp Lys Val Thr Leu Gly Thr Gly Ile Gln Ile			
	250	255	260
tca gtt cct gat gag gtg gca gca gag gtt cgc aac aac ccg gat cgc			931
Ser Val Pro Asp Glu Val Ala Ala Glu Val Arg Asn Asn Pro Asp Arg			
	265	270	275
ttt gag ggt cgt cca gtc att gtt ggt gct cgt ccc gag cac atg tat			979
Phe Glu Gly Arg Pro Val Ile Val Gly Ala Arg Pro Glu His Met Tyr			
	280	285	290
ttg acc acg gcg aat gag agt ggt gct gta ttg ggc gaa gtc agc cac			1027
Leu Thr Thr Ala Asn Glu Ser Gly Ala Val Leu Gly Glu Val Ser His			
	295	300	305
att gat gag ctc ggc gcg gat tca atg gtc tac gta ttg gcg tct ggt			1075
Ile Asp Glu Leu Gly Ala Asp Ser Met Val Tyr Val Leu Ala Ser Gly			
	310	315	320
gtg aag aac ccg aat act gat ctt ttg ggt gag ggc att cca gag gat			1123
Val Lys Asn Pro Asn Thr Asp Leu Leu Gly Glu Gly Ile Pro Glu Asp			
	330	335	340
atg cgc gtg acc gtt gtc ggt gct gaa gag acc gat aag gcc cgg ctg			1171
Met Arg Val Thr Val Val Gly Ala Glu Glu Thr Asp Lys Ala Arg Leu			
	345	350	355
ggt att cgt gtt gag cgc cat cac ggt ctg aag gcc ggc gat aag gtg			1219
Gly Ile Arg Val Glu Arg His His Gly Leu Lys Ala Gly Asp Lys Val			
	360	365	370
cac gtt gtt gct gca ccg aag gat gtt cac ctc ttc gac ggt ctt gat			1267
His Val Val Ala Ala Pro Lys Asp Val His Leu Phe Asp Gly Leu Asp			
	375	380	385

ggc cgt cga atc ggt gca tcg gtt cta gct cca gcc cat aca gtc cag 1315
 Gly Arg Arg Ile Gly Ala Ser Val Leu Ala Pro Ala His Thr Val Gln
 390 395 400 405

tct ggt cac tagattatct accagtgtcaa ctc 1347
 Ser Gly His

<210> 164

<211> 408

<212> PRT

<213> Corynebacterium glutamicum

<400> 164

Met Ala Ser Ile Val Phe Glu Asn Val Thr Arg Lys Tyr Ser Pro Gly
 1 5 10 15

Ala Arg Pro Ala Val Asp Lys Leu Asn Leu Glu Ile Ala Asp Gly Glu
 20 25 30

Phe Leu Val Leu Val Gly Pro Ser Gly Cys Gly Lys Ser Thr Ser Leu
 35 40 45

Arg Met Leu Ala Gly Leu Glu Pro Ile Asp Glu Gly Arg Leu Leu Ile
 50 55 60

Asp Gly Lys Asp Ala Thr Glu Leu Arg Pro Gln Asp Arg Asp Ile Ala
 65 70 75 80

Met Val Phe Gln Ser Tyr Ala Leu Tyr Pro Asn Met Thr Val Arg Asp
 85 90 95

Asn Met Gly Phe Ala Leu Lys Asn Gln Lys Val Ala Lys Ala Glu Ile
 100 105 110

Glu Lys Arg Val Ala Glu Ala Ser Arg Ile Leu Gln Leu Asp Pro Tyr
 115 120 125

Leu Asp Arg Lys Pro Ala Ala Leu Ser Gly Gly Gln Arg Gln Arg Val
 130 135 140

Ala Met Gly Arg Ala Ile Val Arg Glu Pro Ser Val Phe Cys Met Asp
 145 150 155 160

Glu Pro Leu Ser Asn Leu Asp Ala Lys Leu Arg Val Ser Thr Arg Ala
 165 170 175

Glu Ile Ser Gly Leu Gln Arg Arg Met Gly Val Thr Thr Val Tyr Val
 180 185 190

Thr His Asp Gln Val Glu Ala Met Thr Met Gly Asp Arg Val Ala Val
 195 200 205

Leu Leu Leu Gly Val Leu Gln Gln Val Asp Thr Pro Gln Asn Leu Tyr
 210 215 220

Asp Tyr Pro Ala Asn Ala Phe Val Ala Ser Phe Ile Gly Ser Pro Ser
 225 230 235 240

Met Asn Leu Ile Glu Gly Thr Ile Arg Gly Asp Lys Val Thr Leu Gly
 245 250 255

Thr Gly Ile Gln Ile Ser Val Pro Asp Glu Val Ala Ala Glu Val Arg
 260 265 270

Asn Asn Pro Asp Arg Phe Glu Gly Arg Pro Val Ile Val Gly Ala Arg
 275 280 285

Pro Glu His Met Tyr Leu Thr Thr Ala Asn Glu Ser Gly Ala Val Leu
 290 295 300

Gly Glu Val Ser His Ile Asp Glu Leu Gly Ala Asp Ser Met Val Tyr
 305 310 315 320

Val Leu Ala Ser Gly Val Lys Asn Pro Asn Thr Asp Leu Leu Gly Glu
 325 330 335

Gly Ile Pro Glu Asp Met Arg Val Thr Val Val Gly Ala Glu Glu Thr
 340 345 350

Asp Lys Ala Arg Leu Gly Ile Arg Val Glu Arg His His Gly Leu Lys
 355 360 365

Ala Gly Asp Lys Val His Val Val Ala Ala Pro Lys Asp Val His Leu
 370 375 380

Phe Asp Gly Leu Asp Gly Arg Arg Ile Gly Ala Ser Val Leu Ala Pro
 385 390 395 400

Ala His Thr Val Gln Ser Gly His
 405

<210> 165
 <211> 843
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(820)
 <223> FRXA01890

<400> 165
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tccgagcaact tcagctacac ctatttaagg aggctgtgac atg gcg tca atc gtc 115
 Met Ala Ser Ile Val
 1 5

ttt gaa aac gtc aca cgc aaa tac tct ccg ggc gca cgc ccg gcc gtc 163
 Phe Glu Asn Val Thr Arg Lys Tyr Ser Pro Gly Ala Arg Pro Ala Val
 10 15 20

gac aag ctt aat ttg gaa atc gcc gac ggc gag ttc cta gtt ctc gtt 211
 Asp Lys Leu Asn Leu Glu Ile Ala Asp Gly Glu Phe Leu Val Leu Val
 25 30 35

gga ccc tca ggc tgt gga aag tcc act tct ttg cgc atg ctg gct ggt 259
 Gly Pro Ser Gly Cys Gly Lys Ser Thr Ser Leu Arg Met Leu Ala Gly

40	45	50	
ctt gag cct atc gac gag gga cgt cta ctc att gat ggt aaa gac gcc			307
Leu Glu Pro Ile Asp Glu Gly Arg Leu Leu Ile Asp Gly Lys Asp Ala			
55	60	65	
acg gaa ctg cgt ccg cag gat cgt gac atc gct atg gtc ttc cag agc			355
Thr Glu Leu Arg Pro Gln Asp Arg Asp Ile Ala Met Val Phe Gln Ser			
70	75	80	85
tac gcg ctg tac ccg aat atg act gtt cgg gac aac atg ggc ttt gcg			403
Tyr Ala Leu Tyr Pro Asn Met Thr Val Arg Asp Asn Met Gly Phe Ala			
	90	95	100
ctg aag aat cag aag gtg gct aag gct gag atc gaa aag cgt gtt gct			451
Leu Lys Asn Gln Lys Val Ala Lys Ala Glu Ile Glu Lys Arg Val Ala			
	105	110	115
gaa gcc tca cgc att ctg cag ctg gat ccg tat ctt gat cgt aag cct			499
Glu Ala Ser Arg Ile Leu Gln Leu Asp Pro Tyr Leu Asp Arg Lys Pro			
	120	125	130
gca gct ttg tct ggt ggt cag cgc cag cgc gtg gcc atg ggc cgt gca			547
Ala Ala Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Met Gly Arg Ala			
	135	140	145
att gtg cgt gag cca tgc gtg ttc tgc atg gat gag cca ctg tcc aac			595
Ile Val Arg Glu Pro Ser Val Phe Cys Met Asp Glu Pro Leu Ser Asn			
150	155	160	165
cta gat gcg aag ctg cgt gtg tct acg cgt gcg gag atc tct ggt ttg			643
Leu Asp Ala Lys Leu Arg Val Ser Thr Arg Ala Glu Ile Ser Gly Leu			
	170	175	180
cag cgt cgc atg ggc gtg acc acg gtg tat gtg act cac gat cag gtc			691
Gln Arg Arg Met Gly Val Thr Thr Val Tyr Val Thr His Asp Gln Val			
	185	190	195
gag gcc atg acc atg ggt gat cgc gtc gct gtg ctt ttg ctc ggt gtg			739
Glu Ala Met Thr Met Gly Asp Arg Val Ala Val Leu Leu Leu Gly Val			
	200	205	210
ctg cag caa gta gac acc ccg cag aac ctg tac gac tac cca gca aat			787
Leu Gln Gln Val Asp Thr Pro Gln Asn Leu Tyr Asp Tyr Pro Ala Asn			
	215	220	225
gcg ttc gtc gcc agc ttc att ggt tcc ctt cca tgaacttgat tgagggcacc			840
Ala Phe Val Ala Ser Phe Ile Gly Ser Leu Pro			
230	235	240	
atc			843

<210> 166

<211> 240

<212> PRT

<213> Corynebacterium glutamicum

<400> 166

Met Ala Ser Ile Val Phe Glu Asn Val Thr Arg Lys Tyr Ser Pro Gly

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5

10

15

Ala Arg Pro Ala Val Asp Lys Leu Asn Leu Glu Ile Ala Asp Gly Glu
 20 25 30

Phe Leu Val Leu Val Gly Pro Ser Gly Cys Gly Lys Ser Thr Ser Leu
 35 40 45

Arg Met Leu Ala Gly Leu Glu Pro Ile Asp Glu Gly Arg Leu Leu Ile
 50 55 60

Asp Gly Lys Asp Ala Thr Glu Leu Arg Pro Gln Asp Arg Asp Ile Ala
 65 70 75 80

Met Val Phe Gln Ser Tyr Ala Leu Tyr Pro Asn Met Thr Val Arg Asp
 85 90 95

Asn Met Gly Phe Ala Leu Lys Asn Gln Lys Val Ala Lys Ala Glu Ile
 100 105 110

Glu Lys Arg Val Ala Glu Ala Ser Arg Ile Leu Gln Leu Asp Pro Tyr
 115 120 125

Leu Asp Arg Lys Pro Ala Ala Leu Ser Gly Gly Gln Arg Gln Arg Val
 130 135 140

Ala Met Gly Arg Ala Ile Val Arg Glu Pro Ser Val Phe Cys Met Asp
 145 150 155 160

Glu Pro Leu Ser Asn Leu Asp Ala Lys Leu Arg Val Ser Thr Arg Ala
 165 170 175

Glu Ile Ser Gly Leu Gln Arg Arg Met Gly Val Thr Thr Val Tyr Val
 180 185 190

Thr His Asp Gln Val Glu Ala Met Thr Met Gly Asp Arg Val Ala Val
 195 200 205

Leu Leu Leu Gly Val Leu Gln Gln Val Asp Thr Pro Gln Asn Leu Tyr
 210 215 220

Asp Tyr Pro Ala Asn Ala Phe Val Ala Ser Phe Ile Gly Ser Leu Pro
 225 230 235 240

<210> 167

<211> 1056

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1033)

<223> RXN02945

<400> 167

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tgggtgcactt gatcgtttcg ccgctggccg cgaggtataa atg acc acc gca ctt 115

Met Thr Thr Ala Leu

1

5

gga acg cgc gtt gtt gcg cgc aac ttt ggc tac cgc cat gct tcc cgg	163
Gly Thr Arg Val Val Ala Arg Asn Phe Gly Tyr Arg His Ala Ser Arg	
10 15 20	
gaa aac ccc gcg ctc aaa gac atc aac ttc gag atc gca cct ggt gaa	211
Glu Asn Pro Ala Leu Lys Asp Ile Asn Phe Glu Ile Ala Pro Gly Glu	
25 30 35	
cgc atc ctg ctc acc ggc gct tcc ggc gcc gga aaa tcc acg cta ctc	259
Arg Ile Leu Leu Thr Gly Ala Ser Gly Ala Gly Lys Ser Thr Leu Leu	
40 45 50	
gcc gcg ctc gct ggc gtt tta ggc ggt tct gat gag ggc gtt tct acg	307
Ala Ala Leu Ala Gly Val Leu Gly Gly Ser Asp Glu Gly Val Ser Thr	
55 60 65	
ggc gaa ttg ctt gtc gac gcc ccc tcc atc ggt ttg gtt ctc caa gat	355
Gly Glu Leu Leu Val Asp Ala Pro Ser Ile Gly Leu Val Leu Gln Asp	
70 75 80 85	
cca gat tcc caa gtc atc gcc tcc cgc atc ggc gat gat gtg gcg ttt	403
Pro Asp Ser Gln Val Ile Ala Ser Arg Ile Gly Asp Asp Val Ala Phe	
90 95 100	
ggc tgc gaa aac ctc caa att ccg cgc gag gaa atc tgg cca cgg gtg	451
Gly Cys Glu Asn Leu Gln Ile Pro Arg Glu Glu Ile Trp Pro Arg Val	
105 110 115	
gaa cga gca ctt gaa ttg gtg ggc ttg gat cta cca ctg agc cac ccc	499
Glu Arg Ala Leu Glu Leu Val Gly Leu Asp Leu Pro Leu Ser His Pro	
120 125 130	
acg aaa tat ctt tcc ggt ggc caa aaa caa cgc ctc gct ctt gcc ggt	547
Thr Lys Tyr Leu Ser Gly Gln Lys Gln Arg Leu Ala Leu Ala Gly	
135 140 145	
gtg atc gcc atg ggt gct cgt ctg att ctg ctt gat gaa ccc acc gca	595
Val Ile Ala Met Gly Ala Arg Leu Ile Leu Leu Asp Glu Pro Thr Ala	
150 155 160 165	
aac ctt gat cct caa ggc caa aaa aat gtg gtc gca gca gtg gat cgc	643
Asn Leu Asp Pro Gln Gly Gln Lys Asn Val Val Ala Ala Val Asp Arg	
170 175 180	
gtt gtt cag gaa act gga gca aca ctc atc gtg gtg gaa cac cgc cat	691
Val Val Gln Glu Thr Gly Ala Thr Leu Ile Val Val Glu His Arg His	
185 190 195	
gag ctg tgg gtc aac atc att gac cgg atc atc agt att act gac ggc	739
Glu Leu Trp Val Asn Ile Ile Asp Arg Ile Ile Ser Ile Thr Asp Gly	
200 205 210	
gaa gat gtc caa cct gca gag ttg atc aag gtg ggc cag ttg cct ggg	787
Glu Asp Val Gln Pro Ala Glu Leu Ile Lys Val Gly Gln Leu Pro Gly	
215 220 225	
gcg cag ccg tcg aca agc aaa ccg atc ttg tgg gcg aat gat ttg ctg	835
Ala Gln Pro Ser Thr Ser Lys Pro Ile Leu Trp Ala Asn Asp Leu Leu	
230 235 240 245	
tgc acc tgg ggc ggc ctg cgt agt ttt gag gtg ccg gaa ggc gcc tcg	883

Cys Thr Trp Gly Gly Leu Arg Ser Phe Glu Val Pro Glu Gly Ala Ser
 250 255 260
 acg gtg atc acc ggg ccg aat ggc gct gga aaa tcc aca ctt gcg ctg 931
 Thr Val Ile Thr Gly Pro Asn Gly Ala Gly Lys Ser Thr Leu Ala Leu
 265 270 275
 acc atg ggt gga ttg ctt ccg cga aaa gtg ggc agc tgg aac tct ctg 979
 Thr Met Gly Gly Leu Leu Pro Arg Lys Val Gly Ser Trp Asn Ser Leu
 280 285 290
 aca cgg tgc gcg gcg gcc tta aca cgc ccc cgc aca agt ggc gtt cag 1027
 Thr Arg Cys Ala Ala Ala Leu Thr Arg Pro Arg Thr Ser Gly Val Gln
 295 300 305
 ctg atc tagctgcacg tattggcact gtc 1056
 Leu Ile
 310
 <210> 168
 <211> 311
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 168
 Met Thr Thr Ala Leu Gly Thr Arg Val Val Ala Arg Asn Phe Gly Tyr
 1 5 10 15
 Arg His Ala Ser Arg Glu Asn Pro Ala Leu Lys Asp Ile Asn Phe Glu
 20 25 30
 Ile Ala Pro Gly Glu Arg Ile Leu Leu Thr Gly Ala Ser Gly Ala Gly
 35 40 45
 Lys Ser Thr Leu Leu Ala Ala Leu Ala Gly Val Leu Gly Gly Ser Asp
 50 55 60
 Glu Gly Val Ser Thr Gly Glu Leu Leu Val Asp Ala Pro Ser Ile Gly
 65 70 75 80
 Leu Val Leu Gln Asp Pro Asp Ser Gln Val Ile Ala Ser Arg Ile Gly
 85 90 95
 Asp Asp Val Ala Phe Gly Cys Glu Asn Leu Gln Ile Pro Arg Glu Glu
 100 105 110
 Ile Trp Pro Arg Val Glu Arg Ala Leu Glu Leu Val Gly Leu Asp Leu
 115 120 125
 Pro Leu Ser His Pro Thr Lys Tyr Leu Ser Gly Gly Gln Lys Gln Arg
 130 135 140
 Leu Ala Leu Ala Gly Val Ile Ala Met Gly Ala Arg Leu Ile Leu Leu
 145 150 155 160
 Asp Glu Pro Thr Ala Asn Leu Asp Pro Gln Gly Gln Lys Asn Val Val
 165 170 175
 Ala Ala Val Asp Arg Val Val Gln Glu Thr Gly Ala Thr Leu Ile Val
 180 185 190

Val Glu His Arg His Glu Leu Trp Val Asn Ile Ile Asp Arg Ile Ile
 195 200 205

Ser Ile Thr Asp Gly Glu Asp Val Gln Pro Ala Glu Leu Ile Lys Val
 210 215 220

Gly Gln Leu Pro Gly Ala Gln Pro Ser Thr Ser Lys Pro Ile Leu Trp
 225 230 235 240

Ala Asn Asp Leu Leu Cys Thr Trp Gly Gly Leu Arg Ser Phe Glu Val
 245 250 255

Pro Glu Gly Ala Ser Thr Val Ile Thr Gly Pro Asn Gly Ala Gly Lys
 260 265 270

Ser Thr Leu Ala Leu Thr Met Gly Gly Leu Leu Pro Arg Lys Val Gly
 275 280 285

Ser Trp Asn Ser Leu Thr Arg Cys Ala Ala Ala Leu Thr Arg Pro Arg
 290 295 300

Thr Ser Gly Val Gln Leu Ile
 305 310

<210> 169
 <211> 357
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(334)
 <223> RXA01247

<400> 169
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cgcgccctct acaccgtccg cgaccgtctc cgccctggcc gtg gcc gcg gca acc 115
 Val Ala Ala Ala Thr
 1 5

gac gca aca cct gaa ggt ccc acc acc tac cag gtc aca ggc atg acc 163
 Asp Ala Thr Pro Glu Gly Pro Thr Thr Tyr Gln Val Thr Gly Met Thr
 10 15 20

tgc gga cac tgc gcc gac aac gtc acc gag gcg gtg agc gct ctg ccc 211
 Cys Gly His Cys Ala Asp Asn Val Thr Glu Ala Val Ser Ala Leu Pro
 25 30 35

cag gtc gac gac gtc cag gtc gac ctg atc gcc ggt ggg gtc tcc atc 259
 Gln Val Asp Asp Val Gln Val Asp Leu Ile Ala Gly Gly Val Ser Ile
 40 45 50

gtc acg gtc acg ggt tcc gtg ccc ctg gaa acc gtc cac cgg gca att 307
 Val Thr Val Thr Gly Ser Val Pro Leu Glu Thr Val His Arg Ala Ile
 55 60 65

gag gag acc ggc tac acc gtc ttg tcc tgcacgattc acccatcatc 354
 Glu Glu Thr Gly Tyr Thr Val Leu Ser

70 75 357

tcg

<210> 170
 <211> 78
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 170
 Val Ala Ala Ala Thr Asp Ala Thr Pro Glu Gly Pro Thr Thr Tyr Gln
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 Val Thr Gly Met Thr Cys Gly His Cys Ala Asp Asn Val Thr Glu Ala
 20 25 30
 Val Ser Ala Leu Pro Gln Val Asp Asp Val Gln Val Asp Leu Ile Ala
 35 40 45
 Gly Gly Val Ser Ile Val Thr Val Thr Gly Ser Val Pro Leu Glu Thr
 50 55 60
 Val His Arg Ala Ile Glu Glu Thr Gly Tyr Thr Val Leu Ser
 65 70 75

<210> 171
 <211> 1296
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1273)
 <223> RXN00099

<400> 171
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 ccgcgcaa at aggtagtcgc ttgcttatag ggtcaggggc gtg aag aat cct cgc 115
 Val Lys Asn Pro Arg
 1 5
 ctg ata gca ctg gcc gct atc atc ctg acc tcg ttc aat ctg cga aca 163
 Leu Ile Ala Leu Ala Ala Ile Ile Leu Thr Ser Phe Asn Leu Arg Thr
 10 15 20
 gct att act gct tta gct ccg ctg gtt tct gag att cgg gat gat tta 211
 Ala Ile Thr Ala Leu Ala Pro Leu Val Ser Glu Ile Arg Asp Asp Leu
 25 30 35
 ggg gtt agt gct tct ctt att ggt gtg ttg ggc atg atc ccg act gct 259
 Gly Val Ser Ala Ser Leu Ile Gly Val Leu Gly Met Ile Pro Thr Ala
 40 45 50
 atg ttc gcg gat gct gcg ttt gcg ctt ccg tcg ttg aag agg aag ttc 307
 Met Phe Ala Asp Ala Ala Phe Ala Leu Pro Ser Leu Lys Arg Lys Phe
 55 60 65
 act act tcc caa ctg ttg atg ttt gcc atg ctg ttg act gct gcc ggt 355

Thr	Thr	Ser	Gln	Leu	Leu	Met	Phe	Ala	Met	Leu	Leu	Thr	Ala	Ala	Gly	
70					75					80					85	
cag	att	att	cgt	gtc	gct	gga	cct	gct	tcg	ctg	ttg	atg	gtc	ggg	act	403
Gln	Ile	Ile	Arg	Val	Ala	Gly	Pro	Ala	Ser	Leu	Leu	Met	Val	Gly	Thr	
				90					95					100		
gtg	ttc	gcg	atg	ttt	gcg	atc	gga	gtt	acc	aat	gtg	ttg	ctt	ccg	att	451
Val	Phe	Ala	Met	Phe	Ala	Ile	Gly	Val	Thr	Asn	Val	Leu	Leu	Pro	Ile	
			105					110					115			
gct	gtt	agg	gag	tat	ttt	ccg	cgt	cac	gtc	ggg	gga	atg	tcg	aca	act	499
Ala	Val	Arg	Glu	Tyr	Phe	Pro	Arg	His	Val	Gly	Gly	Met	Ser	Thr	Thr	
		120					125					130				
tat	ctg	gtg	tcg	ttc	cag	att	gtt	cag	gca	ctt	gct	ccg	acg	ctt	gcc	547
Tyr	Leu	Val	Ser	Phe	Gln	Ile	Val	Gln	Ala	Leu	Ala	Pro	Thr	Leu	Ala	
	135					140					145					
gtg	ccg	att	tct	cag	tgg	gct	aca	cat	gtg	ggg	ttg	acc	ggg	tgg	agg	595
Val	Pro	Ile	Ser	Gln	Trp	Ala	Thr	His	Val	Gly	Leu	Thr	Gly	Trp	Arg	
150					155					160					165	
gtg	tcg	ctc	ggg	tcg	tgg	gcg	ctg	ctg	ggg	ttg	gtt	gcg	gcg	att	tcg	643
Val	Ser	Leu	Gly	Ser	Trp	Ala	Leu	Leu	Gly	Leu	Val	Ala	Ala	Ile	Ser	
				170					175					180		
tgg	att	ccg	ctg	ttg	agt	ttg	cag	ggg	gcc	agg	gtt	gtt	gcg	gcg	ccg	691
Trp	Ile	Pro	Leu	Leu	Ser	Leu	Gln	Gly	Ala	Arg	Val	Val	Ala	Ala	Pro	
			185					190					195			
tcg	aag	gtt	tct	ctt	cct	gtg	tgg	aag	tct	tcg	gtt	ggg	gtg	ggg	ctc	739
Ser	Lys	Val	Ser	Leu	Pro	Val	Trp	Lys	Ser	Ser	Val	Gly	Val	Gly	Leu	
	200						205					210				
ggg	ttg	atg	ttt	ggg	ttt	act	tcg	ttt	gcg	acg	tat	atc	ctc	atg	ggg	787
Gly	Leu	Met	Phe	Gly	Phe	Thr	Ser	Phe	Ala	Thr	Tyr	Ile	Leu	Met	Gly	
	215					220					225					
ttt	atg	ccg	cag	atg	gta	ggg	gat	cct	cag	ctc	ggg	gcg	gtg	ttg	tta	835
Phe	Met	Pro	Gln	Met	Val	Gly	Asp	Pro	Gln	Leu	Gly	Ala	Val	Leu	Leu	
230					235					240					245	
ggc	tgg	tgg	tca	att	ttg	gga	ttg	ccg	ctg	aac	att	ctg	gga	ccg	tgg	883
Gly	Trp	Trp	Ser	Ile	Leu	Gly	Leu	Pro	Leu	Asn	Ile	Leu	Gly	Pro	Trp	
			250					255						260		
ttg	gtg	acg	cgt	ttc	act	aac	tgc	ttc	ccg	atg	gtt	gtt	atc	gcc	agt	931
Leu	Val	Thr	Arg	Phe	Thr	Asn	Cys	Phe	Pro	Met	Val	Val	Ile	Ala	Ser	
			265					270					275			
gtc	atg	ttt	ctc	atc	ggg	aat	ggg	ggg	ttt	tgt	ttg	gct	ccg	gat	gtt	979
Val	Met	Phe	Leu	Ile	Gly	Asn	Gly	Gly	Phe	Cys	Leu	Ala	Pro	Asp	Val	
		280					285					290				
gcg	ccg	tgg	ttg	tgg	gcg	acg	ttg	tct	ggg	ctt	ggg	ccc	ctt	gcg	ttc	1027
Ala	Pro	Trp	Leu	Trp	Ala	Thr	Leu	Ser	Gly	Leu	Gly	Pro	Leu	Ala	Phe	
	295						300				305					
ccg	atg	gcg	ttg	acg	ctc	att	aat	att	cgt	gct	gaa	act	agt	gct	ggg	1075
Pro	Met	Ala	Leu	Thr	Leu	Ile	Asn	Ile	Arg	Ala	Glu	Thr	Ser	Ala	Gly	

310	315	320	325	
gct tct gcg ttg agt tcc ttc ggg cag ggt ttg ggt tat acg att gcg				1123
Ala Ser Ala Leu Ser Ser Phe Gly Gln Gly Leu Gly Tyr Thr Ile Ala	330	335	340	
tgt ttc ggt ccc ttg ttg act ggt ttc att gtc gat gcg aca ggc agc				1171
Cys Phe Gly Pro Leu Leu Thr Gly Phe Ile Val Asp Ala Thr Gly Ser	345	350	355	
ttc cga aca atc ttt gtg ctt ttt gcg gtt gca aca ctc ttc gtt att				1219
Phe Arg Thr Ile Phe Val Leu Phe Ala Val Ala Thr Leu Phe Val Ile	360	365	370	
aga ggc ggt tac ttt gcg aca agg cag gtt tac gtc gaa aag ctt tta				1267
Arg Gly Gly Tyr Phe Ala Thr Arg Gln Val Tyr Val Glu Lys Leu Leu	375	380	385	
aat cgc taggatggcg ctatgccgca aag				1296
Asn Arg				
390				

<210> 172

<211> 391

<212> PRT

<213> Corynebacterium glutamicum

<400> 172

Val Lys Asn Pro Arg Leu Ile Ala Leu Ala Ala Ile Ile Leu Thr Ser	1	5	10	15
Phe Asn Leu Arg Thr Ala Ile Thr Ala Leu Ala Pro Leu Val Ser Glu	20	25	30	
Ile Arg Asp Asp Leu Gly Val Ser Ala Ser Leu Ile Gly Val Leu Gly	35	40	45	
Met Ile Pro Thr Ala Met Phe Ala Asp Ala Ala Phe Ala Leu Pro Ser	50	55	60	
Leu Lys Arg Lys Phe Thr Thr Ser Gln Leu Leu Met Phe Ala Met Leu	65	70	75	80
Leu Thr Ala Ala Gly Gln Ile Ile Arg Val Ala Gly Pro Ala Ser Leu	85	90	95	
Leu Met Val Gly Thr Val Phe Ala Met Phe Ala Ile Gly Val Thr Asn	100	105	110	
Val Leu Leu Pro Ile Ala Val Arg Glu Tyr Phe Pro Arg His Val Gly	115	120	125	
Gly Met Ser Thr Thr Tyr Leu Val Ser Phe Gln Ile Val Gln Ala Leu	130	135	140	
Ala Pro Thr Leu Ala Val Pro Ile Ser Gln Trp Ala Thr His Val Gly	145	150	155	160
Leu Thr Gly Trp Arg Val Ser Leu Gly Ser Trp Ala Leu Leu Gly Leu	165	170	175	

Val Ala Ala Ile Ser Trp Ile Pro Leu Leu Ser Leu Gln Gly Ala Arg
 180 185 190
 Val Val Ala Ala Pro Ser Lys Val Ser Leu Pro Val Trp Lys Ser Ser
 195 200 205
 Val Gly Val Gly Leu Gly Leu Met Phe Gly Phe Thr Ser Phe Ala Thr
 210 215 220
 Tyr Ile Leu Met Gly Phe Met Pro Gln Met Val Gly Asp Pro Gln Leu
 225 230 235 240
 Gly Ala Val Leu Leu Gly Trp Trp Ser Ile Leu Gly Leu Pro Leu Asn
 245 250 255
 Ile Leu Gly Pro Trp Leu Val Thr Arg Phe Thr Asn Cys Phe Pro Met
 260 265 270
 Val Val Ile Ala Ser Val Met Phe Leu Ile Gly Asn Gly Gly Phe Cys
 275 280 285
 Leu Ala Pro Asp Val Ala Pro Trp Leu Trp Ala Thr Leu Ser Gly Leu
 290 295 300
 Gly Pro Leu Ala Phe Pro Met Ala Leu Thr Leu Ile Asn Ile Arg Ala
 305 310 315 320
 Glu Thr Ser Ala Gly Ala Ser Ala Leu Ser Ser Phe Gly Gln Gly Leu
 325 330 335
 Gly Tyr Thr Ile Ala Cys Phe Gly Pro Leu Leu Thr Gly Phe Ile Val
 340 345 350
 Asp Ala Thr Gly Ser Phe Arg Thr Ile Phe Val Leu Phe Ala Val Ala
 355 360 365
 Thr Leu Phe Val Ile Arg Gly Gly Tyr Phe Ala Thr Arg Gln Val Tyr
 370 375 380
 Val Glu Lys Leu Leu Asn Arg
 385 390

<210> 173
 <211> 1296
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1273)
 <223> FRXA00099

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ccgcgcaa at aggtagtcgc ttgcttatag ggtcaggggc gtg aag aat cct cgc 115
 Val Lys Asn Pro Arg
 1 5

ctc	ata	gca	ctg	gcc	gct	atc	atc	ctg	acc	tgc	ttc	aat	ctg	cga	aca	163
Leu	Ile	Ala	Leu	Ala	Ala	Ile	Ile	Leu	Thr	Ser	Phe	Asn	Leu	Arg	Thr	
			10						15					20		
gct	att	act	gct	tta	gct	ccg	ctg	gtt	tct	gag	att	cgg	gat	gat	tta	211
Ala	Ile	Thr	Ala	Leu	Ala	Pro	Leu	Val	Ser	Glu	Ile	Arg	Asp	Asp	Leu	
		25						30					35			
ggg	gtt	agt	gct	tct	ctt	att	ggg	gtg	ttg	ggc	atg	atc	ccg	act	gct	259
Gly	Val	Ser	Ala	Ser	Leu	Ile	Gly	Val	Leu	Gly	Met	Ile	Pro	Thr	Ala	
		40					45					50				
atg	ttc	gcg	gat	gct	gcg	ttt	gcg	ctt	ccg	tgc	ttg	aag	agg	aag	ttc	307
Met	Phe	Ala	Asp	Ala	Ala	Phe	Ala	Leu	Pro	Ser	Leu	Lys	Arg	Lys	Phe	
	55					60					65					
act	act	tcc	caa	ctg	ttg	atg	ttt	gcc	atg	ctg	ttg	act	gct	gcc	ggg	355
Thr	Thr	Ser	Gln	Leu	Leu	Met	Phe	Ala	Met	Leu	Leu	Thr	Ala	Ala	Gly	
	70				75					80					85	
cag	att	att	cgt	gtc	gct	gga	cct	gct	tgc	ctg	ttg	atg	gtc	ggg	act	403
Gln	Ile	Ile	Arg	Val	Ala	Gly	Pro	Ala	Ser	Leu	Leu	Met	Val	Gly	Thr	
			90					95						100		
gtg	ttc	gcg	atg	ttt	gcg	atc	gga	gtt	acc	aat	gtg	ttg	ctt	ccg	att	451
Val	Phe	Ala	Met	Phe	Ala	Ile	Gly	Val	Thr	Asn	Val	Leu	Leu	Pro	Ile	
		105					110						115			
gct	gtt	agg	gag	tat	ttt	ccg	cgt	cac	gtc	ggg	gga	atg	tgc	aca	act	499
Ala	Val	Arg	Glu	Tyr	Phe	Pro	Arg	His	Val	Gly	Gly	Met	Ser	Thr	Thr	
		120					125					130				
tat	ctg	gtg	tgc	ttc	cag	att	gtt	cag	gca	ctt	gct	ccg	acg	ctt	gcc	547
Tyr	Leu	Val	Ser	Phe	Gln	Ile	Val	Gln	Ala	Leu	Ala	Pro	Thr	Leu	Ala	
	135					140					145					
gtg	ccg	att	tct	cag	tgg	gct	aca	cat	gtg	ggg	ttg	acc	ggg	tgg	agg	595
Val	Pro	Ile	Ser	Gln	Trp	Ala	Thr	His	Val	Gly	Leu	Thr	Gly	Trp	Arg	
	150				155					160					165	
gtg	tgc	ctc	ggg	tgc	tgg	gcg	ctg	ctg	ggg	ttg	gtt	gcg	gcg	att	tgc	643
Val	Ser	Leu	Gly	Ser	Trp	Ala	Leu	Leu	Gly	Leu	Val	Ala	Ala	Ile	Ser	
			170					175						180		
tgg	att	ccg	ctg	ttg	agt	ttg	cag	ggg	gcc	agg	gtt	gtt	gcg	gcg	ccg	691
Trp	Ile	Pro	Leu	Leu	Ser	Leu	Gln	Gly	Ala	Arg	Val	Val	Ala	Ala	Pro	
			185					190					195			
tgc	aag	gtt	tct	ctt	cct	gtg	tgg	aag	tct	tgc	gtt	ggg	gtg	ggg	ctc	739
Ser	Lys	Val	Ser	Leu	Pro	Val	Trp	Lys	Ser	Ser	Val	Gly	Val	Gly	Leu	
		200					205					210				
ggg	ttg	atg	ttt	ggg	ttt	act	tgc	ttt	gcg	acg	tat	atc	ctc	atg	ggg	787
Gly	Leu	Met	Phe	Gly	Phe	Thr	Ser	Phe	Ala	Thr	Tyr	Ile	Leu	Met	Gly	
	215					220					225					
ttt	atg	ccg	cag	atg	gta	ggg	gat	cct	cag	ctc	ggg	gcg	gtg	ttg	tta	835
Phe	Met	Pro	Gln	Met	Val	Gly	Asp	Pro	Gln	Leu	Gly	Ala	Val	Leu	Leu	
	230				235					240					245	
ggc	tgg	tgg	tca	att	ttg	gga	ttg	ccg	ctg	aac	att	ctg	gga	ccg	tgg	883

Gly Trp Trp Ser Ile Leu Gly Leu Pro Leu Asn Ile Leu Gly Pro Trp
 250 255 260
 ttg gtg acg cgt ttc act aac tgc ttc ccg atg gtt gtt atc gcc agt 931
 Leu Val Thr Arg Phe Thr Asn Cys Phe Pro Met Val Val Ile Ala Ser
 265 270 275
 gtc atg ttt ctc atc ggt aat ggt ggg ttt tgt ttg gct ccg gat gtt 979
 Val Met Phe Leu Ile Gly Asn Gly Gly Phe Cys Leu Ala Pro Asp Val
 280 285 290
 gcg ccg tgg ttg tgg gcg acg ttg tct ggt ctt ggt ccc ctt gcg ttc 1027
 Ala Pro Trp Leu Trp Ala Thr Leu Ser Gly Leu Gly Pro Leu Ala Phe
 295 300 305
 ccg atg gcg ttg acg ctc att aat att cgt gct gaa act agt gct ggt 1075
 Pro Met Ala Leu Thr Leu Ile Asn Ile Arg Ala Glu Thr Ser Ala Gly
 310 315 320 325
 gct tct gcg ttg agt tcc ttc ggg cag ggt ttg ggt tat acg att gcg 1123
 Ala Ser Ala Leu Ser Ser Phe Gly Gln Gly Leu Gly Tyr Thr Ile Ala
 330 335 340
 tgt ttc ggt ccc ttg ttg act ggt ttc att gtc gat gca aca ggc agc 1171
 Cys Phe Gly Pro Leu Leu Thr Gly Phe Ile Val Asp Ala Thr Gly Ser
 345 350 355
 ttc cga aca atc ttt ttg ctt ttt gcg ggt gca aca ctc ttc gtt att 1219
 Phe Arg Thr Ile Phe Leu Leu Phe Ala Gly Ala Thr Leu Phe Val Ile
 360 365 370
 aga ggc ggt tac ttt gcg aca agg cag gtt tac gtc gaa aag ctt tta 1267
 Arg Gly Tyr Phe Ala Thr Arg Gln Val Tyr Val Glu Lys Leu Leu
 375 380 385
 aat cgc taggatggcg ctatgccgca aag 1296
 Asn Arg
 390

<210> 174

<211> 391

<212> PRT

<213> Corynebacterium glutamicum

<400> 174

Val Lys Asn Pro Arg Leu Ile Ala Leu Ala Ala Ile Ile Leu Thr Ser
 1 5 10 15
 Phe Asn Leu Arg Thr Ala Ile Thr Ala Leu Ala Pro Leu Val Ser Glu
 20 25 30
 Ile Arg Asp Asp Leu Gly Val Ser Ala Ser Leu Ile Gly Val Leu Gly
 35 40 45
 Met Ile Pro Thr Ala Met Phe Ala Asp Ala Ala Phe Ala Leu Pro Ser
 50 55 60
 Leu Lys Arg Lys Phe Thr Thr Ser Gln Leu Leu Met Phe Ala Met Leu
 65 70 75 80

Leu Thr Ala Ala Gly Gln Ile Ile Arg Val Ala Gly Pro Ala Ser Leu
 85 90 95

Leu Met Val Gly Thr Val Phe Ala Met Phe Ala Ile Gly Val Thr Asn
 100 105 110

Val Leu Leu Pro Ile Ala Val Arg Glu Tyr Phe Pro Arg His Val Gly
 115 120 125

Gly Met Ser Thr Thr Tyr Leu Val Ser Phe Gln Ile Val Gln Ala Leu
 130 135 140

Ala Pro Thr Leu Ala Val Pro Ile Ser Gln Trp Ala Thr His Val Gly
 145 150 155 160

Leu Thr Gly Trp Arg Val Ser Leu Gly Ser Trp Ala Leu Leu Gly Leu
 165 170 175

Val Ala Ala Ile Ser Trp Ile Pro Leu Leu Ser Leu Gln Gly Ala Arg
 180 185 190

Val Val Ala Ala Pro Ser Lys Val Ser Leu Pro Val Trp Lys Ser Ser
 195 200 205

Val Gly Val Gly Leu Gly Leu Met Phe Gly Phe Thr Ser Phe Ala Thr
 210 215 220

Tyr Ile Leu Met Gly Phe Met Pro Gln Met Val Gly Asp Pro Gln Leu
 225 230 235 240

Gly Ala Val Leu Leu Gly Trp Trp Ser Ile Leu Gly Leu Pro Leu Asn
 245 250 255

Ile Leu Gly Pro Trp Leu Val Thr Arg Phe Thr Asn Cys Phe Pro Met
 260 265 270

Val Val Ile Ala Ser Val Met Phe Leu Ile Gly Asn Gly Gly Phe Cys
 275 280 285

Leu Ala Pro Asp Val Ala Pro Trp Leu Trp Ala Thr Leu Ser Gly Leu
 290 295 300

Gly Pro Leu Ala Phe Pro Met Ala Leu Thr Leu Ile Asn Ile Arg Ala
 305 310 315 320

Glu Thr Ser Ala Gly Ala Ser Ala Leu Ser Ser Phe Gly Gln Gly Leu
 325 330 335

Gly Tyr Thr Ile Ala Cys Phe Gly Pro Leu Leu Thr Gly Phe Ile Val
 340 345 350

Asp Ala Thr Gly Ser Phe Arg Thr Ile Phe Leu Leu Phe Ala Gly Ala
 355 360 365

Thr Leu Phe Val Ile Arg Gly Gly Tyr Phe Ala Thr Arg Gln Val Tyr
 370 375 380

Val Glu Lys Leu Leu Asn Arg
 385 390

<210> 175
 <211> 1506
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1483)
 <223> RXA00634

<400> 175
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ggttagggttc aaaagcgcaa cctcaataat cagtattgaa atg tgg gag cga ttc 115
 Met Trp Glu Arg Phe
 1 5

agc ttc tac ggc atg caa gca ctc ttg gtg tac tac ctg tat ttt gat 163
 Ser Phe Tyr Gly Met Gln Ala Leu Leu Val Tyr Tyr Leu Tyr Phe Asp
 10 15 20

gtt gca gcc ggt gga tta ggc ctt gat caa acc caa gca aca gga ctg 211
 Val Ala Ala Gly Gly Leu Gly Leu Asp Gln Thr Gln Ala Thr Gly Leu
 25 30 35

gtc ggc gtt tat ggc gca ctg ctc tac ctc tgc tgt tgg gca ggc ggt 259
 Val Gly Val Tyr Gly Ala Leu Leu Tyr Leu Cys Cys Trp Ala Gly Gly
 40 45 50

tgg gtc agt gac aga gtc ctg ggc gca gaa aaa acc ctg ctg ggc ggt 307
 Trp Val Ser Asp Arg Val Leu Gly Ala Glu Lys Thr Leu Leu Gly Gly
 55 60 65

gcg atc tca gta acc atc gga cac ctt gtg ctt gct ggc ctc ggc ggg 355
 Ala Ile Ser Val Thr Ile Gly His Leu Val Leu Ala Gly Leu Gly Gly
 70 75 80 85

aaa att ggt cta gcc att ggc ctt gga tgc atc gcg atc ggt tca gga 403
 Lys Ile Gly Leu Ala Ile Gly Leu Gly Cys Ile Ala Ile Gly Ser Gly
 90 95 100

ttt gtg aaa aca gca gcc atc acc gtg ctg gga tcc agg cat ggt gaa 451
 Phe Val Lys Thr Ala Ala Ile Thr Val Leu Gly Ser Arg His Gly Glu
 105 110 115

caa gaa gga gac gca aag gca gat ccc gca ttc caa ctc ttc tac cta 499
 Gln Glu Gly Asp Ala Lys Ala Asp Pro Ala Phe Gln Leu Phe Tyr Leu
 120 125 130

ggc atc aac gtt ggt gca ctg ctc gga cca ctc ctg acc ggt tgg ctc 547
 Gly Ile Asn Val Gly Ala Leu Leu Gly Pro Leu Leu Thr Gly Trp Leu
 135 140 145

tcc agc agg tat tcc ttt gaa atg gga ttc ggc gca gcc gca gtc ctt 595
 Ser Ser Arg Tyr Ser Phe Glu Met Gly Phe Gly Ala Ala Ala Val Leu
 150 155 160 165

atg atc ggc gga ttg gga atc tac gca gcg ttg cgg aaa cca atg ctg 643
 Met Ile Gly Gly Leu Gly Ile Tyr Ala Ala Leu Arg Lys Pro Met Leu
 170 175 180

caa tgc ttc ccg ctc gag gtg aag aaa gcg ctg ctc cgc gcc caa aac	691
Gln Ser Phe Pro Leu Glu Val Lys Lys Ala Leu Leu Arg Ala Gln Asn	
185 190 195	
cct gca gaa aaa cat gtg att agc acg gca ttt gct gca gtg gct gtg	739
Pro Ala Glu Lys His Val Ile Ser Thr Ala Phe Ala Val Ala Val	
200 205 210	
ctt tgc gga gtg ctg ctt tat ctt ctc ctt aca gaa aca gtc agc gca	787
Leu Cys Gly Val Leu Leu Tyr Leu Leu Leu Thr Glu Thr Val Ser Ala	
215 220 225	
gac caa cta gct gga gct ctg ctt tta gta aca atc ggt gca gca cta	835
Asp Gln Leu Ala Gly Ala Leu Leu Leu Val Thr Ile Gly Ala Ala Leu	
230 235 240 245	
tgg ctc att atc cag ccc tta cga cac cca caa gtc agc tcc gaa gag	883
Trp Leu Ile Ile Gln Pro Leu Arg His Pro Gln Val Ser Ser Glu Glu	
250 255 260	
aaa cga aaa gtg ctg gca ttc atc ccg atc ttc gtc tgc tca acc gca	931
Lys Arg Lys Val Leu Ala Phe Ile Pro Ile Phe Val Cys Ser Thr Ala	
265 270 275	
ttc tgg gca gtg caa gca caa acc tac ggc gta cta gct gtg tac tcc	979
Phe Trp Ala Val Gln Ala Gln Thr Tyr Gly Val Leu Ala Val Tyr Ser	
280 285 290	
caa gaa cgt gtt gac cgc atg gtt ggc gat ttt gag atc cca gca gcc	1027
Gln Glu Arg Val Asp Arg Met Val Gly Asp Phe Glu Ile Pro Ala Ala	
295 300 305	
tgg tca caa tca ctc aat cct ttt ttc atc ctg gcg ctg tcc atc ccg	1075
Trp Ser Gln Ser Leu Asn Pro Phe Phe Ile Leu Ala Leu Ser Ile Pro	
310 315 320 325	
att tcc ctg tgg ttt atg cgc gga tca cgc gcc cca aga gtg aaa att	1123
Ile Ser Leu Trp Phe Met Arg Gly Ser Arg Ala Pro Arg Val Lys Ile	
330 335 340	
gga atc agc att gga gtg atc att gcg gga agt ggg ctt cta gtt ctt	1171
Gly Ile Ser Ile Gly Val Ile Ile Ala Gly Ser Gly Leu Leu Val Leu	
345 350 355	
att cca ttt gtt gga atg ccg ctc gcg cca gtg tgg gtg ctg cct tta	1219
Ile Pro Phe Val Gly Met Pro Leu Ala Pro Val Trp Val Leu Pro Leu	
360 365 370	
agt gtt ttc ctc atc tca ctg gga gaa ctt ttc atc gga ccc gga gga	1267
Ser Val Phe Leu Ile Ser Leu Gly Glu Leu Phe Ile Gly Pro Gly Gly	
375 380 385	
atg gct gcg act gcg cac cac gca cca cga ata ttt gcc aca cga ttc	1315
Met Ala Ala Thr Ala His His Ala Pro Arg Ile Phe Ala Thr Arg Phe	
390 395 400 405	
tcc gcc ctg tat ttc ctc aca ctc gcc atc ggc atg tct att gca ggt	1363
Ser Ala Leu Tyr Phe Leu Thr Leu Ala Ile Gly Met Ser Ile Ala Gly	
410 415 420	
aat gtg tcc aaa ttt tac gac ccc acc aac cac acc tcc gag ctc cga	1411

Asn Val Ser Lys Phe Tyr Asp Pro Thr Asn His Thr Ser Glu Leu Arg
 425 430 435

tac ttc gcg gta ttt ggc att tcg atc atc gtc atc ggt gtc ggt tca 1459
 Tyr Phe Ala Val Phe Gly Ile Ser Ile Ile Val Ile Gly Val Gly Ser
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 Leu Met Val Ala Lys Lys Val Gly
 455 460

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<211> 461

<212> PRT

<213> Corynebacterium glutamicum

<400> 176

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Tyr Leu Tyr Phe Asp Val Ala Ala Gly Gly Leu Gly Leu Asp Gln Thr
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Gln Ala Thr Gly Leu Val Gly Val Tyr Gly Ala Leu Leu Tyr Leu Cys
 35 40 45

Cys Trp Ala Gly Gly Trp Val Ser Asp Arg Val Leu Gly Ala Glu Lys
 50 55 60

Thr Leu Leu Gly Gly Ala Ile Ser Val Thr Ile Gly His Leu Val Leu
 65 70 75 80

Ala Gly Leu Gly Gly Lys Ile Gly Leu Ala Ile Gly Leu Gly Cys Ile
 85 90 95

Ala Ile Gly Ser Gly Phe Val Lys Thr Ala Ala Ile Thr Val Leu Gly
 100 105 110

Ser Arg His Gly Glu Gln Glu Gly Asp Ala Lys Ala Asp Pro Ala Phe
 115 120 125

Gln Leu Phe Tyr Leu Gly Ile Asn Val Gly Ala Leu Leu Gly Pro Leu
 130 135 140

Leu Thr Gly Trp Leu Ser Ser Arg Tyr Ser Phe Glu Met Gly Phe Gly
 145 150 155 160

Ala Ala Ala Val Leu Met Ile Gly Gly Leu Gly Ile Tyr Ala Ala Leu
 165 170 175

Arg Lys Pro Met Leu Gln Ser Phe Pro Leu Glu Val Lys Lys Ala Leu
 180 185 190

Leu Arg Ala Gln Asn Pro Ala Glu Lys His Val Ile Ser Thr Ala Phe
 195 200 205

Ala Ala Val Ala Val Leu Cys Gly Val Leu Leu Tyr Leu Leu Leu Thr
 210 215 220

Glu Thr Val Ser Ala Asp Gln Leu Ala Gly Ala Leu Leu Leu Val Thr

225		230		235		240
Ile Gly Ala Ala	Leu Trp Leu Ile Ile	Gln Pro Leu Arg His	Pro Gln			
	245	250	255			
Val Ser Ser Glu Glu Lys Arg Lys	Val Leu Ala Phe Ile	Pro Ile Phe				
	260	265	270			
Val Cys Ser Thr Ala Phe Trp Ala Val	Gln Ala Gln Thr Tyr Gly Val					
	275	280	285			
Leu Ala Val Tyr Ser Gln Glu Arg Val Asp Arg	Met Val Gly Asp Phe					
	290	295	300			
Glu Ile Pro Ala Ala Trp Ser Gln Ser Leu Asn Pro	Phe Phe Ile Leu					
	305	310	315			320
Ala Leu Ser Ile Pro Ile Ser Leu Trp Phe Met Arg Gly Ser Arg Ala						
	325	330	335			
Pro Arg Val Lys Ile Gly Ile Ser Ile Gly Val Ile Ile Ala Gly Ser						
	340	345	350			
Gly Leu Leu Val Leu Ile Pro Phe Val Gly Met Pro Leu Ala Pro Val						
	355	360	365			
Trp Val Leu Pro Leu Ser Val Phe Leu Ile Ser Leu Gly Glu Leu Phe						
	370	375	380			
Ile Gly Pro Gly Gly Met Ala Ala Thr Ala His His Ala Pro Arg Ile						
	385	390	395			400
Phe Ala Thr Arg Phe Ser Ala Leu Tyr Phe Leu Thr Leu Ala Ile Gly						
	405	410	415			
Met Ser Ile Ala Gly Asn Val Ser Lys Phe Tyr Asp Pro Thr Asn His						
	420	425	430			
Thr Ser Glu Leu Arg Tyr Phe Ala Val Phe Gly Ile Ser Ile Ile Val						
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<211> 1647

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1624)

<223> RXA02451

<400> 177

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Met Asn Thr Asp Thr

1

5

act	caa	gac	ggt	gtg	agt	cct	gaa	cct	tcc	gac	ccc	cac	cta	ggg	tct	163
Thr	Gln	Asp	Gly	Val	Ser	Pro	Glu	Pro	Ser	Asp	Pro	His	Leu	Gly	Ser	
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gaa	gtg	gcg	gaa	act	cac	cgc	gaa	aag	aaa	ttc	ttc	ggc	cag	cct	tgg	211
Glu	Val	Ala	Glu	Thr	His	Arg	Glu	Lys	Lys	Phe	Phe	Gly	Gln	Pro	Trp	
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Gly	Leu	Ala	Asn	Leu	Phe	Gly	Val	Glu	Met	Trp	Glu	Arg	Phe	Ser	Phe	
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Tyr	Gly	Met	Gln	Ser	Ile	Leu	Ala	Phe	Tyr	Leu	Tyr	Tyr	Ser	Val	Thr	
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Asp	Gly	Gly	Leu	Gly	Met	Asn	Gln	Thr	Ala	Ala	Leu	Ser	Ile	Val	Gly	
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gcc	tac	ggc	ggc	ttc	gtc	tac	atg	acc	tcc	ctc	gtg	gct	tgc	ttc	att	403
Ala	Tyr	Gly	Gly	Phe	Val	Tyr	Met	Thr	Ser	Leu	Val	Ala	Ser	Phe	Ile	
				90					95					100		
gca	gac	cga	gta	ttg	ggc	tct	gaa	cgt	aca	ctc	ttc	tac	tcc	gcg	atc	451
Ala	Asp	Arg	Val	Leu	Gly	Ser	Glu	Arg	Thr	Leu	Phe	Tyr	Ser	Ala	Ile	
			105					110					115			
atc	gtc	atg	ctg	ggc	cac	att	gcc	ctg	gcc	ttg	att	ccg	gga	tat	acg	499
Ile	Val	Met	Leu	Gly	His	Ile	Ala	Leu	Ala	Leu	Ile	Pro	Gly	Tyr	Thr	
		120					125					130				
gga	ctg	tcc	atc	ggc	ttg	gtc	ctc	atc	ggc	ctt	ggc	tca	ggt	ggc	gtg	547
Gly	Leu	Ser	Ile	Gly	Leu	Val	Leu	Ile	Gly	Leu	Gly	Ser	Gly	Gly	Val	
	135					140					145					
aag	acg	gca	gcg	cag	gtt	gtg	ctg	ggc	cag	ctg	tac	tca	cgc	acg	gac	595
Lys	Thr	Ala	Ala	Gln	Val	Val	Leu	Gly	Gln	Leu	Tyr	Ser	Arg	Thr	Asp	
	150				155				160						165	
acg	cgt	cga	gac	gca	ggc	ttc	tcc	atc	ttc	tac	atg	ggc	gtc	aac	ctc	643
Thr	Arg	Arg	Asp	Ala	Gly	Phe	Ser	Ile	Phe	Tyr	Met	Gly	Val	Asn	Leu	
			170					175						180		
ggt	ggc	ctc	ttt	ggc	ccg	ctg	atc	acc	aac	gct	ctg	tgg	gga	tgg	gga	691
Gly	Gly	Leu	Phe	Gly	Pro	Leu	Ile	Thr	Asn	Ala	Leu	Trp	Gly	Trp	Gly	
		185						190					195			
gga	ttc	cac	tgg	ggc	ttc	ggt	atc	gcc	gca	gtc	ggc	atg	gct	ttg	ggt	739
Gly	Phe	His	Trp	Gly	Phe	Gly	Ile	Ala	Ala	Val	Gly	Met	Ala	Leu	Gly	
		200					205					210				
ctc	atc	caa	tac	gtg	gcg	atg	cgt	aaa	acc	acc	atc	ggt	gcg	gca	ggc	787
Leu	Ile	Gln	Tyr	Val	Ala	Met	Arg	Lys	Thr	Thr	Ile	Gly	Ala	Ala	Gly	
	215					220					225					
cat	act	gtt	cct	aac	cca	ctg	cct	aag	aat	gaa	tat	gcg	cgc	tgg	att	835
His	Thr	Val	Pro	Asn	Pro	Leu	Pro	Lys	Asn	Glu	Tyr	Ala	Arg	Trp	Ile	
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Ile Gly Ala Val Val Val Val Ala Ala Val Val Ala Leu Ile Ala Thr	
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ggc atc atc aag ctg gaa tgg ctg tcc aac atc acc gca gcg atc gca	931
Gly Ile Ile Lys Leu Glu Trp Leu Ser Asn Ile Thr Ala Ala Ile Ala	
265 270 275	
ctg att gcg gct att gct ctg ctt gct cag atg tac gtt tcc cca ctg	979
Leu Ile Ala Ala Ile Ala Leu Leu Ala Gln Met Tyr Val Ser Pro Leu	
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Thr Thr Ala Ala Glu Lys Ser Arg Leu Leu Gly Phe Ile Pro Met Phe	
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Ile Gly Gly Val Leu Phe Phe Ala Ile Phe Gln Thr Gln Phe Thr Val	
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Leu Ala Val Tyr Ser Asp Thr Arg Leu Asp Arg Asn Phe Phe Gly Ile	
330 335 340	
gai ctt cct cca gga ttg atc aac tcc ttc aac cca atc ttc atc atc	1171
Asp Leu Pro Pro Gly Leu Ile Asn Ser Phe Asn Pro Ile Phe Ile Ile	
345 350 355	
atc ttc tcc gga atc ttt gcc acc ttg tgg aca aaa ctc gga gca aag	1219
Ile Phe Ser Gly Ile Phe Ala Thr Leu Trp Thr Lys Leu Gly Ala Lys	
360 365 370	
cag tgg tct act gca gtg aag ttc ggt gtc gcc aac att gtc att ggt	1267
Gln Trp Ser Thr Ala Val Lys Phe Gly Val Ala Asn Ile Val Ile Gly	
375 380 385	
tgc gcg ctg ttc ttc ttc ctg ccg ttc gcc ggc ggt gca gag aac tct	1315
Cys Ala Leu Phe Phe Phe Leu Pro Phe Ala Gly Gly Ala Glu Asn Ser	
390 395 400 405	
acc cca atg gca ctg atc att tgg gtc tac ttc ctc ttc acc atc gct	1363
Thr Pro Met Ala Leu Ile Ile Trp Val Tyr Phe Leu Phe Thr Ile Ala	
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Glu Leu Leu Leu Ser Pro Val Gly Asn Ser Leu Ala Thr Lys Val Ala	
425 430 435	
ccc gag gca ttc cag tcc cgc atg ttc gcc gtg tgg ctg atg gct gtc	1459
Pro Glu Ala Phe Gln Ser Arg Met Phe Ala Val Trp Leu Met Ala Val	
440 445 450	
tcc atg ggt acg tcc ctg tcc ggc acc ctg ggt ggt tac tac gat cca	1507
Ser Met Gly Thr Ser Leu Ser Gly Thr Leu Gly Gly Tyr Tyr Asp Pro	
455 460 465	
acc gat gca gga tct gaa aag gtc ttc ttc att acc gtt ggc gtt gca	1555
Thr Asp Ala Gly Ser Glu Lys Val Phe Phe Ile Thr Val Gly Val Ala	
470 475 480 485	
gcc atc gtt ctt ggt gca atc gtc ata gca gcc aag ggc tgg gtg ctg	1603

Ala Ile Val Leu Gly Ala Ile Val Ile Ala Ala Lys Gly Trp Val Leu
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 Lys Lys Phe Ile Asp Val Arg
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<210> 178
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 178
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 Phe Gly Gln Pro Trp Gly Leu Ala Asn Leu Phe Gly Val Glu Met Trp
 35 40 45
 Glu Arg Phe Ser Phe Tyr Gly Met Gln Ser Ile Leu Ala Phe Tyr Leu
 50 55 60
 Tyr Tyr Ser Val Thr Asp Gly Gly Leu Gly Met Asn Gln Thr Ala Ala
 65 70 75 80
 Leu Ser Ile Val Gly Ala Tyr Gly Gly Phe Val Tyr Met Thr Ser Leu
 85 90 95
 Val Ala Ser Phe Ile Ala Asp Arg Val Leu Gly Ser Glu Arg Thr Leu
 100 105 110
 Phe Tyr Ser Ala Ile Ile Val Met Leu Gly His Ile Ala Leu Ala Leu
 115 120 125
 Ile Pro Gly Tyr Thr Gly Leu Ser Ile Gly Leu Val Leu Ile Gly Leu
 130 135 140
 Gly Ser Gly Gly Val Lys Thr Ala Ala Gln Val Val Leu Gly Gln Leu
 145 150 155 160
 Tyr Ser Arg Thr Asp Thr Arg Arg Asp Ala Gly Phe Ser Ile Phe Tyr
 165 170 175
 Met Gly Val Asn Leu Gly Gly Leu Phe Gly Pro Leu Ile Thr Asn Ala
 180 185 190
 Leu Trp Gly Trp Gly Gly Phe His Trp Gly Phe Gly Ile Ala Ala Val
 195 200 205
 Gly Met Ala Leu Gly Leu Ile Gln Tyr Val Ala Met Arg Lys Thr Thr
 210 215 220
 Ile Gly Ala Ala Gly His Thr Val Pro Asn Pro Leu Pro Lys Asn Glu
 225 230 235 240
 Tyr Ala Arg Trp Ile Ile Gly Ala Val Val Val Ala Ala Val Val
 245 250 255

Ala Leu Ile Ala Thr Gly Ile Ile Lys Leu Glu Trp Leu Ser Asn Ile
 260 265 270
 Thr Ala Ala Ile Ala Leu Ile Ala Ala Ile Ala Leu Leu Ala Gln Met
 275 280 285
 Tyr Val Ser Pro Leu Thr Thr Ala Ala Glu Lys Ser Arg Leu Leu Gly
 290 295 300
 Phe Ile Pro Met Phe Ile Gly Gly Val Leu Phe Phe Ala Ile Phe Gln
 305 310 315 320
 Thr Gln Phe Thr Val Leu Ala Val Tyr Ser Asp Thr Arg Leu Asp Arg
 325 330 335
 Asn Phe Phe Gly Ile Asp Leu Pro Pro Gly Leu Ile Asn Ser Phe Asn
 340 345 350
 Pro Ile Phe Ile Ile Ile Phe Ser Gly Ile Phe Ala Thr Leu Trp Thr
 355 360 365
 Lys Leu Gly Ala Lys Gln Trp Ser Thr Ala Val Lys Phe Gly Val Ala
 370 375 380
 Asn Ile Val Ile Gly Cys Ala Leu Phe Phe Phe Leu Pro Phe Ala Gly
 385 390 395 400
 Gly Ala Glu Asn Ser Thr Pro Met Ala Leu Ile Ile Trp Val Tyr Phe
 405 410 415
 Leu Phe Thr Ile Ala Glu Leu Leu Leu Ser Pro Val Gly Asn Ser Leu
 420 425 430
 Ala Thr Lys Val Ala Pro Glu Ala Phe Gln Ser Arg Met Phe Ala Val
 435 440 445
 Trp Leu Met Ala Val Ser Met Gly Thr Ser Leu Ser Gly Thr Leu Gly
 450 455 460
 Gly Tyr Tyr Asp Pro Thr Asp Ala Gly Ser Glu Lys Val Phe Phe Ile
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 Lys Gly Trp Val Leu Lys Lys Phe Ile Asp Val Arg
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<211> 1426

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (93)..(1403)

<223> RXA02394

<400> 179

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Val	Pro	Val	Ala	Ile	Ala	Ile	Gly	Leu	Pro	Ser	Leu	Phe	Ala	Ala	Met	
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gcc	gtg	ctt	ggc	cca	gaa	aac	gcc	gcg	cag	gcc	gtc	gcg	cag	cgc	atg	257
Ala	Val	Leu	Gly	Pro	Glu	Asn	Ala	Ala	Gln	Ala	Val	Ala	Gln	Arg	Met	
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Phe	Thr	Gly	Thr	Asn	Ser	Phe	Thr	Leu	Leu	Ala	Ile	Pro	Phe	Phe	Val	
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Leu	Ala	Gly	Leu	Leu	Met	Asn	Ser	Gly	Gly	Ile	Ala	Thr	Arg	Leu	Ile	
			75					80					85			
gac	gcc	gcg	aag	gtg	ctt	gtc	ggc	cgc	atg	cct	gcc	tcc	atg	gcc	aat	401
Asp	Ala	Ala	Lys	Val	Leu	Val	Gly	Arg	Met	Pro	Ala	Ser	Met	Ala	Asn	
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Thr	Asn	Ile	Ala	Ala	Asn	Gly	Leu	Phe	Gly	Ala	Val	Ser	Gly	Ala	Ala	
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Val	Ala	Ser	Ala	Ser	Ala	Val	Gly	Thr	Val	Met	Thr	Pro	Lys	Met	Lys	
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gaa	gag	ggc	tac	tgc	cgc	gct	tac	gca	gcg	gcc	gtc	aac	gtg	gct	tca	545
Glu	Glu	Gly	Tyr	Ser	Arg	Ala	Tyr	Ala	Ala	Ala	Val	Asn	Val	Ala	Ser	
				140				145					150			
gca	cct	gcg	ggc	atg	ctg	atc	ccg	cca	tca	aac	act	ttt	att	gtg	tat	593
Ala	Pro	Ala	Gly	Met	Leu	Ile	Pro	Pro	Ser	Asn	Thr	Phe	Ile	Val	Tyr	
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tcc	ttg	gtg	tcc	tgc	aca	tca	att	gca	gca	cta	ttt	atg	gcc	ggc	gtt	641
Ser	Leu	Val	Ser	Ser	Thr	Ser	Ile	Ala	Ala	Leu	Phe	Met	Ala	Gly	Val	
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Gly	Pro	Gly	Leu	Leu	Trp	Ile	Leu	Ala	Cys	Val	Ile	Val	Gly	Thr	Trp	
	185					190					195					
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 Ile Val Ile Val Val Gly Gly Ile Leu Leu Gly Trp Phe Thr Pro Thr
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gaa tcc gct gct att gct gta gtg tac tgc ctg gtc ttg ggc ttt att 881
 Glu Ser Ala Ala Ile Ala Val Val Tyr Cys Leu Val Leu Gly Phe Ile
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 265 270 275

act cgc acc aca tca att gtc atg ttg ctc att gca gtt tct gca gca 977
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 Leu Ser Trp Val Met Ala Phe Ala Lys Ile Pro Gln Met Ile Ser Asp
 300 305 310

gcg ctt ctt tgc gta tcc gat tcc aag gtt gtc atc ttg ttg atc atg 1073
 Ala Leu Leu Ser Val Ser Asp Ser Lys Val Val Ile Leu Leu Ile Met
 315 320 325

atg ttc atc ctg tta ctc atc ggt acc gta atg gac cca aca cca gca 1121
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 330 335 340

att ttg atc ttc gtc ccg atc ttc ctt cca gtg gtt acc gaa ctt ggt 1169
 Ile Leu Ile Phe Val Pro Ile Phe Leu Pro Val Val Thr Glu Leu Gly
 345 350 355

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 Val Asp Pro Val His Phe Gly Ala Met Val Val Met Asn Leu Ser Val
 360 365 370 375

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 Gly Val Ile Thr Pro Pro Val Gly Asn Val Leu Phe Val Gly Ser Gln
 380 385 390

gtg gca ggg ctg cgt gtg gaa act gtg atc aga cga ctg tgg ccg tat 1313
 Val Ala Gly Leu Arg Val Glu Thr Val Ile Arg Arg Leu Trp Pro Tyr
 395 400 405

ctc att gcc att att gtt gcg ctg ttc gtg gtt gtt ttc gta ccg cag 1361
 Leu Ile Ala Ile Ile Val Ala Leu Phe Val Val Val Phe Val Pro Gln
 410 415 420

atc tct atc tgg ctg ccc aca aca atg gga ttg atg gga ggc 1403
 Ile Ser Ile Trp Leu Pro Thr Thr Met Gly Leu Met Gly Gly
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<210> 180

<211> 437

<212> PRT

<213> Corynebacterium glutamicum

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Pro	Ser	Leu 35	Phe	Ala	Ala	Met	Ala 40	Val	Leu	Gly	Pro	Glu 45	Asn	Ala	Ala
Gln	Ala 50	Val	Ala	Gln	Arg	Met 55	Phe	Thr	Gly	Thr	Asn 60	Ser	Phe	Thr	Leu
Leu 65	Ala	Ile	Pro	Phe	Phe 70	Val	Leu	Ala	Gly	Leu 75	Leu	Met	Asn	Ser	Gly
Gly	Ile	Ala	Thr	Arg 85	Leu	Ile	Asp	Ala	Ala 90	Lys	Val	Leu	Val	Gly 95	Arg
Met	Pro	Ala	Ser 100	Met	Ala	Asn	Thr	Asn 105	Ile	Ala	Ala	Asn	Gly 110	Leu	Phe
Gly	Ala	Val 115	Ser	Gly	Ala	Ala	Val 120	Ala	Ser	Ala	Ser	Ala 125	Val	Gly	Thr
Val 130	Met	Thr	Pro	Lys	Met	Lys 135	Glu	Glu	Gly	Tyr	Ser 140	Arg	Ala	Tyr	Ala
Ala 145	Ala	Val	Asn	Val	Ala	Ser	Ala	Pro	Ala	Gly 155	Met	Leu	Ile	Pro	Pro 160
Ser	Asn	Thr	Phe	Ile 165	Val	Tyr	Ser	Leu	Val 170	Ser	Ser	Thr	Ser	Ile 175	Ala
Ala	Leu	Phe	Met 180	Ala	Gly	Val	Gly	Pro 185	Gly	Leu	Leu	Trp	Ile 190	Leu	Ala
Cys	Val	Ile 195	Val	Gly	Thr	Trp	Leu 200	Ala	Arg	Lys	Glu	Asn 205	Tyr	Lys	Arg
Glu 210	Gln	Ile	His	Pro	Thr	Phe 215	Lys	Gln	Ser	Leu	Val 220	Val	Leu	Trp	Arg
Ala 225	Leu	Pro	Ser	Leu	Leu 230	Met	Ile	Val	Ile	Val 235	Val	Gly	Gly	Ile	Leu 240
Leu	Gly	Trp	Phe	Thr 245	Pro	Thr	Glu	Ser	Ala 250	Ala	Ile	Ala	Val	Val 255	Tyr
Cys	Leu	Val 260	Leu	Gly	Phe	Ile	Tyr 265	Arg	Thr	Ile	Lys	Val 270	Gly	Asp	Leu
Ala	Asp	Ile 275	Leu	Leu	Lys	Ala	Thr 280	Arg	Thr	Thr	Ser	Ile 285	Val	Met	Leu
Leu 290	Ile	Ala	Val	Ser	Ala	Ala 295	Leu	Ser	Trp	Val	Met 300	Ala	Phe	Ala	Lys
Ile 305	Pro	Gln	Met	Ile	Ser	Asp 310	Ala	Leu	Leu	Ser 315	Val	Ser	Asp	Ser	Lys 320

Val Val Ile Leu Leu Ile Met Met Phe Ile Leu Leu Leu Ile Gly Thr
 325 330 335

Val Met Asp Pro Thr Pro Ala Ile Leu Ile Phe Val Pro Ile Phe Leu
 340 345 350

Pro Val Val Thr Glu Leu Gly Val Asp Pro Val His Phe Gly Ala Met
 355 360 365

Val Val Met Asn Leu Ser Val Gly Val Ile Thr Pro Pro Val Gly Asn
 370 375 380

Val Leu Phe Val Gly Ser Gln Val Ala Gly Leu Arg Val Glu Thr Val
 385 390 395 400

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 Met Thr Thr Pro Leu
 1 5

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 Val His Ala Val Asn Asn Val Ser Leu Glu Val His Pro Gly Gln Ile
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 Thr Ala Ile Val Gly Glu Ser Gly Ser Gly Lys Ser Thr Thr Ala Gln
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 Ala Val Ile Gly Leu Leu Ala Asp Asn Ala Glu Val Asp Ser Gly Arg
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Lys Asn Val Arg Gly Thr Lys Ile Gly Leu Ile Pro Gln Asp Pro Asn	
90 95 100	
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Asn Ser Leu Asn Pro Val Lys Thr Ile Gly Ala Ser Val Gly Glu Gly	
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Leu Ala Ile His Lys Arg Gly Thr Ala Ala Glu Arg Lys Lys Lys Val	
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Ile Glu Leu Leu Glu Arg Val Gly Ile Asp Asn Pro Glu Val Arg Tyr	
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Asp Gln Tyr Pro His Glu Leu Ser Gly Gly Met Lys Gln Arg Ala Leu	
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Ile Ala Ala Ala Ile Ala Leu Glu Pro Glu Leu Ile Ile Ala Asp Glu	
170 175 180	
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Pro Thr Ser Ala Leu Asp Val Thr Val Gln Lys Ile Ile Leu Asp Leu	
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Leu Glu Asp Met Gln Arg Glu Leu Gly Met Gly Ile Leu Phe Ile Thr	
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His Asp Leu Ala Val Ala Gly Asp Arg Ala Asp Arg Ile Val Val Met	
215 220 225	
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Gln Lys Gly Glu Val Arg Glu Ser Gly Tyr Ala Ala Ser Val Leu Thr	
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Asp Pro Gln His Glu Tyr Ser Lys Lys Leu Leu Ala Asp Ala Pro Ser	
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Leu Thr Ile Gly Glu Ile Pro Thr Arg Val Pro Ala Val Asp Pro Glu	
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Val Ala Gln Ala Lys Gly Pro Leu Leu Val Val Asp Lys Phe Arg Lys	
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Glu His Gln Arg Gly Lys Glu Gly Ala Phe Val Ala Ala Asn Asp Ile	
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 375 380 385

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 Asp Glu Lys Val Ala His Tyr Leu Glu Leu Val Ala Leu Asp Pro Ala
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 Leu Ala Thr Arg Arg Pro Arg Glu Leu Ser Gly Gly Gln Arg Gln Arg
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gtc gcc att gct cgt gcc atg att ttg gaa cct gaa ttg gtg gtt ttc 1459
 Val Ala Ile Ala Arg Ala Met Ile Leu Glu Pro Glu Leu Val Val Phe
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 Asp Glu Ala Val Ser Ala Leu Asp Val Thr Val Gln Ala Gln Ile Leu
 455 460 465

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cca gga tgc cgc tat cgt ggt ggc gaa ctc aat ctt gga cta 1741
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<211> 547

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 182

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 Thr Ile Gly Ser Thr Ile Ala Glu Pro Leu Arg Asn Phe Thr Lys Val
 385 390 395 400
 Ser Lys Gln Glu Ala Asp Glu Lys Val Ala His Tyr Leu Glu Leu Val
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 Glu Leu Val Val Phe Asp Glu Ala Val Ser Ala Leu Asp Val Thr Val
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 Lys Thr Ala Glu Val Phe Asn Asn Pro Gln Thr Asp Phe Thr Arg Arg
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<223> RXA02660

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Arg Glu Ala Asn Gly Leu Asn Asp Pro Met Met Val Arg Tyr Phe Asp		
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Phe Ile Leu Gly Met Leu Lys Gly Asp Leu Gly Thr Ser Ser Gly Gly		
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Val Ala Val Thr Asp Ile Val Ala Arg Ala Phe Pro Ile Thr Leu Gln		
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Leu Thr Phe Trp Gly Leu Ile Ile Ala Val Val Ala Leu Ile Leu		
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105 110 115		
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Arg Val Val Ser Ile Ala Ala Leu Ala Thr Pro Ser Phe Trp Leu Ala		
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Ile Leu Leu Ile Gln Trp Leu Gly Thr Ile Pro Gly Ala Trp Gly Phe		
135 140 145		
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Phe Pro Ala Leu Val Thr Arg Trp Val Pro Phe Ser Glu Asp Pro Ala		
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acc tac ttc aac aac atc gca ctt cag cga ttg cgt tgg cag tcc ccg	643	
Thr Tyr Phe Asn Asn Ile Ala Leu Gln Arg Leu Arg Trp Gln Ser Pro		
170 175 180		
ttg cag gtt ctt tgg ccc gcg ttg ttc gta cct cca tgg tgg aag aac	691	
Leu Gln Val Leu Trp Pro Ala Leu Phe Val Pro Pro Trp Trp Lys Asn		
185 190 195		
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 <213> Corynebacterium glutamicum

<400> 184

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Pro Asp Gln Leu Ile Arg Val Val Ser Ile Ala Ala Leu Ala Thr Pro
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Ser Phe Trp Leu Ala Ile Leu Leu Ile Gln Trp Leu Gly Thr Ile Pro
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Gly Ala Trp Gly Phe Phe Pro Ala Leu Val Thr Arg Trp Val Pro Phe
      145             150             155             160

Ser Glu Asp Pro Ala Thr Tyr Phe Asn Asn Ile Ala Leu Gln Arg Leu
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Arg Trp Gln Ser Pro Leu Gln Val Leu Trp Pro Ala Leu Phe Val Pro
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Pro Trp Trp Lys Asn Trp Thr Arg Thr Thr Ser Ala Gln Gln Ser Val
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Gln Asp Pro Gln Asn
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 Val Ile Gly Leu Arg
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gtt ggt tcc ctc atg ggt ggt gcg gtg atc att gag atc atc ttc aac 163
 Val Gly Ser Leu Met Gly Gly Ala Val Ile Ile Glu Ile Ile Phe Asn
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 Ile Gln Ala Met Gly Gln Leu Ile Leu Asp Gly Val Thr Arg Asn Asp
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 Val Tyr Leu Val Gln Gly Val Thr Leu Thr Val Ala Ile Ala Phe Ile
 40 45 50

atc gtc aat atc gcc gtg gac ctg ctc tac gtc ctg gtc aat cca cgt 307
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Ile	Ile	Phe	Val	Leu	Ile	Arg	Val	Ile	Pro	Gly	Asp	Pro	Ala	Ala	Val					
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Gln	Leu	Gly	Thr	Asp	Gln	Pro	Leu	Phe	Gln	Gln	Tyr	Phe	Ser	Trp	Ile					
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Ser	Ala	Val	Met	Asp	Val	Met	Gly	Gln	Asp	Phe	Met	Arg	Thr	Ala	Arg					
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Tyr Phe Ser Trp Ile Gly Gly Met Leu Thr Gly Asp Phe Gly Thr Ser				
65	70	75	80	
Leu Ser Ser Gly Gln Asp Leu Ser Pro Ile Ile Phe Asp Arg Leu Gln				
85	90	95		
Val Ser Leu Ile Leu Val Gly Cys Ser Ile Val Leu Ser Leu Leu Ile				
100	105	110		
Ala Ile Pro Leu Gly Val Leu Ser Ala Arg Arg Gly Gly Val Ile Ile				
115	120	125		
Ser Gly Ile Ser Gln Ile Gly Ile Ala Ile Pro Ser Phe Leu Ala Gly				
130	135	140		
Ile Leu Leu Val Ala Val Phe Ala Val Gly Leu Gly Trp Leu Pro Ala				
145	150	155	160	

Asn Gly Trp Ile Pro Pro Ser Glu Asn Phe Gly Gly Phe Leu Ala Arg
 165 170 175
 Leu Ile Leu Pro Val Leu Ala Leu Thr Ala Val Gln Ala Ala Ile Leu
 180 185 190
 Thr Arg Tyr Val Arg Ser Ala Val Met Asp Val Met Gly Gln Asp Phe
 195 200 205
 Met Arg Thr Ala Arg Ser Lys Gly Met Ser Phe Asn Arg Ala Leu Ile
 210 215 220
 Ile His Gly Leu Arg Asn Ala Ala Leu Pro Val Leu Thr Val Thr Gly
 225 230 235 240
 Leu Gln Leu Thr Thr Leu Val Ile Gly Ala Val Val Ile Glu Gln Val
 245 250 255
 Phe Val Ile Pro Gly ile Gly Ser Met Leu Leu Glu Ser Val Ser Asn
 260 265 270
 Arg Asp Leu Ile Ala Val Gln Ser Ile Val Met Leu Leu Val Ala Phe
 275 280 285
 Thr Leu Leu Val Asn Leu Val Val Asp Leu Leu Tyr Gln Val Val Asp
 290 295 300
 Pro Arg Val Gly Ala Val Gly Val Ala Ser Thr Lys Val Pro Gly Ser
 305 310 315 320
 Val Ala

<210> 189
 <211> 818
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(795)
 <223> RXA01013

<400> 189
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 Leu Gly Asn Pro Trp Thr Arg Pro Ala Ala Val Ile Ser Ile Val Val
 1 5 10 15
 ctc gcc gtt gcg gtg ctg atg gca ctt gtt cct gga ctg ttt acc tcc 96
 Leu Ala Val Ala Val Leu Met Ala Leu Val Pro Gly Leu Phe Thr Ser
 20 25 30
 cag gat ccg ttc act ggc gat gat gtg gcg ctg ctt ggg cca agt ggc 144
 Gln Asp Pro Phe Thr Gly Asp Asp Val Ala Leu Leu Gly Pro Ser Gly
 35 40 45
 acc cac tgg ttt ggt acc gat tcc gtg gga cgc gat ctc tac agt cgt 192
 Thr His Trp Phe Gly Thr Asp Ser Val Gly Arg Asp Leu Tyr Ser Arg
 50 55 60

gtt gtt tac ggc gcg agg gaa acc ctg ctc ggt gca ctg atc gca gtg 240
 Val Val Tyr Gly Ala Arg Glu Thr Leu Leu Gly Ala Leu Ile Ala Val
 65 70 75 80
 ctg gtt ggt ctg atc gtg gga acc ctg atc gga ctg ctc gca ggt gca 288
 Leu Val Gly Leu Ile Val Gly Thr Leu Ile Gly Leu Leu Ala Gly Ala
 85 90 95
 cag cgc ggt tgg gtt gac act gta tta atg cgt ttc gtg gat gtg ctg 336
 Gln Arg Gly Trp Val Asp Thr Val Leu Met Arg Phe Val Asp Val Leu
 100 105 110
 ttg tcc atc ccg gca ctg ctg ctc agc ttg act gtc att atc ctt ttg 384
 Leu Ser Ile Pro Ala Leu Leu Leu Ser Leu Thr Val Ile Ile Leu Leu
 115 120 125
 gga ttc ggc acc atg aac gca gcg atc gca gtc ggt att acc tct gtt 432
 Gly Phe Gly Thr Met Asn Ala Ala Ile Ala Val Gly Ile Thr Ser Val
 130 135 140
 gcc acc ttc gcg cgt ctg gcg cgt tcc cag gtg atg act gtt gca ggt 480
 Ala Thr Phe Ala Arg Leu Ala Arg Ser Gln Val Met Thr Val Ala Gly
 145 150 155 160
 tcc gat ttc gtg gaa gct gca tac ggt tcc ggt ggc acc cag gcg cag 528
 Ser Asp Phe Val Glu Ala Ala Tyr Gly Ser Gly Gly Thr Gln Ala Gln
 165 170 175
 gtg ttg ttc cgc cac att ctg cct aac tct ctg acc cca gtg ttt gct 576
 Val Leu Phe Arg His Ile Leu Pro Asn Ser Leu Thr Pro Val Phe Ala
 180 185 190
 ctt gca gca ctg cag ttc ggt tcc gcg att ttg cag ctg tcc gtg ttg 624
 Leu Ala Ala Leu Gln Phe Gly Ser Ala Ile Leu Gln Leu Ser Val Leu
 195 200 205
 ggc ttc ttg ggc tac ggc gct ccg gca cca aca cca gag tgg ggt ctg 672
 Gly Phe Leu Gly Tyr Gly Ala Pro Ala Pro Thr Pro Glu Trp Gly Leu
 210 215 220
 ctg atc tct gat gcc cgc gac tac atg gcg acc tca tgg tgg ctg act 720
 Leu Ile Ser Asp Ala Arg Asp Tyr Met Ala Thr Ser Trp Trp Leu Thr
 225 230 235 240
 gtg ctg cct ggt ttt gtc atc atc gcc gtg gtt atg tct gcc aac tac 768
 Val Leu Pro Gly Phe Val Ile Ile Ala Val Val Met Ser Ala Asn Tyr
 245 250 255
 cta agc cgc atc att cag aag gag gca tagaaaaatga ctactccott gtt 818
 Leu Ser Arg Ile Ile Gln Lys Glu Ala
 260 265

<210> 190

<211> 265

<212> PRT

<213> Corynebacterium glutamicum

<400> 190

Leu Gly Asn Pro Trp Thr Arg Pro Ala Ala Val Ile Ser Ile Val Val
 1 5 10 15

Leu Ala Val Ala Val Leu Met Ala Leu Val Pro Gly Leu Phe Thr Ser
 20 25 30
 Gln Asp Pro Phe Thr Gly Asp Asp Val Ala Leu Leu Gly Pro Ser Gly
 35 40 45
 Thr His Trp Phe Gly Thr Asp Ser Val Gly Arg Asp Leu Tyr Ser Arg
 50 55 60
 Val Val Tyr Gly Ala Arg Glu Thr Leu Leu Gly Ala Leu Ile Ala Val
 65 70 75 80
 Leu Val Gly Leu Ile Val Gly Thr Leu Ile Gly Leu Leu Ala Gly Ala
 85 90 95
 Gln Arg Gly Trp Val Asp Thr Val Leu Met Arg Phe Val Asp Val Leu
 100 105 110
 Leu Ser Ile Pro Ala Leu Leu Leu Ser Leu Thr Val Ile Ile Leu Leu
 115 120 125
 Gly Phe Gly Thr Met Asn Ala Ala Ile Ala Val Gly Ile Thr Ser Val
 130 135 140
 Ala Thr Phe Ala Arg Leu Ala Arg Ser Gln Val Met Thr Val Ala Gly
 145 150 155 160
 Ser Asp Phe Val Glu Ala Ala Tyr Gly Ser Gly Gly Thr Gln Ala Gln
 165 170 175
 Val Leu Phe Arg His Ile Leu Pro Asn Ser Leu Thr Pro Val Phe Ala
 180 185 190
 Leu Ala Ala Leu Gln Phe Gly Ser Ala Ile Leu Gln Leu Ser Val Leu
 195 200 205
 Gly Phe Leu Gly Tyr Gly Ala Pro Ala Pro Thr Pro Glu Trp Gly Leu
 210 215 220
 Leu Ile Ser Asp Ala Arg Asp Tyr Met Ala Thr Ser Trp Trp Leu Thr
 225 230 235 240
 Val Leu Pro Gly Phe Val Ile Ile Ala Val Val Met Ser Ala Asn Tyr
 245 250 255
 Leu Ser Arg Ile Ile Gln Lys Glu Ala
 260 265

<210> 191

<211> 933

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(910)

<223> RXN02933

<400> 191

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ggttccaggg agcgtggctt aagtgacaac gatcaaaaaac atg ccc ctt tca ggg	115
Met Pro Leu Ser Gly	5
1	
aaa atc ggc ggc ttc atc gtt gcc gtt gta ttt gtt ctt gct gcg ctg	163
Lys Ile Gly Gly Phe Ile Val Ala Val Val Phe Val Leu Ala Ala Leu	
10 15 20	
tct ttc att tgg act ccg ttt gat cca gtt caa gct ttc cca cag gag	211
Ser Phe Ile Trp Thr Pro Phe Asp Pro Val Gln Ala Phe Pro Gln Glu	
25 30 35	
cgc ctt gag gga agt tct ttg agg cac ctg ttg gga acg gat cgt tat	259
Arg Leu Glu Gly Ser Ser Leu Arg His Leu Leu Gly Thr Asp Arg Tyr	
40 45 50	
ggt cgc gat gtt tta tcc cag atc atg gtt ggt tcc cgc gtc acg ttg	307
Gly Arg Asp Val Leu Ser Gln Ile Met Val Gly Ser Arg Val Thr Leu	
55 60 65	
ttg gtg ggc atc att gcg gtg gcg atc gca gca tta atc ggc acg cca	355
Leu Val Gly Ile Ile Ala Val Ala Ile Ala Ala Leu Ile Gly Thr Pro	
70 75 80 85	
ctg ggt att gct gcg gga atg cgc cgt ggc atg gtg gaa acc ttt gtc	403
Leu Gly Ile Ala Ala Gly Met Arg Arg Gly Met Val Glu Thr Phe Val	
90 95 100	
atg cgt ggt gcc gat tta atg ttg gcg ttc cca gca ctg ttg ttg gcg	451
Met Arg Gly Ala Asp Leu Met Leu Ala Phe Pro Ala Leu Leu Leu Ala	
105 110 115	
att att tcc ggc gcc gtt ttc ggc gcc tcc acg tgg tcc gcg atg gtc	499
Ile Ile Ser Gly Ala Val Phe Gly Ala Ser Thr Trp Ser Ala Met Val	
120 125 130	
gcg atc ggc atc gca ggc atc cct agt ttt gcc cgc gtg gct cgt gca	547
Ala Ile Gly Ile Ala Gly Ile Pro Ser Phe Ala Arg Val Ala Arg Ala	
135 140 145	
ggc aca ttg cag gtg acc agt cag gat ttc atc gca gct gct cgg cta	595
Gly Thr Leu Gln Val Thr Ser Gln Asp Phe Ile Ala Ala Ala Arg Leu	
150 155 160 165	
tca aaa gta agt tcc gcc cgg atc gcg ctt cgc cat att ttg ccc aac	643
Ser Lys Val Ser Ser Ala Arg Ile Ala Leu Arg His Ile Leu Pro Asn	
170 175 180	
atc acc agc atg ttg atc gtt cag gca tca gta gct ttt gcc ctg gcg	691
Ile Thr Ser Met Leu Ile Val Gln Ala Ser Val Ala Phe Ala Leu Ala	
185 190 195	
atc ctg gcg gaa gcc gca ttg agt ttc ctc ggt ttg ggc acc act ccc	739
Ile Leu Ala Glu Ala Ala Leu Ser Phe Leu Gly Leu Gly Thr Thr Pro	
200 205 210	
ccg gat ccc agc tgg ggt cgc atg ttg caa acc gct caa gca tcc atc	787
Pro Asp Pro Ser Trp Gly Arg Met Leu Gln Thr Ala Gln Ala Ser Ile	
215 220 225	

ggc gtc acc ccc atg ttg gcg gtg tgg ccc ggt gct gcg atc gct ttg 835
 Gly Val Thr Pro Met Leu Ala Val Trp Pro Gly Ala Ala Ile Ala Leu
 230 235 240 245

acg gtc ctt ggt ttt aat ctt ttc ggt gat ggt tta cgc gat gcc atc 883
 Thr Val Leu Gly Phe Asn Leu Phe Gly Asp Gly Leu Arg Asp Ala Ile
 250 255 260

gat cca aag cgg gag gtc ggc cgt gct taaagtttct gatttaacgg ttg 933
 Asp Pro Lys Arg Glu Val Gly Arg Ala
 265 270

<210> 192

<211> 270

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 192

Met Pro Leu Ser Gly Lys Ile Gly Gly Phe Ile Val Ala Val Val Phe
 1 5 10 15

Val Leu Ala Ala Leu Ser Phe Ile Trp Thr Pro Phe Asp Pro Val Gln
 20 25 30

Ala Phe Pro Gln Glu Arg Leu Glu Gly Ser Ser Leu Arg His Leu Leu
 35 40 45

Gly Thr Asp Arg Tyr Gly Arg Asp Val Leu Ser Gln Ile Met Val Gly
 50 55 60

Ser Arg Val Thr Leu Leu Val Gly Ile Ile Ala Val Ala Ile Ala Ala
 65 70 75 80

Leu Ile Gly Thr Pro Leu Gly Ile Ala Ala Gly Met Arg Arg Gly Met
 85 90 95

Val Glu Thr Phe Val Met Arg Gly Ala Asp Leu Met Leu Ala Phe Pro
 100 105 110

Ala Leu Leu Leu Ala Ile Ile Ser Gly Ala Val Phe Gly Ala Ser Thr
 115 120 125

Trp Ser Ala Met Val Ala Ile Gly Ile Ala Gly Ile Pro Ser Phe Ala
 130 135 140

Arg Val Ala Arg Ala Gly Thr Leu Gln Val Thr Ser Gln Asp Phe Ile
 145 150 155 160

Ala Ala Ala Arg Leu Ser Lys Val Ser Ser Ala Arg Ile Ala Leu Arg
 165 170 175

His Ile Leu Pro Asn Ile Thr Ser Met Leu Ile Val Gln Ala Ser Val
 180 185 190

Ala Phe Ala Leu Ala Ile Leu Ala Glu Ala Ala Leu Ser Phe Leu Gly
 195 200 205

Leu Gly Thr Thr Pro Pro Asp Pro Ser Trp Gly Arg Met Leu Gln Thr
 210 215 220

Ala Gln Ala Ser Ile Gly Val Thr Pro Met Leu Ala Val Trp Pro Gly
225 230 235 240

Ala Ala Ile Ala Leu Thr Val Leu Gly Phe Asn Leu Phe Gly Asp Gly
245 250 255

Leu Arg Asp Ala Ile Asp Pro Lys Arg Glu Val Gly Arg Ala
260 265 270

<210> 193

<211> 900

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(889)

<223> FRXA02033

<400> 193

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ggttccaggg agcgtggctt aagtgacaac gatcaaaaac atg ccc ctt tca ggg 115
Met Pro Leu Ser Gly
1 5

aaa atc ggc ggc ttc atc gtt gcc gtt gta ttt gtt ctt gct gcg ctg 163
Lys Ile Gly Gly Phe Ile Val Ala Val Val Phe Val Leu Ala Ala Leu
10 15 20

tct ttc att tgg act ccg ttt gat cca gtt caa gct ttc cca cag gag 211
Ser Phe Ile Trp Thr Pro Phe Asp Pro Val Gln Ala Phe Pro Gln Glu
25 30 35

cgc ctt gag gga agt tct ttg agg cac ctg ttg gga acg gat cgt tat 259
Arg Leu Glu Gly Ser Ser Leu Arg His Leu Leu Gly Thr Asp Arg Tyr
40 45 50

ggt cgc gat gtt tta tcc cag atc atg gtt ggt tcc cgc gtc acg ttg 307
Gly Arg Asp Val Leu Ser Gln Ile Met Val Gly Ser Arg Val Thr Leu
55 60 65

ttg gtg ggc atc att gcg gtg gcg atc gca gca tta atc ggc acg cca 355
Leu Val Gly Ile Ile Ala Val Ala Ile Ala Ala Leu Ile Gly Thr Pro
70 75 80 85

ctg ggt att gct gcg gga atg cgc cgt ggc atg gtg gaa acc ttt gtc 403
Leu Gly Ile Ala Ala Gly Met Arg Arg Gly Met Val Glu Thr Phe Val
90 95 100

atg cgt ggt gcc gat tta atg ttg gcg ttc cca gca ctg ttg ttg gcg 451
Met Arg Gly Ala Asp Leu Met Leu Ala Phe Pro Ala Leu Leu Leu Ala
105 110 115

att att tcc ggc gcc gtt ttc ggc gcc tcc acg tgg tcc gcg atg gtc 499
Ile Ile Ser Gly Ala Val Phe Gly Ala Ser Thr Trp Ser Ala Met Val
120 125 130

gcg atc ggc atc gca ggc atc cct agt ttt gcc cgc gtg gct cgt gca 547

Ala Ile Gly Ile Ala Gly Ile Pro Ser Phe Ala Arg Val Ala Arg Ala
 135 140 145

ggc aca ttg cag gtg acc agt cag gat ttc atc gca gct gct cgg cta 595
 Gly Thr Leu Gln Val Thr Ser Gln Asp Phe Ile Ala Ala Ala Arg Leu
 150 155 160 165

tca aaa gta agt tcc gcc cgg atc gcg ctt cgc cat att ttg ccc aac 643
 Ser Lys Val Ser Ser Ala Arg Ile Ala Leu Arg His Ile Leu Pro Asn
 170 175 180

atc acc agc atg ttg atc gtt cag gca tca gta gct ttt gcc ctg gcg 691
 Ile Thr Ser Met Leu Ile Val Gln Ala Ser Val Ala Phe Ala Leu Ala
 185 190 195

atc ctg gcg gaa gcc gca ttg agt ttc ctc ggt ttg ggc acc act ccc 739
 Ile Leu Ala Glu Ala Ala Leu Ser Phe Leu Gly Leu Gly Thr Thr Pro
 200 205 210

ccg gat ccc agc tgg ggt cgc atg ttg caa acc gct caa gca tcc atc 787
 Pro Asp Pro Ser Trp Gly Arg Met Leu Gln Thr Ala Gln Ala Ser Ile
 215 220 225

ggc gtc acc ccc atg ttg gcg gtg tgg ccc ggt gct gcg atc gct ttg 835
 Gly Val Thr Pro Met Leu Ala Val Trp Pro Gly Ala Ala Ile Ala Leu
 230 235 240 245

acg gtc ctt ggt ttt aat ctt ttc ggt gat ggt tta cgc gat gcc atc 883
 Thr Val Leu Gly Phe Asn Leu Phe Gly Asp Gly Leu Arg Asp Ala Ile
 250 255 260

gat cca tagtattata t 900
 Asp Pro

<210> 194

<211> 263

<212> PRT

<213> Corynebacterium glutamicum

<400> 194

Met Pro Leu Ser Gly Lys Ile Gly Gly Phe Ile Val Ala Val Val Phe
 1 5 10 15

Val Leu Ala Ala Leu Ser Phe Ile Trp Thr Pro Phe Asp Pro Val Gln
 20 25 30

Ala Phe Pro Gln Glu Arg Leu Glu Gly Ser Ser Leu Arg His Leu Leu
 35 40 45

Gly Thr Asp Arg Tyr Gly Arg Asp Val Leu Ser Gln Ile Met Val Gly
 50 55 60

Ser Arg Val Thr Leu Leu Val Gly Ile Ile Ala Val Ala Ile Ala Ala
 65 70 75 80

Leu Ile Gly Thr Pro Leu Gly Ile Ala Ala Gly Met Arg Arg Gly Met
 85 90 95

Val Glu Thr Phe Val Met Arg Gly Ala Asp Leu Met Leu Ala Phe Pro

100					105					110					
Ala	Leu	Leu	Leu	Ala	Ile	Ile	Ser	Gly	Ala	Val	Phe	Gly	Ala	Ser	Thr
	115						120					125			
Trp	Ser	Ala	Met	Val	Ala	Ile	Gly	Ile	Ala	Gly	Ile	Pro	Ser	Phe	Ala
	130					135					140				
Arg	Val	Ala	Arg	Ala	Gly	Thr	Leu	Gln	Val	Thr	Ser	Gln	Asp	Phe	Ile
145					150					155					160
Ala	Ala	Ala	Arg	Leu	Ser	Lys	Val	Ser	Ser	Ala	Arg	Ile	Ala	Leu	Arg
			165					170						175	
His	Ile	Leu	Pro	Asn	Ile	Thr	Ser	Met	Leu	Ile	Val	Gln	Ala	Ser	Val
			180					185					190		
Ala	Phe	Ala	Leu	Ala	Ile	Leu	Ala	Glu	Ala	Ala	Leu	Ser	Phe	Leu	Gly
	195						200					205			
Leu	Gly	Thr	Thr	Pro	Pro	Asp	Pro	Ser	Trp	Gly	Arg	Met	Leu	Gln	Thr
	210					215					220				
Ala	Gln	Ala	Ser	Ile	Gly	Val	Thr	Pro	Met	Leu	Ala	Val	Trp	Pro	Gly
225					230				235					240	
Ala	Ala	Ile	Ala	Leu	Thr	Val	Leu	Gly	Phe	Asn	Leu	Phe	Gly	Asp	Gly
			245					250						255	
Leu	Arg	Asp	Ala	Ile	Asp	Pro									
			260												

<210> 195

<211> 958

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(958)

<223> RXA01006

<400> 195

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				Met	Thr	Thr	Ser	Gln	
				1				5	

att	ctg	cgc	cgc	atc	ggc	caa	gcc	gtc	ttg	gtc	ttg	ttg	gtc	acc	ttt	163
Ile	Leu	Arg	Arg	Ile	Gly	Gln	Ala	Val	Leu	Val	Leu	Leu	Val	Thr	Phe	
			10					15						20		

acc	ttg	gcg	ttc	atc	atg	ctt	tcc	gcc	ctc	cct	ggc	gat	gct	gtg	tcc	211
Thr	Leu	Ala	Phe	Ile	Met	Leu	Ser	Ala	Leu	Pro	Gly	Asp	Ala	Val	Ser	
		25						30					35			

gcc	cgc	tat	tcc	agc	cct	gat	ttg	ggc	ctg	tca	cct	gag	cag	atc	gca	259
Ala	Arg	Tyr	Ser	Ser	Pro	Asp	Leu	Gly	Leu	Ser	Pro	Glu	Gln	Ile	Ala	
		40					45					50				

cag atc cgt gaa tcc tat ggt gcc gat gaa tcc ctg atc gct cag tac	307
Gln Ile Arg Glu Ser Tyr Gly Ala Asp Glu Ser Leu Ile Ala Gln Tyr	
55 60 65	
ttc tcc acc ttg ggt ggc ttc ctt gta ggt aac ttc ggt tac tcc gta	355
Phe Ser Thr Leu Gly Gly Phe Leu Val Gly Asn Phe Gly Tyr Ser Val	
70 75 80 85	
caa acc gga act gcc gtg gca acc cag ctg gca gaa gcc cta cca ggc	403
Gln Thr Gly Thr Ala Val Ala Thr Gln Leu Ala Glu Ala Leu Pro Gly	
90 95 100	
acc ttg acc ttg gct att ttg gca ttc ttg ctc gca gcc att ttg gca	451
Thr Leu Thr Leu Ala Ile Leu Ala Phe Leu Leu Ala Ala Ile Leu Ala	
105 110 115	
ctg gtt att tcc att ctt gcc acc atg gat cgc ttt gca tgg atc aag	499
Leu Val Ile Ser Ile Leu Ala Thr Met Asp Arg Phe Ala Trp Ile Lys	
120 125 130	
ggc atc ttc cag gct ctg cct cca ttc ttt gtg tcc ctt cca agt ttc	547
Gly Ile Phe Gln Ala Leu Pro Pro Phe Phe Val Ser Leu Pro Ser Phe	
135 140 145	
tgg ttg ggc atc atc ttg atc cag atc gtg tcc ttc cgc ctt ggt tgg	595
Trp Leu Gly Ile Ile Leu Ile Gln Ile Val Ser Phe Arg Leu Gly Trp	
150 155 160 165	
gtc ccc gtt att ggg acc acc ccg gca caa gga ctg atc ctg ccg acc	643
Val Pro Val Ile Gly Thr Thr Pro Ala Gln Gly Leu Ile Leu Pro Thr	
170 175 180	
atc acc ttg tcc atc cca att acc gct ccg ctt gca cag gtg ctc atc	691
Ile Thr Leu Ser Ile Pro Ile Thr Ala Pro Leu Ala Gln Val Leu Ile	
185 190 195	
cgc tcg att gaa gag gtc aag gca caa ccg ttc atc gcg gct gtt cgt	739
Arg Ser Ile Glu Glu Val Lys Ala Gln Pro Phe Ile Ala Ala Val Arg	
200 205 210	
gct cgc ggt gcg ggt gaa atg tgg atc ttc ttc cgc aac atc att cgc	787
Ala Arg Gly Ala Gly Glu Met Trp Ile Phe Phe Arg Asn Ile Ile Arg	
215 220 225	
aac gcc ctt ttg cca acc ctg acg att gcc ggc atc ttg ttt ggt gaa	835
Asn Ala Leu Leu Pro Thr Leu Thr Ile Ala Gly Ile Leu Phe Gly Glu	
230 235 240 245	
cta gtc ggt ggg gcc gtg gtc acc gag gca gtg ttc ggc cgc gct gga	883
Leu Val Gly Gly Ala Val Val Thr Glu Ala Val Phe Gly Arg Ala Gly	
250 255 260	
ctt ggc caa atg acc gtc aac gca gtg gcc aac cgc gat atg cca gtg	931
Leu Gly Gln Met Thr Val Asn Ala Val Ala Asn Arg Asp Met Pro Val	
265 270 275	
atg ctt gcc atc gtg gtg atc gca gct	958
Met Leu Ala Ile Val Val Ile Ala Ala	
280 285	

<210> 196

<211> 286

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 196

Met Thr Thr Ser Gln Ile Leu Arg Arg Ile Gly Gln Ala Val Leu Val
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Leu Leu Val Thr Phe Thr Leu Ala Phe Ile Met Leu Ser Ala Leu Pro
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Gly Asp Ala Val Ser Ala Arg Tyr Ser Ser Pro Asp Leu Gly Leu Ser
 35 40 45

Pro Glu Gln Ile Ala Gln Ile Arg Glu Ser Tyr Gly Ala Asp Glu Ser
 50 55 60

Leu Ile Ala Gln Tyr Phe Ser Thr Leu Gly Gly Phe Leu Val Gly Asn
 65 70 75 80

Phe Gly Tyr Ser Val Gln Thr Gly Thr Ala Val Ala Thr Gln Leu Ala
 85 90 95

Glu Ala Leu Pro Gly Thr Leu Thr Leu Ala Ile Leu Ala Phe Leu Leu
 100 105 110

Ala Ala Ile Leu Ala Leu Val Ile Ser Ile Leu Ala Thr Met Asp Arg
 115 120 125

Phe Ala Trp Ile Lys Gly Ile Phe Gln Ala Leu Pro Pro Phe Phe Val
 130 135 140

Ser Leu Pro Ser Phe Trp Leu Gly Ile Ile Leu Ile Gln Ile Val Ser
 145 150 155 160

Phe Arg Leu Gly Trp Val Pro Val Ile Gly Thr Thr Pro Ala Gln Gly
 165 170 175

Leu Ile Leu Pro Thr Ile Thr Leu Ser Ile Pro Ile Thr Ala Pro Leu
 180 185 190

Ala Gln Val Leu Ile Arg Ser Ile Glu Glu Val Lys Ala Gln Pro Phe
 195 200 205

Ile Ala Ala Val Arg Ala Arg Gly Ala Gly Glu Met Trp Ile Phe Phe
 210 215 220

Arg Asn Ile Ile Arg Asn Ala Leu Leu Pro Thr Leu Thr Ile Ala Gly
 225 230 235 240

Ile Leu Phe Gly Glu Leu Val Gly Gly Ala Val Val Thr Glu Ala Val
 245 250 255

Phe Gly Arg Ala Gly Leu Gly Gln Met Thr Val Asn Ala Val Ala Asn
 260 265 270

Arg Asp Met Pro Val Met Leu Ala Ile Val Val Ile Ala Ala
 275 280 285

<210> 197
 <211> 1482
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1459)
 <223> RXA02312

<400> 197

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agcagtcacg gagaatcacg aaccgcacct caagcgcggt ttg agc aat aga cac 115
                                   Leu Ser Asn Arg His
                                   1 5

ctt cag ctc atc gcc atc ggc gga gcg atc ggt acg ggt ctg ttc atg 163
Leu Gln Leu Ile Ala Ile Gly Gly Ala Ile Gly Thr Gly Leu Phe Met
                                   10 15 20

ggg tcc ggc aag acg atc tcc gtt gcg ggg cca tca gta att ttg gtg 211
Gly Ser Gly Lys Thr Ile Ser Val Ala Gly Pro Ser Val Ile Leu Val
                                   25 30 35

tac gcc att att ggt ttc atg ctt ttc ttc gtc atg cgt gcc atg gga 259
Tyr Ala Ile Ile Gly Phe Met Leu Phe Phe Val Met Arg Ala Met Gly
                                   40 45 50

gag ctg ctg ctc gcc aat ttg aat tac aaa tct ttg cgc gat gcg gtc 307
Glu Leu Leu Leu Ala Asn Leu Asn Tyr Lys Ser Leu Arg Asp Ala Val
                                   55 60 65

tct gat att ttg ggt cct ggc gca ggt ttt gtc acc ggc tgg aca tat 355
Ser Asp Ile Leu Gly Pro Gly Ala Gly Phe Val Thr Gly Trp Thr Tyr
                                   70 75 80 85

tgg ttc tgc tgg att gcc aca ggc atg gcg gac atc gtg gcg atc act 403
Trp Phe Cys Trp Ile Ala Thr Gly Met Ala Asp Ile Val Ala Ile Thr
                                   90 95 100

gga tac acc caa tac tgg tgg cct gag atc cca ttg tgg ctt cca ggt 451
Gly Tyr Thr Gln Tyr Trp Trp Pro Glu Ile Pro Leu Trp Leu Pro Gly
                                   105 110 115

gtg ctc acc att gcg ttg ctg ttt gcc ctg aac ttg gct gcg gta cga 499
Val Leu Thr Ile Ala Leu Leu Phe Ala Leu Asn Leu Ala Ala Val Arg
                                   120 125 130

ctg ttc ggt gag atg gag ttt tgg ttc gcc atc atc aaa atc gtg gct 547
Leu Phe Gly Glu Met Glu Phe Trp Phe Ala Ile Ile Lys Ile Val Ala
                                   135 140 145

atc gtg tcc ttg atc gtc gtg gga ctt ttc atg gtg gtc aca gcc ttt 595
Ile Val Ser Leu Ile Val Val Gly Leu Phe Met Val Val Thr Ala Phe
                                   150 155 160 165

gaa tca cct aat ggc acc acc gcg cag ttc aac aac ctc att gag cat 643
Glu Ser Pro Asn Gly Thr Thr Ala Gln Phe Asn Asn Leu Ile Glu His
                                   170 175 180

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ggc gga ttt ttc ccc aac ggc atc acc ggt ttc ttg gct ggt ttc cag	691
Gly Gly Phe Phe Pro Asn Gly Ile Thr Gly Phe Leu Ala Gly Phe Gln	
185 190 195	
atc gct atc ttt gcg ttc gtc ggg att gaa ctt gcc ggc act gca gct	739
Ile Ala Ile Phe Ala Phe Val Gly Ile Glu Leu Ala Gly Thr Ala Ala	
200 205 210	
gca gag act gag aat ccc acc aag acg ctt cct cgg gca atc aac tcc	787
Ala Glu Thr Glu Asn Pro Thr Lys Thr Leu Pro Arg Ala Ile Asn Ser	
215 220 225	
att ccc atc cgc atc gtg gtg ttc tat gtt ttg gcg ttg gct gtc atc	835
Ile Pro Ile Arg Ile Val Val Phe Tyr Val Leu Ala Leu Ala Val Ile	
230 235 240 245	
atg atg gtc acc cca tgg gat cag gtc cgt gct gac aac agc cca ttc	883
Met Met Val Thr Pro Trp Asp Gln Val Arg Ala Asp Asn Ser Pro Phe	
250 255 260	
gtg cag atg ttc gcg ctg gca gga atc cca gcg gcg gca ggc atc att	931
Val Gln Met Phe Ala Leu Ala Gly Ile Pro Ala Ala Ala Gly Ile Ile	
265 270 275	
aac ttt gtg gtc atc act tct gca gcg tcg tct gcc aac agt ggt att	979
Asn Phe Val Val Ile Thr Ser Ala Ala Ser Ser Ala Asn Ser Gly Ile	
280 285 290	
ttc tcc acc tcc cgc atg ttg tat gga ttg tct ttg gaa ggc gca gct	1027
Phe Ser Thr Ser Arg Met Leu Tyr Gly Leu Ser Leu Glu Gly Ala Ala	
295 300 305	
ccg aaa cgg tgg agc cgg ttg tcc aag aac ttg gtg cca gcc agg gga	1075
Pro Lys Arg Trp Ser Arg Leu Ser Lys Asn Leu Val Pro Ala Arg Gly	
310 315 320 325	
ttg act ttt tct gtg att tgc ctc att cca gcg gtg ggt ttg ctg tac	1123
Leu Thr Phe Ser Val Ile Cys Leu Ile Pro Ala Val Gly Leu Leu Tyr	
330 335 340	
gct ggc ggc act gtc atc gag gca ttc aca ctg atc acc acg gtt tct	1171
Ala Gly Gly Thr Val Ile Glu Ala Phe Thr Leu Ile Thr Thr Val Ser	
345 350 355	
tcg gtg ttg ttc atg gtg gtg tgg tcc tac att ttg gtg gct tat atc	1219
Ser Val Leu Phe Met Val Val Trp Ser Tyr Ile Leu Val Ala Tyr Ile	
360 365 370	
gtc tac cgc cgc aac agc ccg gaa tta cac aaa aag tcg att ttc aaa	1267
Val Tyr Arg Arg Asn Ser Pro Glu Leu His Lys Lys Ser Ile Phe Lys	
375 380 385	
atg cct ggc ggc gtg gtc atg gca gtt gtg gtg ttg gtg ttc ttc gca	1315
Met Pro Gly Gly Val Val Met Ala Val Val Val Leu Val Phe Phe Ala	
390 395 400 405	
gcg atg ttg gtg gtg ctg tcc ctg gag ccg gat acc cgt gca gcg ctc	1363
Ala Met Leu Val Val Leu Ser Leu Glu Pro Asp Thr Arg Ala Ala Leu	
410 415 420	

atc gcg acg cca gtg tgg ttc atc att ttg ggt atc ggt tgg ttg tcc 1411
 Ile Ala Thr Pro Val Trp Phe Ile Ile Leu Gly Ile Gly Trp Leu Ser
 425 430 435

atc ggt gga gct aag ggc gct aag cat cgc agc caa ata acc tcc cac 1459
 Ile Gly Gly Ala Lys Gly Ala Lys His Arg Ser Gln Ile Thr Ser His
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taaagctcct gggtttagact cga 1482

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<211> 453

<212> PRT

<213> Corynebacterium glutamicum

<400> 198

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 20 25 30

Ser Val Ile Leu Val Tyr Ala Ile Ile Gly Phe Met Leu Phe Phe Val
 35 40 45

Met Arg Ala Met Gly Glu Leu Leu Leu Ala Asn Leu Asn Tyr Lys Ser
 50 55 60

Leu Arg Asp Ala Val Ser Asp Ile Leu Gly Pro Gly Ala Gly Phe Val
 65 70 75 80

Thr Gly Trp Thr Tyr Trp Phe Cys Trp Ile Ala Thr Gly Met Ala Asp
 85 90 95

Ile Val Ala Ile Thr Gly Tyr Thr Gln Tyr Trp Trp Pro Glu Ile Pro
 100 105 110

Leu Trp Leu Pro Gly Val Leu Thr Ile Ala Leu Leu Phe Ala Leu Asn
 115 120 125

Leu Ala Ala Val Arg Leu Phe Gly Glu Met Glu Phe Trp Phe Ala Ile
 130 135 140

Ile Lys Ile Val Ala Ile Val Ser Leu Ile Val Val Gly Leu Phe Met
 145 150 155 160

Val Val Thr Ala Phe Glu Ser Pro Asn Gly Thr Thr Ala Gln Phe Asn
 165 170 175

Asn Leu Ile Glu His Gly Gly Phe Phe Pro Asn Gly Ile Thr Gly Phe
 180 185 190

Leu Ala Gly Phe Gln Ile Ala Ile Phe Ala Phe Val Gly Ile Glu Leu
 195 200 205

Ala Gly Thr Ala Ala Ala Glu Thr Glu Asn Pro Thr Lys Thr Leu Pro
 210 215 220

Arg Ala Ile Asn Ser Ile Pro Ile Arg Ile Val Val Phe Tyr Val Leu
 225 230 235 240

Ala Leu Ala Val Ile Met Met Val Thr Pro Trp Asp Gln Val Arg Ala
 245 250 255
 Asp Asn Ser Pro Phe Val Gln Met Phe Ala Leu Ala Gly Ile Pro Ala
 260 265 270
 Ala Ala Gly Ile Ile Asn Phe Val Val Ile Thr Ser Ala Ala Ser Ser
 275 280 285
 Ala Asn Ser Gly Ile Phe Ser Thr Ser Arg Met Leu Tyr Gly Leu Ser
 290 295 300
 Leu Glu Gly Ala Ala Pro Lys Arg Trp Ser Arg Leu Ser Lys Asn Leu
 305 310 315 320
 Val Pro Ala Arg Gly Leu Thr Phe Ser Val Ile Cys Leu Ile Pro Ala
 325 330 335
 Val Gly Leu Leu Tyr Ala Gly Gly Thr Val Ile Glu Ala Phe Thr Leu
 340 345 350
 Ile Thr Thr Val Ser Ser Val Leu Phe Met Val Val Trp Ser Tyr Ile
 355 360 365
 Leu Val Ala Tyr Ile Val Tyr Arg Arg Asn Ser Pro Glu Leu His Lys
 370 375 380
 Lys Ser Ile Phe Lys Met Pro Gly Gly Val Val Met Ala Val Val Val
 385 390 395 400
 Leu Val Phe Phe Ala Ala Met Leu Val Val Leu Ser Leu Glu Pro Asp
 405 410 415
 Thr Arg Ala Ala Leu Ile Ala Thr Pro Val Trp Phe Ile Ile Leu Gly
 420 425 430
 Ile Gly Trp Leu Ser Ile Gly Gly Ala Lys Gly Ala Lys His Arg Ser
 435 440 445
 Gln Ile Thr Ser His
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<210> 199
 <211> 1242
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1219)
 <223> RXA00090

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 atcggcgcag tggctcttcgt gatcatgatt gtgaggcaac gtg gcc gtg gat aaa 115
 Val Ala Val Asp Lys
 1 5

gat att gaa aac cgc acc tca gac ctt tct cga tgg gaa act atg gag	163
Asp Ile Glu Asn Arg Thr Ser Asp Leu Ser Arg Trp Glu Thr Met Glu	
10 15 20	
gaa tca gca acg gtc gag gga cgc acc gat gtc gaa cta gca tca gcg	211
Glu Ser Ala Thr Val Glu Gly Arg Thr Asp Val Glu Leu Ala Ser Ala	
25 30 35	
ccg agc aaa cga cgc acc tca ggt gca ttc caa aca gcg cgc gcc aag	259
Pro Ser Lys Arg Arg Thr Ser Gly Ala Phe Gln Thr Ala Arg Ala Lys	
40 45 50	
cgc cgc tac tgg atc atc atg gcc gcg ctg ctg gtc acc gcg ctt gcc	307
Arg Arg Tyr Trp Ile Ile Met Ala Ala Leu Leu Val Thr Ala Leu Ala	
55 60 65	
ttc acc tgg ggc ctc att tgg tac aag aac ccg atg ccc gtt ggg cat	355
Phe Thr Trp Gly Leu Ile Trp Tyr Lys Asn Pro Met Pro Val Gly His	
70 75 80 85	
ccg gcc ttc gcg ctg att gca gaa cga cgc atg gag tcg gtc ttt gtc	403
Pro Ala Phe Ala Leu Ile Ala Glu Arg Arg Met Glu Ser Val Phe Val	
90 95 100	
atg ctg att gtt gcg gtt tgc caa ggc ttt gcg acg gtt gcg ttc cag	451
Met Leu Ile Val Ala Val Cys Gln Gly Phe Ala Thr Val Ala Phe Gln	
105 110 115	
acc gtc acc aac aac cgc att atc acg ccg tcg atc atg ggc ttt gaa	499
Thr Val Thr Asn Asn Arg Ile Ile Thr Pro Ser Ile Met Gly Phe Glu	
120 125 130	
tct ctc tac aca ctg att cat acc tcc aca gtg ttc ttc ttc ggc gca	547
Ser Leu Tyr Thr Leu Ile His Thr Ser Thr Val Phe Phe Gly Ala	
135 140 145	
act gca ctg ctg gcc acc aga aat ctc gaa atg ttt gtc ggc cag ctg	595
Thr Ala Leu Leu Ala Thr Arg Asn Leu Glu Met Phe Val Gly Gln Leu	
150 155 160 165	
gtg atc atg gtt ctt ttg acc ttg gtc ctc tac acc tgg ctg ctt tcc	643
Val Ile Met Val Leu Leu Thr Leu Val Leu Tyr Thr Trp Leu Leu Ser	
170 175 180	
gga aaa cgc ggc gat atg cac gcc atg ctg ctt gtc ggc atc atc att	691
Gly Lys Arg Gly Asp Met His Ala Met Leu Leu Val Gly Ile Ile Ile	
185 190 195	
ggt ggc gga ctc gga tcc atc tcc acc ttt atg cag cgc att ctg acc	739
Gly Gly Gly Leu Gly Ser Ile Ser Thr Phe Met Gln Arg Ile Leu Thr	
200 205 210	
cca tca gaa ttc gat att ctt tcc gcc cga ctt ttc gga tca gta aac	787
Pro Ser Glu Phe Asp Ile Leu Ser Ala Arg Leu Phe Gly Ser Val Asn	
215 220 225	
aac gcg gaa acc gaa tac ttc cca att gct gtt cca cta gta gta gtg	835
Asn Ala Glu Thr Glu Tyr Phe Pro Ile Ala Val Pro Leu Val Val Val	
230 235 240 245	
gcg tcc gtc ttg ttg ctg cta agc tct cga cgc ctc aac gtt gta ggg	883

<400> 200															
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Trp	Glu	Thr	Met	Glu	Glu	Ser	Ala	Thr	Val	Glu	Gly	Arg	Thr	Asp	Val
			20					25					30		
Glu	Leu	Ala	Ser	Ala	Pro	Ser	Lys	Arg	Arg	Thr	Ser	Gly	Ala	Phe	Gln
		35					40					45			
Thr	Ala	Arg	Ala	Lys	Arg	Arg	Tyr	Trp	Ile	Ile	Met	Ala	Ala	Leu	Leu
	50					55					60				
Val	Thr	Ala	Leu	Ala	Phe	Thr	Trp	Gly	Leu	Ile	Trp	Tyr	Lys	Asn	Pro
65					70					75					80
Met	Pro	Val	Gly	His	Pro	Ala	Phe	Ala	Leu	Ile	Ala	Glu	Arg	Arg	Met
				85					90					95	
Glu	Ser	Val	Phe	Val	Met	Leu	Ile	Val	Ala	Val	Cys	Gln	Gly	Phe	Ala
			100					105					110		

Thr Val Ala Phe Gln Thr Val Thr Asn Asn Arg Ile Ile Thr Pro Ser
 115 120 125
 Ile Met Gly Phe Glu Ser Leu Tyr Thr Leu Ile His Thr Ser Thr Val
 130 135 140
 Phe Phe Phe Gly Ala Thr Ala Leu Leu Ala Thr Arg Asn Leu Glu Met
 145 150 155 160
 Phe Val Gly Gln Leu Val Ile Met Val Leu Leu Thr Leu Val Leu Tyr
 165 170 175
 Thr Trp Leu Leu Ser Gly Lys Arg Gly Asp Met His Ala Met Leu Leu
 180 185 190
 Val Gly Ile Ile Ile Gly Gly Gly Leu Gly Ser Ile Ser Thr Phe Met
 195 200 205
 Gln Arg Ile Leu Thr Pro Ser Glu Phe Asp Ile Leu Ser Ala Arg Leu
 210 215 220
 Phe Gly Ser Val Asn Asn Ala Glu Thr Glu Tyr Phe Pro Ile Ala Val
 225 230 235 240
 Pro Leu Val Val Val Ala Ser Val Leu Leu Leu Leu Ser Ser Arg Arg
 245 250 255
 Leu Asn Val Val Gly Leu Gly Lys Asp Ala Ala Thr Asn Leu Gly Ile
 260 265 270
 Asn His Arg Arg Ser Ser Ile Tyr Thr Leu Val Leu Val Ser Val Leu
 275 280 285
 Met Ala Val Ser Thr Ala Leu Val Gly Pro Met Thr Phe Leu Gly Phe
 290 295 300
 Leu Val Ala Thr Leu Ala Tyr Gln Phe Ala Asp Thr Tyr Asp His Arg
 305 310 315 320
 Tyr Ile Leu Pro Met Ser Ala Leu Ile Gly Phe Val Val Leu Ser Gly
 325 330 335
 Ala Tyr Phe Val Met Asn His Val Phe Arg Ala Gln Gly Val Val Ser
 340 345 350
 Ile Ile Ile Glu Met Val Gly Gly Thr Val Phe Leu Ile Val Ile Leu
 355 360 365
 Arg Lys Gly Arg Leu
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<211> 1122

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1099)

<223> RXA00089

<400> 201

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tgacacacaaa tcggtttaac agggaagggg atcggcactg atg gca aca cca gca 115
Met Ala Thr Pro Ala
1 5

tcg gct ccc act tcc gaa cca cgt ctc aaa cgc acc aga gcc aag ctt 163
Ser Ala Pro Thr Ser Glu Pro Arg Leu Lys Arg Thr Arg Ala Lys Leu
10 15 20

ttt gat tgg aag ctt ctc atc ggc atc att ttc gtc gcc ggc ctc gtg 211
Phe Asp Trp Lys Leu Leu Ile Gly Ile Ile Phe Val Ala Gly Leu Val
25 30 35

gtg ctt tcc ctc ctc acc ggc caa tac gac att ttc ggt ggc gat gat 259
Val Leu Ser Leu Leu Thr Gly Gln Tyr Asp Ile Phe Gly Gly Asp Asp
40 45 50

ggc caa ctg atg ttc gag gca gtt cgc atc ccg cgt acc gtt tcc ctc 307
Gly Gln Leu Met Phe Glu Ala Val Arg Ile Pro Arg Thr Val Ser Leu
55 60 65

att ttg toc ggt gca gca atg gcg atg tgt ggc tta gtc atg cag ctg 355
Ile Leu Ser Gly Ala Ala Met Ala Met Cys Gly Leu Val Met Gln Leu
70 75 80 85

ttg acc caa aac aaa ttc gtg gaa ccc agc acc aca gga aca acc gaa 403
Leu Thr Gln Asn Lys Phe Val Glu Pro Ser Thr Thr Gly Thr Thr Glu
90 95 100

tgg gca ggt ctt ggc ctc ctc ttc gtg att tac ttc gtg cca gcc gcg 451
Trp Ala Gly Leu Gly Leu Leu Phe Val Ile Tyr Phe Val Pro Ala Ala
105 110 115

acc gtt ttg gat cgc atg ctc ggt gcc gtg gtg ttt tcc ttc atc gga 499
Thr Val Leu Asp Arg Met Leu Gly Ala Val Val Phe Ser Phe Ile Gly
120 125 130

acc atg gtg ttc ttc ctc ttt cta cgc cga gta aca ctg cgt tcc tca 547
Thr Met Val Phe Phe Leu Phe Leu Arg Arg Val Thr Leu Arg Ser Ser
135 140 145

ttg atc gtc ccg att atc ggc atc atg ctc ggt gcc gtg gtg tca tcg 595
Leu Ile Val Pro Ile Ile Gly Ile Met Leu Gly Ala Val Val Ser Ser
150 155 160 165

atc tcc agc ttc ttc gcc ttg caa ttc gac atg ctc cag caa ttg gga 643
Ile Ser Ser Phe Phe Ala Leu Gln Phe Asp Met Leu Gln Gln Leu Gly
170 175 180

aca tgg ttt gcg ggt tcc ttt aat aca gtg ttc cgc gga cag tac gaa 691
Thr Trp Phe Ala Gly Ser Phe Asn Thr Val Phe Arg Gly Gln Tyr Glu
185 190 195

gtg ctg tgg atc gtt gtc atc gtc gtt att gca gtg ttc ttc ttc gca 739
Val Leu Trp Ile Val Val Ile Val Val Ile Ala Val Phe Phe Phe Ala
200 205 210

gac cgg ctc acc gta gct ggc ctt ggc gag gaa atc gcg aca aac gtg 787

Asp Arg Leu Thr Val Ala Gly Leu Gly Glu Glu Ile Ala Thr Asn Val
 215 220 225
 ggt ctc aat tac aac cgc atg gtc ctt atc gga act ggc ctc atc gcc 835
 Gly Leu Asn Tyr Asn Arg Met Val Leu Ile Gly Thr Gly Leu Ile Ala
 230 235 240 245
 atc gca aca ggt gtg gtc acc gtc gtg gtt ggt agc ctg cca ttc ctc 883
 Ile Ala Thr Gly Val Val Thr Val Val Val Gly Ser Leu Pro Phe Leu
 250 255 260
 gga ctc atc gtg ccc aac gtt gtg tcc atg ttc cgt ggc gat gac ctg 931
 Gly Leu Ile Val Pro Asn Val Val Ser Met Phe Arg Gly Asp Asp Leu
 265 270 275
 cgc tcg aac ctg cca tgg gta tgc cta acc ggc atc gcg atc gta acc 979
 Arg Ser Asn Leu Pro Trp Val Cys Leu Thr Gly Ile Ala Ile Val Thr
 280 285 290
 att tgt gac ttg atc agc cga acc atc atc gcg cct ttc gaa att cca 1027
 Ile Cys Asp Leu Ile Ser Arg Thr Ile Ile Ala Pro Phe Glu Ile Pro
 295 300 305
 gtt tca gta atc ctg ggc atc atc ggc gca gtg gtc ttc gtg atc atg 1075
 Val Ser Val Ile Leu Gly Ile Ile Gly Ala Val Val Phe Val Ile Met
 310 315 320 325
 att gtg agg caa cgt ggc cgt gga taaagatat gaaaaccgca cct 1122
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<210> 202

<211> 333

<212> PRT

<213> Corynebacterium glutamicum

<400> 202

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 20 25 30
 Val Ala Gly Leu Val Val Leu Ser Leu Leu Thr Gly Gln Tyr Asp Ile
 35 40 45
 Phe Gly Gly Asp Asp Gly Gln Leu Met Phe Glu Ala Val Arg Ile Pro
 50 55 60
 Arg Thr Val Ser Leu Ile Leu Ser Gly Ala Ala Met Ala Met Cys Gly
 65 70 75 80
 Leu Val Met Gln Leu Leu Thr Gln Asn Lys Phe Val Glu Pro Ser Thr
 85 90 95
 Thr Gly Thr Thr Glu Trp Ala Gly Leu Gly Leu Leu Phe Val Ile Tyr
 100 105 110
 Phe Val Pro Ala Ala Thr Val Leu Asp Arg Met Leu Gly Ala Val Val
 115 120 125

Phe Ser Phe Ile Gly Thr Met Val Phe Phe Leu Phe Leu Arg Arg Val
 130 135 140
 Thr Leu Arg Ser Ser Leu Ile Val Pro Ile Ile Gly Ile Met Leu Gly
 145 150 155 160
 Ala Val Val Ser Ser Ile Ser Ser Phe Phe Ala Leu Gln Phe Asp Met
 165 170 175
 Leu Gln Gln Leu Gly Thr Trp Phe Ala Gly Ser Phe Asn Thr Val Phe
 180 185 190
 Arg Gly Gln Tyr Glu Val Leu Trp Ile Val Val Ile Val Val Ile Ala
 195 200 205
 Val Phe Phe Phe Ala Asp Arg Leu Thr Val Ala Gly Leu Gly Glu Glu
 210 215 220
 Ile Ala Thr Asn Val Gly Leu Asn Tyr Asn Arg Met Val Leu Ile Gly
 225 230 235 240
 Thr Gly Leu Ile Ala Ile Ala Thr Gly Val Val Thr Val Val Val Gly
 245 250 255
 Ser Leu Pro Phe Leu Gly Leu Ile Val Pro Asn Val Val Ser Met Phe
 260 265 270
 Arg Gly Asp Asp Leu Arg Ser Asn Leu Pro Trp Val Cys Leu Thr Gly
 275 280 285
 Ile Ala Ile Val Thr Ile Cys Asp Leu Ile Ser Arg Thr Ile Ile Ala
 290 295 300
 Pro Phe Glu Ile Pro Val Ser Val Ile Leu Gly Ile Ile Gly Ala Val
 305 310 315 320
 Val Phe Val Ile Met Ile Val Arg Gln Arg Gly Arg Gly
 325 330

<210> 203

<211> 749

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(726)

<223> RXN01285

<400> 203

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aac ggc tgc ggc aaa tcc acc ctg ctc cgc ggt ttc tcc cgc gtg ctc 96
 Asn Gly Cys Gly Lys Ser Thr Leu Leu Arg Gly Phe Ser Arg Val Leu
 20 25 30

aat ccg cag cac ggc aaa gtg ctt ctc gac ggt cgg caa ctc gat tca 144

Asn	Pro	Gln	His	Gly	Lys	Val	Leu	Leu	Asp	Gly	Arg	Gln	Leu	Asp	Ser		
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ttc	aag	cct	aaa	gag	atc	gcc	cga	gaa	cta	ggc	ctg	ctg	cca	cag	acc	192	
Phe	Lys	Pro	Lys	Glu	Ile	Ala	Arg	Glu	Leu	Gly	Leu	Leu	Pro	Gln	Thr		
	50					55				60							
tcc	atc	gcc	cca	gaa	ggc	atc	cgg	gtt	tac	gat	ctc	atc	gcg	cgc	ggg	240	
Ser	Ile	Ala	Pro	Glu	Gly	Ile	Arg	Val	Tyr	Asp	Leu	Ile	Ala	Arg	Gly		
	65				70					75					80		
cgc	gct	ccc	tac	caa	agc	ctc	ata	caa	caa	tgg	cgc	acc	tcc	gac	gaa	288	
Arg	Ala	Pro	Tyr	Gln	Ser	Leu	Ile	Gln	Gln	Trp	Arg	Thr	Ser	Asp	Glu		
				85					90						95		
gac	gcc	gtc	gcg	caa	gcg	ctc	gcc	tcc	acg	aat	ctc	acc	gaa	ctt	gca	336	
Asp	Ala	Val	Ala	Gln	Ala	Leu	Ala	Ser	Thr	Asn	Leu	Thr	Glu	Leu	Ala		
			100					105					110				
gct	cgc	ctc	gtc	gat	gaa	ctc	tcc	ggg	ggc	cag	cgc	caa	cga	gtg	tgg	384	
Ala	Arg	Leu	Val	Asp	Glu	Leu	Ser	Gly	Gly	Gln	Arg	Gln	Arg	Val	Trp		
	115						120						125				
gtg	gcc	atg	ttg	ctc	gcc	cag	caa	aca	ccg	atc	atg	ctt	ctc	gac	gag	432	
Val	Ala	Met	Leu	Leu	Ala	Gln	Gln	Thr	Pro	Ile	Met	Leu	Leu	Asp	Glu		
	130					135					140						
ccc	acc	acc	ttc	ctc	gac	atc	gcc	cac	caa	tac	gaa	ctc	ttg	gaa	ttg	480	
Pro	Thr	Thr	Phe	Leu	Asp	Ile	Ala	His	Gln	Tyr	Glu	Leu	Leu	Glu	Leu		
	145				150					155					160		
ctg	cgc	gca	ttc	aac	gag	gcc	ggg	aaa	act	gtg	gtc	act	gtg	ctt	cac	528	
Leu	Arg	Ala	Phe	Asn	Glu	Ala	Gly	Lys	Thr	Val	Val	Thr	Val	Leu	His		
				165					170					175			
gat	ctc	aac	caa	gcc	gcc	cgc	tac	gcc	gac	cac	ctc	atc	gtg	atg	aaa	576	
Asp	Leu	Asn	Gln	Ala	Ala	Arg	Tyr	Ala	Asp	His	Leu	Ile	Val	Met	Lys		
			180					185						190			
gat	ggg	cac	gta	cat	gcc	acg	ggc	aca	ccg	gag	gaa	gtc	tta	act	gcc	624	
Asp	Gly	His	Val	His	Ala	Thr	Gly	Thr	Pro	Glu	Glu	Val	Leu	Thr	Ala		
		195					200					205					
gag	atg	gtt	caa	gga	gtt	ttt	ggc	ctg	ccc	tgc	atc	atc	tcc	cca	gac	672	
Glu	Met	Val	Gln	Gly	Val	Phe	Gly	Leu	Pro	Cys	Ile	Ile	Ser	Pro	Asp		
	210					215					220						
ccc	gtc	aca	gga	acc	ccc	acc	gtc	gtt	ccc	ctc	agt	cgg	tct	cgc	gca	720	
Pro	Val	Thr	Gly	Thr	Pro	Thr	Val	Val	Pro	Leu	Ser	Arg	Ser	Arg	Ala		
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gga	gct	taagtagcta	ccccccaac	gga												749	
Gly	Ala																

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<211> 242

<212> PRT

<213> Corynebacterium glutamicum

<400> 204

Leu Asn Val Thr Ile Pro Asp Asn Thr Phe Thr Ala Ile Ile Gly Pro
 1 5 10 15

Asn Gly Cys Gly Lys Ser Thr Leu Leu Arg Gly Phe Ser Arg Val Leu
 20 25 30

Asn Pro Gln His Gly Lys Val Leu Leu Asp Gly Arg Gln Leu Asp Ser
 35 40 45

Phe Lys Pro Lys Glu Ile Ala Arg Glu Leu Gly Leu Leu Pro Gln Thr
 50 55 60

Ser Ile Ala Pro Glu Gly Ile Arg Val Tyr Asp Leu Ile Ala Arg Gly
 65 70 75 80

Arg Ala Pro Tyr Gln Ser Leu Ile Gln Gln Trp Arg Thr Ser Asp Glu
 85 90 95

Asp Ala Val Ala Gln Ala Leu Ala Ser Thr Asn Leu Thr Glu Leu Ala
 100 105 110

Ala Arg Leu Val Asp Glu Leu Ser Gly Gly Gln Arg Gln Arg Val Trp
 115 120 125

Val Ala Met Leu Leu Ala Gln Gln Thr Pro Ile Met Leu Leu Asp Glu
 130 135 140

Pro Thr Thr Phe Leu Asp Ile Ala His Gln Tyr Glu Leu Leu Glu Leu
 145 150 155 160

Leu Arg Ala Phe Asn Glu Ala Gly Lys Thr Val Val Thr Val Leu His
 165 170 175

Asp Leu Asn Gln Ala Ala Arg Tyr Ala Asp His Leu Ile Val Met Lys
 180 185 190

Asp Gly His Val His Ala Thr Gly Thr Pro Glu Glu Val Leu Thr Ala
 195 200 205

Glu Met Val Gln Gly Val Phe Gly Leu Pro Cys Ile Ile Ser Pro Asp
 210 215 220

Pro Val Thr Gly Thr Pro Thr Val Val Pro Leu Ser Arg Ser Arg Ala
 225 230 235 240

Gly Ala

<210> 205

<211> 566

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(543)

<223> FRXA01285

<400> 205

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gcg cgc ggg cgc gct ccc tac caa agc ctc ata caa caa tgg cgc acc 96
 Ala Arg Gly Arg Ala Pro Tyr Gln Ser Leu Ile Gln Gln Trp Arg Thr
 20 25 30

tcc gac gaa gac gcc gtc gcg caa gcg ctc gcc tcc acg aat ctc acc 144
 Ser Asp Glu Asp Ala Val Ala Gln Ala Leu Ala Ser Thr Asn Leu Thr
 35 40 45

gaa ctt gca gct cgc ctc gtc gat gaa ctc tcc ggt ggc cag cgc caa 192
 Glu Leu Ala Ala Arg Leu Val Asp Glu Leu Ser Gly Gly Gln Arg Gln
 50 55 60

cga gtg tgg gtg gcc atg ttg ctc gcc cag caa aca ccg atc atg ctt 240
 Arg Val Trp Val Ala Met Leu Leu Ala Gln Gln Thr Pro Ile Met Leu
 65 70 75 80

ctc gac gag ccc acc acc ttc ctc gac atc gcc cac caa tac gaa ctc 288
 Leu Asp Glu Pro Thr Thr Phe Leu Asp Ile Ala His Gln Tyr Glu Leu
 85 90 95

ttg gaa ttg ctg cgc gca ttc aac gag gcc ggg aaa act gtg gtc act 336
 Leu Glu Leu Leu Arg Ala Phe Asn Glu Ala Gly Lys Thr Val Val Thr
 100 105 110

gtg ctt cac gat ctc aac caa gcc gcc cgc tac gcc gac cac ctc atc 384
 Val Leu His Asp Leu Asn Gln Ala Ala Arg Tyr Ala Asp His Leu Ile
 115 120 125

gtg atg aaa gat ggg cac gta cat gcc acg ggc aca ccg gag gaa gtc 432
 Val Met Lys Asp Gly His Val His Ala Thr Gly Thr Pro Glu Glu Val
 130 135 140

tta act gcc gag atg gtt caa gga gtt ttt ggc ctg ccc tgc atc atc 480
 Leu Thr Ala Glu Met Val Gln Gly Val Phe Gly Leu Pro Cys Ile Ile
 145 150 155 160

tcc cca gac ccc gtc aca gga acc ccc acc gtc gtt ccc ctc agt cgg 528
 Ser Pro Asp Pro Val Thr Gly Thr Pro Thr Val Val Pro Leu Ser Arg
 165 170 175

tct cgc gca gga gct taagtagcta cccctccaac gga 566
 Ser Arg Ala Gly Ala
 180

<210> 206

<211> 181

<212> PRT

<213> Corynebacterium glutamicum

<400> 206

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Ala Arg Gly Arg Ala Pro Tyr Gln Ser Leu Ile Gln Gln Trp Arg Thr
 20 25 30

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Met Ala Ile Val Ser
1 5

ctc gac aac gtc acc gta tcc att gaa gga aaa aag ctt ctc gac gcc 163
Leu Asp Asn Val Thr Val Ser Ile Glu Gly Lys Lys Leu Leu Asp Ala
10 15 20

gtc tcc ctc aag gcc tac ccc ggg gaa gtg ttg gga ctc atc ggc cca 211
Val Ser Leu Lys Ala Tyr Pro Gly Glu Val Leu Gly Leu Ile Gly Pro
25 30 35

aac ggt gcc gga aaa tcc act ctg ctg agt gtc ctt tca ggc gat cgg 259
Asn Gly Ala Gly Lys Ser Thr Leu Leu Ser Val Leu Ser Gly Asp Arg
40 45 50

ctt ccc gat tca ggc gaa gtc aac gtc ggt ggc tta gat ccc gca aca 307

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Leu	Pro	Asp	Ser	Gly	Glu	Val	Asn	Val	Gly	Gly	Leu	Asp	Pro	Ala	Thr		
	55					60					65						
gca	gcg	gca	tcc	gat	atg	gcc	agg	gtg	cga	gca	gtc	atg	ctt	caa	gat	355	
Ala	Ala	Ala	Ser	Asp	Met	Ala	Arg	Val	Arg	Ala	Val	Met	Leu	Gln	Asp		
70					75				80						85		
gtc	agc	gtg	gca	ttt	tcc	ttc	ctc	gtg	tgg	gac	gtc	gta	gaa	atg	ggc	403	
Val	Ser	Val	Ala	Phe	Ser	Phe	Leu	Val	Trp	Asp	Val	Val	Glu	Met	Gly		
				90					95						100		
agg	cgg	ccg	tgg	cag	aag	gcg	tca	acc	ccc	gaa	gag	gat	cat	gaa	atc	451	
Arg	Arg	Pro	Trp	Gln	Lys	Ala	Ser	Thr	Pro	Glu	Glu	Asp	His	Glu	Ile		
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Ile	Glu	Ala	Ala	Leu	Ala	Ala	Thr	Ser	Val	Ser	His	Leu	Ala	Glu	Arg		
			120					125					130				
gaa	atc	acc	aca	ctg	tca	ggc	ggc	gag	cgg	gca	cgc	gtt	gcc	ttg	tcc	547	
Glu	Ile	Thr	Thr	Leu	Ser	Gly	Gly	Glu	Arg	Ala	Arg	Val	Ala	Leu	Ser		
			135				140					145					
cgt	gtc	ctt	gct	cag	caa	acc	ccc	att	gtg	ctg	ttg	gac	gaa	cca	aca	595	
Arg	Val	Leu	Ala	Gln	Gln	Thr	Pro	Ile	Val	Leu	Leu	Asp	Glu	Pro	Thr		
150					155					160					165		
gcc	gcg	atg	gat	atc	agc	cac	caa	gaa	caa	act	ctg	ggc	aca	gcg	cga	643	
Ala	Ala	Met	Asp	Ile	Ser	His	Gln	Glu	Gln	Thr	Leu	Gly	Thr	Ala	Arg		
				170					175						180		
gca	ctg	gca	gcc	gcc	ggg	gca	gca	gtg	att	gtg	gtc	ctt	cat	gat	ctc	691	
Ala	Leu	Ala	Ala	Ala	Gly	Ala	Ala	Val	Ile	Val	Val	Leu	His	Asp	Leu		
			185					190						195			
aat	gcg	gcc	gct	gca	tat	tgc	gac	agc	att	gtg	tgt	ctc	agt	gat	ggt	739	
Asn	Ala	Ala	Ala	Ala	Tyr	Cys	Asp	Ser	Ile	Val	Cys	Leu	Ser	Asp	Gly		
			200				205						210				
cga	gtg	att	gcc	tcc	ggt	tct	gtt	gat	cag	gtg	tat	tcc	acg	gaa	acg	787	
Arg	Val	Ile	Ala	Ser	Gly	Ser	Val	Asp	Gln	Val	Tyr	Ser	Thr	Glu	Thr		
			215				220					225					
ctg	tcc	cgt	gtt	tac	ggt	tgg	cct	atc	agg	gtc	gat	cat	agt	gga	aaa	835	
Leu	Ser	Arg	Val	Tyr	Gly	Trp	Pro	Ile	Arg	Val	Asp	His	Ser	Gly	Lys		
230					235					240					245		
tat	gtt	cga	gtg	gag	ccg	gac	cgt	tct	gag	gcg	aat	tta	ccc	tcc	gta	883	
Tyr	Val	Arg	Val	Glu	Pro	Asp	Arg	Ser	Glu	Ala	Asn	Leu	Pro	Ser	Val		
				250					255						260		
cta	cag	gtg	aaa	aat	acg	gtt	tca	cca	gct	tagatacatg	actaactaag					933	
Leu	Gln	Val	Lys	Asn	Thr	Val	Ser	Pro	Ala								
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gtt																	936

<210> 208

<211> 271

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 208

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Lys Leu Leu Asp Ala Val Ser Leu Lys Ala Tyr Pro Gly Glu Val Leu
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Gly Leu Ile Gly Pro Asn Gly Ala Gly Lys Ser Thr Leu Leu Ser Val
 35             40             45

Leu Ser Gly Asp Arg Leu Pro Asp Ser Gly Glu Val Asn Val Gly Gly
 50             55             60

Leu Asp Pro Ala Thr Ala Ala Ala Ser Asp Met Ala Arg Val Arg Ala
 65             70             75             80

Val Met Leu Gln Asp Val Ser Val Ala Phe Ser Phe Leu Val Trp Asp
          85             90             95

Val Val Glu Met Gly Arg Arg Pro Trp Gln Lys Ala Ser Thr Pro Glu
 100             105             110

Glu Asp His Glu Ile Ile Glu Ala Ala Leu Ala Ala Thr Ser Val Ser
 115             120             125

His Leu Ala Glu Arg Glu Ile Thr Thr Leu Ser Gly Gly Glu Arg Ala
 130             135             140

Arg Val Ala Leu Ser Arg Val Leu Ala Gln Gln Thr Pro Ile Val Leu
 145             150             155             160

Leu Asp Glu Pro Thr Ala Ala Met Asp Ile Ser His Gln Glu Gln Thr
          165             170             175

Leu Gly Thr Ala Arg Ala Leu Ala Ala Ala Gly Ala Ala Val Ile Val
          180             185             190

Val Leu His Asp Leu Asn Ala Ala Ala Tyr Cys Asp Ser Ile Val
          195             200             205

Cys Leu Ser Asp Gly Arg Val Ile Ala Ser Gly Ser Val Asp Gln Val
 210             215             220

Tyr Ser Thr Glu Thr Leu Ser Arg Val Tyr Gly Trp Pro Ile Arg Val
 225             230             235             240

Asp His Ser Gly Lys Tyr Val Arg Val Glu Pro Asp Arg Ser Glu Ala
          245             250             255

Asn Leu Pro Ser Val Leu Gln Val Lys Asn Thr Val Ser Pro Ala
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<210> 209

<211> 903

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS
 <222> (101)..(880)
 <223> RXN03080

<400> 209

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cagcatgcgc aagcgacgcg gattggggct gtaaaaactc atg cct caa tta gtt 115
                                         Met Pro Gln Leu Val
                                         1                               5

gaa att cgt gat ctc aac gtt gaa ttc ccc tct cgc cat gca gtg aaa 163
Glu Ile Arg Asp Leu Asn Val Glu Phe Pro Ser Arg His Ala Val Lys
                               10                               15                               20

aac gtg tct ttt tct gca cct gct gga aaa gtc acc gca ctg att ggc 211
Asn Val Ser Phe Ser Ala Pro Ala Gly Lys Val Thr Ala Leu Ile Gly
                               25                               30                               35

cca aat ggt gct ggt aaa agt act gcc ctt tcg gcg att gca gga ttg 259
Pro Asn Gly Ala Gly Lys Ser Thr Ala Leu Ser Ala Ile Ala Gly Leu
                               40                               45                               50

gtt gaa tcc acc ggc gag gta atg gtt ggt ggg agt ggg gtt gcg tcg 307
Val Glu Ser Thr Gly Glu Val Met Val Gly Gly Ser Gly Val Ala Ser
                               55                               60                               65

aaa agc gct aaa gcc cga gcc cgc ctg ctc tca ctc gtg ccg caa aac 355
Lys Ser Ala Lys Ala Arg Ala Arg Leu Leu Ser Leu Val Pro Gln Asn
                               70                               75                               80                               85

acc gag ttg cgc att ggt ttt agt gca cgc gac gtt gtc gcg atg ggc 403
Thr Glu Leu Arg Ile Gly Phe Ser Ala Arg Asp Val Val Ala Met Gly
                               90                               95                               100

cgc tac ccg cat cgt ggc cgc ttc gcc gtg gag acc gac gca gat cga 451
Arg Tyr Pro His Arg Gly Arg Phe Ala Val Glu Thr Asp Ala Asp Arg
                               105                               110                               115

cgc gcc acc gat gac gcc ctg cgc gcc atc aac gcg ctc gac atc gcc 499
Arg Ala Thr Asp Asp Ala Leu Arg Ala Ile Asn Ala Leu Asp Ile Ala
                               120                               125                               130

gag cag ccc gtc aac gaa tta tcg ggc ggc cag cag cag ctc atc cac 547
Glu Gln Pro Val Asn Glu Leu Ser Gly Gly Gln Gln Gln Leu Ile His
                               135                               140                               145

atc ggc cga gcg ctc gcc caa gac acc gcc gtc gtg ctt ctc gac gag 595
Ile Gly Arg Ala Leu Ala Gln Asp Thr Ala Val Val Leu Leu Asp Glu
                               150                               155                               160                               165

ccc gtc tcc gcc ctt gat cta cgg cac caa gtt gaa gtc ctt caa ctc 643
Pro Val Ser Ala Leu Asp Leu Arg His Gln Val Glu Val Leu Gln Leu
                               170                               175                               180

ctg cgc gcc cga gct aat tcc ggc acc acc gtg atc gtc gtc ctt cac 691
Leu Arg Ala Arg Ala Asn Ser Gly Thr Thr Val Ile Val Val Leu His
                               185                               190                               195

gat ctc aac cac gtt gcc cgt tgg tgc gac cat gca gtg ttg atg gcc 739
Asp Leu Asn His Val Ala Arg Trp Cys Asp His Ala Val Leu Met Ala

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200	205	210	
gac ggc gaa gtt gtc tcc caa ggt gac atc cgc gag gtg ctc gaa cct			787
Asp Gly Glu Val Val Ser Gln Gly Asp Ile Arg Glu Val Leu Glu Pro			
215	220	225	
gcc aca ctg tcc acc gtg tac gga ctg ccc att gcg gtg cgc gat gat			835
Ala Thr Leu Ser Thr Val Tyr Gly Leu Pro Ile Ala Val Arg Asp Asp			
230	235	240	245
ccc gaa acc agc tca ctt cgc gtg atc ccg cat cca aat ccc ttt			880
Pro Glu Thr Ser Ser Leu Arg Val Ile Pro His Pro Asn Pro Phe			
250	255	260	
tgattgaaag tttgacttaa aaa			903
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<213> Corynebacterium glutamicum			
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Arg His Ala Val Lys Asn Val Ser Phe Ser Ala Pro Ala Gly Lys Val			
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Thr Ala Leu Ile Gly Pro Asn Gly Ala Gly Lys Ser Thr Ala Leu Ser			
35	40	45	
Ala Ile Ala Gly Leu Val Glu Ser Thr Gly Glu Val Met Val Gly Gly			
50	55	60	
Ser Gly Val Ala Ser Lys Ser Ala Lys Ala Arg Ala Arg Leu Leu Ser			
65	70	75	80
Leu Val Pro Gln Asn Thr Glu Leu Arg Ile Gly Phe Ser Ala Arg Asp			
85	90	95	
Val Val Ala Met Gly Arg Tyr Pro His Arg Gly Arg Phe Ala Val Glu			
100	105	110	
Thr Asp Ala Asp Arg Arg Ala Thr Asp Asp Ala Leu Arg Ala Ile Asn			
115	120	125	
Ala Leu Asp Ile Ala Glu Gln Pro Val Asn Glu Leu Ser Gly Gly Gln			
130	135	140	
Gln Gln Leu Ile His Ile Gly Arg Ala Leu Ala Gln Asp Thr Ala Val			
145	150	155	160
Val Leu Leu Asp Glu Pro Val Ser Ala Leu Asp Leu Arg His Gln Val			
165	170	175	
Glu Val Leu Gln Leu Leu Arg Ala Arg Ala Asn Ser Gly Thr Thr Val			
180	185	190	
Ile Val Val Leu His Asp Leu Asn His Val Ala Arg Trp Cys Asp His			
195	200	205	

Ala Val Leu Met Ala Asp Gly Glu Val Val Ser Gln Gly Asp Ile Arg
 210 215 220

Glu Val Leu Glu Pro Ala Thr Leu Ser Thr Val Tyr Gly Leu Pro Ile
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Ala Val Arg Asp Asp Pro Glu Thr Ser Ser Leu Arg Val Ile Pro His
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Pro Asn Pro Phe
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<210> 211
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <223> FRXA02864

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 Met Pro Gln Leu Val
 1 5

gaa att cgt gat ctc aac gtt gaa ttc ccc tct cgc cat gca gtg aaa 163
 Glu Ile Arg Asp Leu Asn Val Glu Phe Pro Ser Arg His Ala Val Lys
 10 15 20

aac gtg tct ttt tct gca cct gct gga aaa gtc acc gca ctg att ggc 211
 Asn Val Ser Phe Ser Ala Pro Ala Gly Lys Val Thr Ala Leu Ile Gly
 25 30 35

cca aat ggt gct ggt aaa agt act gcc ctt tcg gcg att gca gga ttg 259
 Pro Asn Gly Ala Gly Lys Ser Thr Ala Leu Ser Ala Ile Ala Gly Leu
 40 45 50

gtt gaa tcc acc ggc gag gta atg gtt ggt ggg agt ggg gtt gcg tcg 307
 Val Glu Ser Thr Gly Glu Val Met Val Gly Gly Ser Gly Val Ala Ser
 55 60 65

aaa agc gct aaa gcc cga gcc cgc ctg ctc tca ctc gtg ccg caa aac 355
 Lys Ser Ala Lys Ala Arg Ala Arg Leu Leu Ser Leu Val Pro Gln Asn
 70 75 80 85

acc gag ttg cgc att ggt ttt agt gca cgc gac gtt gtc gcg atg ggc 403
 Thr Glu Leu Arg Ile Gly Phe Ser Ala Arg Asp Val Val Ala Met Gly
 90 95 100

cgc tac ccg cat cgt ggc cgc ttc gcc gtg gag acc gac gca gat cga 451
 Arg Tyr Pro His Arg Gly Arg Phe Ala Val Glu Thr Asp Ala Asp Arg
 105 110 115

cgc gcc acc gat gac gcc ctg cgc gcc atc aac gcg ctc gac atc gcc 499
 Arg Ala Thr Asp Asp Ala Leu Arg Ala Ile Asn Ala Leu Asp Ile Ala

120	125	130	
gag cag ccc gtc aac gaa tta tgc ggc ggc cag cag cag ctc atc cac			547
Glu Gln Pro Val Asn Glu Leu Ser Gly Gly Gln Gln Gln Leu Ile His			
135	140	145	
atc ggc cga gcg ctc gcc caa gac acc gcc gtc gtg ctt ctc gac gag			595
Ile Gly Arg Ala Leu Ala Gln Asp Thr Ala Val Val Leu Leu Asp Glu			
150	155	160	165
ccc gtc tcc gcc ctt gat cta cgg cac caa gtt gaa gtc ctt caa ctc			643
Pro Val Ser Ala Leu Asp Leu Arg His Gln Val Glu Val Leu Gln Leu			
170	175	180	
ctg cgc gcc cga gct aat tcc ggc acc acc gtg atc gtc gtc ctt cac			691
Leu Arg Ala Arg Ala Asn Ser Gly Thr Thr Val Ile Val Val Leu His			
185	190	195	
gat ctc aac cac gtt gcc cgt tgg tgc gac cat gca gtg ttg atg gcc			739
Asp Leu Asn His Val Ala Arg Trp Cys Asp His Ala Val Leu Met Ala			
200	205	210	
gac ggc gaa gtt gtc tcc caa ggt gac atc cgc gag gtg ctc gaa cct			787
Asp Gly Glu Val Val Ser Gln Gly Asp Ile Arg Glu Val Leu Glu Pro			
215	220	225	
gcc aca ctg tcc acc gtg tac gga ctg ccc att gcg gtg cgc gat gat			835
Ala Thr Leu Ser Thr Val Tyr Gly Leu Pro Ile Ala Val Arg Asp Asp			
230	235	240	245
ccc gaa acc agc tca ctt cgc gtg atc ccg cat cca aat ccc ttt			880
Pro Glu Thr Ser Ser Leu Arg Val Ile Pro His Pro Asn Pro Phe			
250	255	260	
tgattgaaag tttgacttaa aaa			903

<210> 212

<211> 260

<212> PRT

<213> Corynebacterium glutamicum

<400> 212

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Arg	His	Ala	Val	Lys	Asn	Val	Ser	Phe	Ser	Ala	Pro	Ala	Gly	Lys	Val
		20						25					30		

Thr	Ala	Leu	Ile	Gly	Pro	Asn	Gly	Ala	Gly	Lys	Ser	Thr	Ala	Leu	Ser
		35					40					45			

Ala	Ile	Ala	Gly	Leu	Val	Glu	Ser	Thr	Gly	Glu	Val	Met	Val	Gly	Gly
	50					55						60			

Ser	Gly	Val	Ala	Ser	Lys	Ser	Ala	Lys	Ala	Arg	Ala	Arg	Leu	Leu	Ser
65					70					75				80	

Leu	Val	Pro	Gln	Asn	Thr	Glu	Leu	Arg	Ile	Gly	Phe	Ser	Ala	Arg	Asp
				85					90					95	

Val Val Ala Met Gly Arg Tyr Pro His Arg Gly Arg Phe Ala Val Glu
 100 105 110

Thr Asp Ala Asp Arg Arg Ala Thr Asp Asp Ala Leu Arg Ala Ile Asn
 115 120 125

Ala Leu Asp Ile Ala Glu Gln Pro Val Asn Glu Leu Ser Gly Gly Gln
 130 135 140

Gln Gln Leu Ile His Ile Gly Arg Ala Leu Ala Gln Asp Thr Ala Val
 145 150 155 160

Val Leu Leu Asp Glu Pro Val Ser Ala Leu Asp Leu Arg His Gln Val
 165 170 175

Glu Val Leu Gln Leu Leu Arg Ala Arg Ala Asn Ser Gly Thr Thr Val
 180 185 190

Ile Val Val Leu His Asp Leu Asn His Val Ala Arg Trp Cys Asp His
 195 200 205

Ala Val Leu Met Ala Asp Gly Glu Val Val Ser Gln Gly Asp Ile Arg
 210 215 220

Glu Val Leu Glu Pro Ala Thr Leu Ser Thr Val Tyr Gly Leu Pro Ile
 225 230 235 240

Ala Val Arg Asp Asp Pro Glu Thr Ser Ser Leu Arg Val Ile Pro His
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Pro Asn Pro Phe
 260

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 <211> 1149
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1126)
 <223> RXN00523

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 Met Ser Leu Ser His
 1 5

caa ctc aag cgc cag cgc gca tcg cgc aac tcc cgc agg tgg ctg att 163
 Gln Leu Lys Arg Gln Arg Ala Ser Arg Asn Ser Arg Arg Trp Leu Ile
 10 15 20

gtt gcg gca ttg ggc gtc gtc acg ctt ggt att ttt gct ttt tct ttg 211
 Val Ala Ala Leu Gly Val Val Thr Leu Gly Ile Phe Ala Phe Ser Leu
 25 30 35

atg tgg ggc gag gtg ttt tat ggc cct gct cag gtg ctg aaa gtg ttg 259
 Met Trp Gly Glu Val Phe Tyr Gly Pro Ala Gln Val Leu Lys Val Leu

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gcg ggc gtg att ttt cag acg gtg ttg cgt aat cag ttg gcg tcg ccg Ala Gly Val Ile Phe Gln Thr Val Leu Arg Asn Gln Leu Ala Ser Pro 90 95 100			403
gat att atc ggc att tct tct ggc gcg tcg gcg gcg ggc gta att tgc Asp Ile Ile Gly Ile Ser Ser Gly Ala Ser Ala Ala Gly Val Ile Cys 105 110 115			451
att gtg ttt ttc ggg atg tcg cag tct gca gtg tcg gcg att tct ttg Ile Val Phe Phe Gly Met Ser Gln Ser Ala Val Ser Ala Ile Ser Leu 120 125 130			499
tgt gcg tcc ttg gct gtg gcg ttg ttg att tat ctg gtg gcg tat cgc Cys Ala Ser Leu Ala Val Ala Leu Leu Ile Tyr Leu Val Ala Tyr Arg 135 140 145			547
ggt ggt ttt tcg gcc acg cgt ctg att ctt acc ggc att ggt att gct Gly Gly Phe Ser Ala Thr Arg Leu Ile Leu Thr Gly Ile Gly Ile Ala 150 155 160 165			595
gcg atg ctg aat tca tta gtg tcg tat tcg ctg tcc aag gct gat tct Ala Met Leu Asn Ser Leu Val Ser Tyr Ser Leu Ser Lys Ala Asp Ser 170 175 180			643
tgg gat ctg ccg acc gcg acg cgc tgg ctt acc ggc tcg ctc aat ggt Trp Asp Leu Pro Thr Ala Thr Arg Trp Leu Thr Gly Ser Leu Asn Gly 185 190 195			691
gcg acg tgg gat cgt gcg atg ccg ctg att gtc acc act gtg gta ctc Ala Thr Trp Asp Arg Ala Met Pro Leu Ile Val Thr Thr Val Val Leu 200 205 210			739
att ccg ctg ctg gtg gct aat gcg cgc aat gtg gat ctt atg cgt ttg Ile Pro Leu Leu Val Ala Asn Ala Arg Asn Val Asp Leu Met Arg Leu 215 220 225			787
ggc aat gat tcc gcg gtg ggt ttg ggc gtt gct act aat cgc acg cgc Gly Asn Asp Ser Ala Val Gly Leu Gly Val Ala Thr Asn Arg Thr Arg 230 235 240 245			835
gtc att gcg att att gcc gct gtt gcg ctc atc gcc gtt gct acc gct Val Ile Ala Ile Ile Ala Ala Val Ala Leu Ile Ala Val Ala Thr Ala 250 255 260			883
gca tgc ggc ccg atc gca ttc gtg gcg ttt gtg tct ggc ccc att gcc Ala Cys Gly Pro Ile Ala Phe Val Ala Phe Val Ser Gly Pro Ile Ala 265 270 275			931
gcg cgc att tta ggc tcc ggc gga tcg ctc atc atc ccc tcc gca ctc Ala Arg Ile Leu Gly Ser Gly Gly Ser Leu Ile Ile Pro Ser Ala Leu 280 285 290			979

atc ggc ggg ttg atc gtg ctc atc gcc gac cta att ggc caa tac ttc 1027
 Ile Gly Gly Leu Ile Val Leu Ile Ala Asp Leu Ile Gly Gln Tyr Phe
 295 300 305

ctc ggc acc cgc tac ccc gtc gga gtt gtc acc ggc gca ttc ggc gcc 1075
 Leu Gly Thr Arg Tyr Pro Val Gly Val Val Thr Gly Ala Phe Gly Ala
 310 315 320 325

cca ttc ctt atc tat tta ctc att cgt tcc aac cgc gcg gga gta acc 1123
 Pro Phe Leu Ile Tyr Leu Leu Ile Arg Ser Asn Arg Ala Gly Val Thr
 330 335 340

ctg tgaccaccaa ccatcaacta tcc 1149
 Leu

<210> 214

<211> 342

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 214

Met Ser Leu Ser His Gln Leu Lys Arg Gln Arg Ala Ser Arg Asn Ser
 1 5 10 15

Arg Arg Trp Leu Ile Val Ala Ala Leu Gly Val Val Thr Leu Gly Ile
 20 25 30

Phe Ala Phe Ser Leu Met Trp Gly Glu Val Phe Tyr Gly Pro Ala Gln
 35 40 45

Val Leu Lys Val Leu Ser Gly Gln Gln Val Pro Gly Ala Ser Tyr Ser
 50 55 60

Val Gly Val Leu Arg Leu Pro Arg Ala Val Met Gly Leu Thr Ala Gly
 65 70 75 80

Leu Ala Phe Gly Ala Ala Gly Val Ile Phe Gln Thr Val Leu Arg Asn
 85 90 95

Gln Leu Ala Ser Pro Asp Ile Ile Gly Ile Ser Ser Gly Ala Ser Ala
 100 105 110

Ala Gly Val Ile Cys Ile Val Phe Phe Gly Met Ser Gln Ser Ala Val
 115 120 125

Ser Ala Ile Ser Leu Cys Ala Ser Leu Ala Val Ala Leu Leu Ile Tyr
 130 135 140

Leu Val Ala Tyr Arg Gly Gly Phe Ser Ala Thr Arg Leu Ile Leu Thr
 145 150 155 160

Gly Ile Gly Ile Ala Ala Met Leu Asn Ser Leu Val Ser Tyr Ser Leu
 165 170 175

Ser Lys Ala Asp Ser Trp Asp Leu Pro Thr Ala Thr Arg Trp Leu Thr
 180 185 190

Gly Ser Leu Asn Gly Ala Thr Trp Asp Arg Ala Met Pro Leu Ile Val

195					200					205					
Thr	Thr	Val	Val	Leu	Ile	Pro	Leu	Leu	Val	Ala	Asn	Ala	Arg	Asn	Val
210						215					220				
Asp	Leu	Met	Arg	Leu	Gly	Asn	Asp	Ser	Ala	Val	Gly	Leu	Gly	Val	Ala
225					230					235					240
Thr	Asn	Arg	Thr	Arg	Val	Ile	Ala	Ile	Ile	Ala	Ala	Val	Ala	Leu	Ile
				245					250					255	
Ala	Val	Ala	Thr	Ala	Ala	Cys	Gly	Pro	Ile	Ala	Phe	Val	Ala	Phe	Val
			260					265					270		
Ser	Gly	Pro	Ile	Ala	Ala	Arg	Ile	Leu	Gly	Ser	Gly	Gly	Ser	Leu	Ile
		275					280					285			
Ile	Pro	Ser	Ala	Leu	Ile	Gly	Gly	Leu	Ile	Val	Leu	Ile	Ala	Asp	Leu
	290					295					300				
Ile	Gly	Gln	Tyr	Phe	Leu	Gly	Thr	Arg	Tyr	Pro	Val	Gly	Val	Val	Thr
305					310					315					320
Gly	Ala	Phe	Gly	Ala	Pro	Phe	Leu	Ile	Tyr	Leu	Leu	Ile	Arg	Ser	Asn
				325					330					335	
Arg	Ala	Gly	Val	Thr	Leu										
			340												

<210> 215

<211> 802

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (30)..(779)

<223> FRXA00523

<400> 215

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			Val	Leu	Arg	Asn	Gln	Leu	Ala	Ser		
			1				5					

cgc	gat	att	atc	ggc	att	tct	tct	ggc	gcg	tcg	gcg	gcg	ggc	gta	att	101
Pro	Asp	Ile	Ile	Gly	Ile	Ser	Ser	Gly	Ala	Ser	Ala	Ala	Gly	Val	Ile	
	10					15					20					

tgc	att	gtg	ttt	ttc	gga	atg	tcg	cag	tct	gca	gtg	tcg	gcg	att	tct	149
Cys	Ile	Val	Phe	Phe	Gly	Met	Ser	Gln	Ser	Ala	Val	Ser	Ala	Ile	Ser	
	25				30					35				40		

ttg	tgt	gcg	tcc	ttg	gct	gtg	gcg	ttg	ttg	att	tat	ctg	gtg	gcg	tat	197
Leu	Cys	Ala	Ser	Leu	Ala	Val	Ala	Leu	Leu	Ile	Tyr	Leu	Val	Ala	Tyr	
				45				50						55		

cgc	ggt	ggt	ttt	tcg	gcc	acg	cgt	ctg	att	ctt	acc	ggc	att	ggt	att	245
Arg	Gly	Gly	Phe	Ser	Ala	Thr	Arg	Leu	Ile	Leu	Thr	Gly	Ile	Gly	Ile	
			60					65						70		

Gly Ala Ser Ala Ala Gly Val Ile Cys Ile Val Phe Phe Gly Met Ser
20 25 30

Gln	Ser	Ala	Val	Ser	Ala	Ile	Ser	Leu	Cys	Ala	Ser	Leu	Ala	Val	Ala	
		35					40					45				
Leu	Leu	Ile	Tyr	Leu	Val	Ala	Tyr	Arg	Gly	Gly	Phe	Ser	Ala	Thr	Arg	
	50					55					60					
Leu	Ile	Leu	Thr	Gly	Ile	Gly	Ile	Ala	Ala	Met	Leu	Asn	Ser	Leu	Val	
65					70					75					80	
Ser	Tyr	Ser	Leu	Ser	Lys	Ala	Asp	Ser	Trp	Asp	Leu	Pro	Thr	Ala	Thr	
				85					90					95		
Arg	Trp	Leu	Thr	Gly	Ser	Leu	Asn	Gly	Ala	Thr	Trp	Asp	Arg	Ala	Met	
			100					105					110			
Pro	Leu	Ile	Val	Thr	Thr	Val	Val	Leu	Ile	Pro	Leu	Leu	Val	Ala	Asn	
		115					120					125				
Ala	Arg	Asn	Val	Asp	Leu	Met	Arg	Leu	Gly	Asn	Asp	Ser	Ala	Val	Gly	
	130					135					140					
Leu	Gly	Val	Ala	Thr	Asn	Arg	Thr	Arg	Val	Ile	Ala	Ile	Ile	Ala	Ala	
145					150					155					160	
Val	Ala	Leu	Ile	Ala	Val	Ala	Thr	Ala	Ala	Cys	Gly	Pro	Ile	Ala	Phe	
				165					170					175		
Val	Ala	Phe	Val	Ser	Gly	Pro	Ile	Ala	Ala	Arg	Ile	Leu	Gly	Ser	Gly	
			180					185					190			
Gly	Ser	Leu	Ile	Ile	Pro	Ser	Ala	Leu	Ile	Gly	Gly	Leu	Ile	Val	Leu	
		195					200					205				
Ile	Ala	Asp	Leu	Ile	Gly	Gln	Tyr	Phe	Leu	Gly	Thr	Arg	Tyr	Pro	Val	
	210					215					220					
Gly	Val	Val	Thr	Gly	Ala	Phe	Gly	Ala	Pro	Phe	Leu	Ile	Tyr	Leu	Leu	
225					230					235					240	
Ile	Arg	Ser	Asn	Arg	Ala	Gly	Val	Thr	Leu							
				245					250							

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<210> 217
<211> 1167
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1144)
<223> RXA01289
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<400> 217
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atactttttct ttccccctcg atcttttagga gtcacgcgat atg acg gcg gtg gcg 115
                                         Met Thr Ala Val Ala
                                         1                               5
gta gag aag caq aag gag acg tcg ata agc aaa aac ctc ggc agg cgc 163

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Val	Glu	Lys	Gln	Lys	Glu	Thr	Ser	Ile	Ser	Lys	Asn	Leu	Gly	Arg	Arg		
				10					15					20			
cga	gcg	ctg	ggc	att	ctc	gga	atc	gtc	gtg	gca	ctg	ggg	gcg	ctt	att	211	
Arg	Ala	Leu	Gly	Ile	Leu	Gly	Ile	Val	Val	Ala	Leu	Gly	Ala	Leu	Ile		
			25					30					35				
gtt	tta	agt	att	gct	gtg	ggg	gcg	aac	cca	ctt	tct	ttt	agc	tcc	gta	259	
Val	Leu	Ser	Ile	Ala	Val	Gly	Ala	Asn	Pro	Leu	Ser	Phe	Ser	Ser	Val		
		40					45					50					
tgg	cag	ggg	ttt	acc	gca	cac	gac	agc	tct	gag	gcg	tcg	att	atc	gtg	307	
Trp	Gln	Gly	Phe	Thr	Ala	His	Asp	Ser	Ser	Glu	Ala	Ser	Ile	Ile	Val		
	55					60					65						
tgg	tca	atg	cgt	att	ccg	cgc	acg	ctg	gtg	ggc	atc	gtg	act	ggc	gct	355	
Trp	Ser	Met	Arg	Ile	Pro	Arg	Thr	Leu	Val	Gly	Ile	Val	Thr	Gly	Ala		
	70				75					80					85		
gct	ttt	ggg	gtg	gcg	ggg	gct	tta	att	caa	gcg	ctg	acg	cgc	aac	ccg	403	
Ala	Phe	Gly	Val	Ala	Gly	Ala	Leu	Ile	Gln	Ala	Leu	Thr	Arg	Asn	Pro		
				90					95					100			
ctt	gcc	gat	ccc	gga	att	ttg	gga	gtt	aac	gcg	ggg	gca	ggg	ttc	gca	451	
Leu	Ala	Asp	Pro	Gly	Ile	Leu	Gly	Val	Asn	Ala	Gly	Ala	Gly	Phe	Ala		
			105					110					115				
gtg	acc	gta	ggg	gtc	gga	ttt	ttc	gga	ctc	agc	agc	gtg	acg	ggc	tac	499	
Val	Thr	Val	Gly	Val	Gly	Phe	Phe	Gly	Leu	Ser	Ser	Val	Thr	Gly	Tyr		
		120					125					130					
atc	tgg	ttc	gca	ttc	ctg	ggc	gct	gcc	gcc	gct	acc	ctg	ctg	gtg	tat	547	
Ile	Trp	Phe	Ala	Phe	Leu	Gly	Ala	Ala	Ala	Ala	Thr	Leu	Leu	Val	Tyr		
	135					140					145						
ttc	att	ggg	gcg	agc	acc	agc	ggc	agc	gtt	aac	cct	gtt	gct	ctg	gtc	595	
Phe	Ile	Gly	Ala	Ser	Thr	Ser	Gly	Ser	Val	Asn	Pro	Val	Ala	Leu	Val		
150					155				160					165			
ctc	gcc	ggc	gtt	gct	ctg	gcc	gcc	gtg	ctt	ggg	ggc	gtc	acg	agc	ttc	643	
Leu	Ala	Gly	Val	Ala	Leu	Ala	Ala	Val	Leu	Gly	Gly	Val	Thr	Ser	Phe		
				170				175						180			
ctc	aca	ctg	att	gat	cct	gag	act	ttt	gaa	agc	atc	cgc	aac	tgg	aat	691	
Leu	Thr	Leu	Ile	Asp	Pro	Glu	Thr	Phe	Glu	Ser	Ile	Arg	Asn	Trp	Asn		
			185					190					195				
ctt	ggg	tct	gtt	gca	cgc	acc	gac	ctc	agc	gac	acc	atg	acc	gta	ttg	739	
Leu	Gly	Ser	Val	Ala	Arg	Thr	Asp	Leu	Ser	Asp	Thr	Met	Thr	Val	Leu		
		200					205					210					
cca	ttc	ctg	gca	gtc	gga	ctg	gcc	atc	gcg	ctc	ctg	ctg	tcg	gga	gca	787	
Pro	Phe	Leu	Ala	Val	Gly	Leu	Ala	Ile	Ala	Leu	Leu	Leu	Ser	Gly	Ala		
	215					220					225						
ctg	aac	tcc	att	gcg	ctt	ggc	gat	gac	ctt	gct	gca	tcc	ctg	ggc	acc	835	
Leu	Asn	Ser	Ile	Ala	Leu	Gly	Asp	Asp	Leu	Ala	Ala	Ser	Leu	Gly	Thr		
230					235				240					245			
aaa	gtg	atg	cgc	acc	cgc	gtg	ctc	ggc	atc	att	tca	gtc	acc	ttg	ttg	883	
Lys	Val	Met	Arg	Thr	Arg	Val	Leu	Gly	Ile	Ile	Ser	Val	Thr	Leu	Leu		

250										255					260					
gcc ggc ggc gcg acc gcc ctt act ggt ggt atc ggc ttc gta ggc ctt	931																			
Ala Gly Gly Ala Thr Ala Leu Thr Gly Gly Ile Gly Phe Val Gly Leu																				
265 270 275																				
atg gtt ccc cac gtt gtg cgc tgg gta gtt ggc ccc gat caa cga tgg	979																			
Met Val Pro His Val Val Arg Trp Val Val Gly Pro Asp Gln Arg Trp																				
280 285 290																				
atc atc acc ttc agc gcc ctg tgc gcc cct gtt ctt gta ctc ggc gca	1027																			
Ile Ile Thr Phe Ser Ala Leu Cys Ala Pro Val Leu Val Leu Gly Ala																				
295 300 305																				
gac att ttg gga cgc atc atc gcc cgc ccc ggc gaa att gaa gta ggc	1075																			
Asp Ile Leu Gly Arg Ile Ile Ala Arg Pro Gly Glu Ile Glu Val Gly																				
310 315 320 325																				
att gtt acc gca gtc atc ggc gca cct gtc ctg atc gca cta gtt cga	1123																			
Ile Val Thr Ala Val Ile Gly Ala Pro Val Leu Ile Ala Leu Val Arg																				
330 335 340																				
cgg agg aaa gcc agt ggt ctt taatatcaaa tctagaactg atg	1167																			
Arg Arg Lys Ala Ser Gly Leu																				
345																				

<210> 218

<211> 348

<212> PRT

<213> Corynebacterium glutamicum

<400> 218

Met Thr Ala Val Ala Val Glu Lys Gln Lys Glu Thr Ser Ile Ser Lys	
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Asn Leu Gly Arg Arg Arg Ala Leu Gly Ile Leu Gly Ile Val Val Ala	
20 25 30	
Leu Gly Ala Leu Ile Val Leu Ser Ile Ala Val Gly Ala Asn Pro Leu	
35 40 45	
Ser Phe Ser Ser Val Trp Gln Gly Phe Thr Ala His Asp Ser Ser Glu	
50 55 60	
Ala Ser Ile Ile Val Trp Ser Met Arg Ile Pro Arg Thr Leu Val Gly	
65 70 75 80	
Ile Val Thr Gly Ala Ala Phe Gly Val Ala Gly Ala Leu Ile Gln Ala	
85 90 95	
Leu Thr Arg Asn Pro Leu Ala Asp Pro Gly Ile Leu Gly Val Asn Ala	
100 105 110	
Gly Ala Gly Phe Ala Val Thr Val Gly Val Gly Phe Phe Gly Leu Ser	
115 120 125	
Ser Val Thr Gly Tyr Ile Trp Phe Ala Phe Leu Gly Ala Ala Ala Ala	
130 135 140	
Thr Leu Leu Val Tyr Phe Ile Gly Ala Ser Thr Ser Gly Ser Val Asn	

145		150		155		160
Pro Val Ala Leu	Val Leu Ala Gly	Val Ala Leu Ala	Ala Val Leu Gly			
	165		170			175
Gly Val Thr Ser	Phe Leu Thr Leu	Ile Asp Pro Glu	Thr Phe Glu Ser			
	180		185			190
Ile Arg Asn Trp	Asn Leu Gly Ser	Val Ala Arg Thr	Asp Leu Ser Asp			
	195		200			205
Thr Met Thr Val	Leu Pro Phe Leu	Ala Val Gly Leu	Ala Ile Ala Leu			
	210		215			220
Leu Leu Ser Gly	Ala Leu Asn Ser	Ile Ala Leu Gly	Asp Asp Leu Ala			
	225		230			235
Ala Ser Leu Gly	Thr Lys Val Met	Arg Thr Arg Val	Leu Gly Ile Ile			
	245		250			255
Ser Val Thr Leu	Leu Ala Gly Gly	Ala Thr Ala Leu	Thr Gly Gly Ile			
	260		265			270
Gly Phe Val Gly	Leu Met Val Pro	His Val Val Arg	Trp Val Val Gly			
	275		280			285
Pro Asp Gln Arg	Trp Ile Ile Thr	Phe Ser Ala Leu	Cys Ala Pro Val			
	290		295			300
Leu Val Leu Gly	Ala Asp Ile Leu	Gly Arg Ile Ile	Ala Arg Pro Gly			
	305		310			315
Glu Ile Glu Val	Gly Ile Val Thr	Ala Val Ile Gly	Ala Pro Val Leu			
	325		330			335
Ile Ala Leu Val	Arg Arg Arg Lys	Ala Ser Gly Leu				
	340		345			

<210> 219
 <211> 1287
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1264)
 <223> RXA01290

<400> 219
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 gcacctgtcc tgatcgcaact agttcgacgg aggaaagcca gtg gtc ttt aat atc 115
 Val Val Phe Asn Ile
 1 5
 aaa tct aga act gat gaa act cct gtt gct gcg tct gag ccg gtg gaa 163
 Lys Ser Arg Thr Asp Glu Thr Pro Val Ala Ala Ser Glu Pro Val Glu
 10 15 20
 tcc act aga cct gtg tct gaa gct tcg aca agc cct gcg ctt aac ccc 211

Ser	Thr	Arg	Pro	Val	Ser	Glu	Ala	Ser	Thr	Ser	Pro	Ala	Leu	Asn	Pro		
			25					30					35				
ggc	tac	cac	gca	gtt	tca	gtg	cag	agg	cgc	cgg	ttc	tct	ttc	cgc	atc	259	
Gly	Tyr	His	Ala	Val	Ser	Val	Gln	Arg	Arg	Arg	Phe	Ser	Phe	Arg	Ile		
		40					45					50					
cca	gcc	cgc	ctc	atg	gtg	gtt	agc	ctt	atc	ctt	ttc	gcc	atc	gcg	cta	307	
Pro	Ala	Arg	Leu	Met	Val	Val	Ser	Leu	Ile	Leu	Phe	Ala	Ile	Ala	Leu		
		55					60				65						
tgc	agc	gcc	aca	tgg	gct	atc	acg	atg	ggc	gat	tac	cca	ctg	tct	ttg	355	
Cys	Ser	Ala	Thr	Trp	Ala	Ile	Thr	Met	Gly	Asp	Tyr	Pro	Leu	Ser	Leu		
	70					75				80					85		
ggg	cag	gtg	att	aat	gca	ctt	gct	ggc	acc	ggc	gag	aaa	ttc	cag	ttg	403	
Gly	Gln	Val	Ile	Asn	Ala	Leu	Ala	Gly	Thr	Gly	Glu	Lys	Phe	Gln	Leu		
				90					95					100			
ttg	gtg	gtg	cgg	gaa	tgg	cgt	cta	cct	gta	gcc	att	gct	gct	gtt	gtc	451	
Leu	Val	Val	Arg	Glu	Trp	Arg	Leu	Pro	Val	Ala	Ile	Ala	Ala	Val	Val		
			105					110					115				
ttc	ggc	gcg	ctg	ctt	ggc	ata	ggt	gga	gcg	att	ttc	cag	tcg	att	act	499	
Phe	Gly	Ala	Leu	Leu	Gly	Ile	Gly	Gly	Ala	Ile	Phe	Gln	Ser	Ile	Thr		
		120					125					130					
cga	aac	ccg	ttg	ggt	tca	cct	gac	gtg	att	ggt	ttc	gat	gca	ggt	tct	547	
Arg	Asn	Pro	Leu	Gly	Ser	Pro	Asp	Val	Ile	Gly	Phe	Asp	Ala	Gly	Ser		
		135					140				145						
tac	acg	gcg	gtg	gtt	ctt	gtc	att	ttg	gtc	ctc	ggc	aac	act	cac	tac	595	
Tyr	Thr	Ala	Val	Val	Leu	Val	Ile	Leu	Val	Leu	Gly	Asn	Thr	His	Tyr		
		150				155				160					165		
tgg	agc	atc	gct	ttc	gct	gcc	atc	gtc	ggt	ggc	att	gtt	acc	gcc	ttt	643	
Trp	Ser	Ile	Ala	Phe	Ala	Ala	Ile	Val	Gly	Gly	Ile	Val	Thr	Ala	Phe		
				170					175					180			
gcc	gtg	tat	gtc	ctg	gcg	tgg	cgt	aaa	ggt	gtg	caa	ggt	ttc	cgc	ttg	691	
Ala	Val	Tyr	Val	Leu	Ala	Trp	Arg	Lys	Gly	Val	Gln	Gly	Phe	Arg	Leu		
			185					190					195				
atc	atc	gtg	ggc	atc	ggt	gtc	tcg	gcc	atg	ctc	agt	tcc	gtt	aac	gcg	739	
Ile	Ile	Val	Gly	Ile	Gly	Val	Ser	Ala	Met	Leu	Ser	Ser	Val	Asn	Ala		
		200					205					210					
tat	cta	atc	acc	cgc	gcc	gat	gtg	gaa	gac	gcc	atg	gtt	gtg	ggc	ttc	787	
Tyr	Leu	Ile	Thr	Arg	Ala	Asp	Val	Glu	Asp	Ala	Met	Val	Val	Gly	Phe		
		215				220					225						
tgg	agt	gcc	ggt	tcc	atc	aac	cgc	att	acc	tgg	caa	tct	ctg	ctc	ccc	835	
Trp	Ser	Ala	Gly	Ser	Ile	Asn	Arg	Ile	Thr	Trp	Gln	Ser	Leu	Leu	Pro		
		230				235				240					245		
tct	ctg	gtg	atc	gct	gct	gtc	atc	atc	gtg	gcc	gcc	att	gtg	ctg	gca	883	
Ser	Leu	Val	Ile	Ala	Ala	Val	Ile	Ile	Val	Ala	Ala	Ile	Val	Leu	Ala		
				250					255					260			
agg	tca	ctg	cgt	ttc	atg	gaa	atg	ggc	gat	gac	gta	gcc	acc	acc	ctc	931	
Arg	Ser	Leu	Arg	Phe	Met	Glu	Met	Gly	Asp	Asp	Val	Ala	Thr	Thr	Leu		

265	270	275	
ggt gtg aaa aca aac tcc acc cgc ttg gca ctc atc gtt gtc ggc gtt			979
Gly Val Lys Thr Asn Ser Thr Arg Leu Ala Leu Ile Val Val Gly Val			
280	285	290	
gct acc tcc gcg ttg gtt aca gca gct gcc gga ccg atc tcc ttc atc			1027
Ala Thr Ser Ala Leu Val Thr Ala Ala Ala Gly Pro Ile Ser Phe Ile			
295	300	305	
gcg ttg gtt gcc cca cag ctg gca cgt cgc ctc act aaa acc cct ggt			1075
Ala Leu Val Ala Pro Gln Leu Ala Arg Arg Leu Thr Lys Thr Pro Gly			
310	315	320	325
gtc agc ctg gtt gct gcc gct gca atg ggt tcc gca ctg ctc agc tgc			1123
Val Ser Leu Val Ala Ala Ala Ala Met Gly Ser Ala Leu Leu Ser Cys			
	330	335	340
gct cac ctc ctt tcc ctg att atc agc tcc ttc tac cgc acc atc ccg			1171
Ala His Leu Leu Ser Leu Ile Ile Ser Ser Phe Tyr Arg Thr Ile Pro			
	345	350	355
gtt ggc ctg ttg act gta tcc atc ggt ggt tgc tac atg atc tgg ctt			1219
Val Gly Leu Leu Thr Val Ser Ile Gly Gly Cys Tyr Met Ile Trp Leu			
	360	365	370
ctg ctg cgc gaa acc cgc cgc caa tac cgc acc ggc acc atc cga			1264
Leu Leu Arg Glu Thr Arg Arg Gln Tyr Arg Thr Gly Thr Ile Arg			
	375	380	385
tagttctttt aaggatccct cat			1287

<210> 220

<211> 388

<212> PRT

<213> Corynebacterium glutamicum

<400> 220

Val Val Phe Asn Ile Lys Ser Arg Thr Asp Glu Thr Pro Val Ala Ala
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Ser Glu Pro Val Glu Ser Thr Arg Pro Val Ser Glu Ala Ser Thr Ser
20 25 30

Pro Ala Leu Asn Pro Gly Tyr His Ala Val Ser Val Gln Arg Arg Arg
35 40 45

Phe Ser Phe Arg Ile Pro Ala Arg Leu Met Val Val Ser Leu Ile Leu
50 55 60

Phe Ala Ile Ala Leu Cys Ser Ala Thr Trp Ala Ile Thr Met Gly Asp
65 70 75 80

Tyr Pro Leu Ser Leu Gly Gln Val Ile Asn Ala Leu Ala Gly Thr Gly
85 90 95

Glu Lys Phe Gln Leu Leu Val Val Arg Glu Trp Arg Leu Pro Val Ala
100 105 110

Ile Ala Ala Val Val Phe Gly Ala Leu Leu Gly Ile Gly Gly Ala Ile

115					120					125					
Phe	Gln	Ser	Ile	Thr	Arg	Asn	Pro	Leu	Gly	Ser	Pro	Asp	Val	Ile	Gly
130						135					140				
Phe	Asp	Ala	Gly	Ser	Tyr	Thr	Ala	Val	Val	Leu	Val	Ile	Leu	Val	Leu
145					150					155					160
Gly	Asn	Thr	His	Tyr	Trp	Ser	Ile	Ala	Phe	Ala	Ala	Ile	Val	Gly	Gly
				165					170					175	
Ile	Val	Thr	Ala	Phe	Ala	Val	Tyr	Val	Leu	Ala	Trp	Arg	Lys	Gly	Val
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Gln	Gly	Phe	Arg	Leu	Ile	Ile	Val	Gly	Ile	Gly	Val	Ser	Ala	Met	Leu
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Ser	Ser	Val	Asn	Ala	Tyr	Leu	Ile	Thr	Arg	Ala	Asp	Val	Glu	Asp	Ala
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Met	Val	Val	Gly	Phe	Trp	Ser	Ala	Gly	Ser	Ile	Asn	Arg	Ile	Thr	Trp
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Gln	Ser	Leu	Leu	Pro	Ser	Leu	Val	Ile	Ala	Ala	Val	Ile	Ile	Val	Ala
				245					250					255	
Ala	Ile	Val	Leu	Ala	Arg	Ser	Leu	Arg	Phe	Met	Glu	Met	Gly	Asp	Asp
			260					265					270		
Val	Ala	Thr	Thr	Leu	Gly	Val	Lys	Thr	Asn	Ser	Thr	Arg	Leu	Ala	Leu
			275				280					285			
Ile	Val	Val	Gly	Val	Ala	Thr	Ser	Ala	Leu	Val	Thr	Ala	Ala	Ala	Gly
	290					295					300				
Pro	Ile	Ser	Phe	Ile	Ala	Leu	Val	Ala	Pro	Gln	Leu	Ala	Arg	Arg	Leu
305					310					315					320
Thr	Lys	Thr	Pro	Gly	Val	Ser	Leu	Val	Ala	Ala	Ala	Ala	Met	Gly	Ser
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Ala	Leu	Leu	Ser	Cys	Ala	His	Leu	Leu	Ser	Leu	Ile	Ile	Ser	Ser	Phe
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<213> Corynebacterium glutamicum

<220>

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<222> (1)..(582)

<223> RXA01822

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Gly Ile Gly Thr Gly Ala Phe Leu Gly Ala Ala Arg Asp Phe Phe Met	
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gtg cgc gca gat att acg ggt gct tcg acg gta cag ctg tgg tct gcc	144
Val Arg Ala Asp Ile Thr Gly Ala Ser Thr Val Gln Leu Trp Ser Ala	
35 40 45	
ggg tcg ttg agc ggc cgc gac tgg aat cat gcc ctg ttg gtg ttg att	192
Gly Ser Leu Ser Gly Arg Asp Trp Asn His Ala Leu Leu Val Leu Ile	
50 55 60	
tcg tgt gca gtg att gtg cca gca ctg tgc att att gtc cgc cgt tta	240
Ser Cys Ala Val Ile Val Pro Ala Leu Cys Ile Ile Val Arg Arg Leu	
65 70 75 80	
cgc ctg atg gaa atg ggt gat gat gca gct ggc gca ctt gga att tca	288
Arg Leu Met Glu Met Gly Asp Asp Ala Ala Gly Ala Leu Gly Ile Ser	
85 90 95	
gtg gag aga aca cgg ttg ata gcc att ttg ttg gct gtg ctg ctg gtg	336
Val Glu Arg Thr Arg Leu Ile Ala Ile Leu Leu Ala Val Leu Leu Val	
100 105 110	
ggg atc gcc acc gca gct gca ggt ccc atc gct ttt att gca ctg gca	384
Gly Ile Ala Thr Ala Ala Ala Gly Pro Ile Ala Phe Ile Ala Leu Ala	
115 120 125	
gca cct cag att gcc cgg gct ctg gcc cgg gag gat gga gtg ctg gtg	432
Ala Pro Gln Ile Ala Arg Ala Leu Ala Arg Glu Asp Gly Val Leu Val	
130 135 140	
gct gcg tcg ata agc att ggc tct ggc ctg tta gtt gcg gcg gat tgc	480
Ala Ala Ser Ile Ser Ile Gly Ser Gly Leu Leu Val Ala Ala Asp Cys	
145 150 155 160	
cta gag caa cac gtt gat act gag ctg cac acg ccc gtt ggc ctg gtg	528
Leu Glu Gln His Val Asp Thr Glu Leu His Thr Pro Val Gly Leu Val	
165 170 175	
acc agt ttg ctg ggc ggc gtg tat ttg atg tgg ctt ttg agc cga aag	576
Thr Ser Leu Leu Gly Gly Val Tyr Leu Met Trp Leu Leu Ser Arg Lys	
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<211> 194

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<213> Corynebacterium glutamicum

<400> 222

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Val Arg Ala Asp Ile Thr Gly Ala Ser Thr Val Gln Leu Trp Ser Ala
 35 40 45

Gly Ser Leu Ser Gly Arg Asp Trp Asn His Ala Leu Leu Val Leu Ile
 50 55 60

Ser Cys Ala Val Ile Val Pro Ala Leu Cys Ile Ile Val Arg Arg Leu
 65 70 75 80

Arg Leu Met Glu Met Gly Asp Asp Ala Ala Gly Ala Leu Gly Ile Ser
 85 90 95

Val Glu Arg Thr Arg Leu Ile Ala Ile Leu Leu Ala Val Leu Leu Val
 100 105 110

Gly Ile Ala Thr Ala Ala Ala Gly Pro Ile Ala Phe Ile Ala Leu Ala
 115 120 125

Ala Pro Gln Ile Ala Arg Ala Leu Ala Arg Glu Asp Gly Val Leu Val
 130 135 140

Ala Ala Ser Ile Ser Ile Gly Ser Gly Leu Leu Val Ala Ala Asp Cys
 145 150 155 160

Leu Glu Gln His Val Asp Thr Glu Leu His Thr Pro Val Gly Leu Val
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Thr Ser Leu Leu Gly Gly Val Tyr Leu Met Trp Leu Leu Ser Arg Lys
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Glu Ala

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<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(1096)

<223> RXN00466

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 Val Gln Ser Arg Leu
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tcc aaa atc ctg cgc agt agc gtc gta ggc gtt gct gtc cta gcc ctg 163
 Ser Lys Ile Leu Arg Ser Ser Val Val Gly Val Ala Val Leu Ala Leu

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Leu	Ala	Gly	Cys	Ser	Asn	Asn	Ala	Asp	Asp	Thr	Asp	Ala	Asp	Ser	Thr					
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Ser	Thr	Gly	Asn	Ser	Ala	Phe	Pro	Val	Ser	Ile	Glu	His	Glu	Phe	Gly					
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Thr	Thr	Thr	Ile	Asp	Asp	Val	Pro	Glu	Arg	Val	Val	Thr	Leu	Gly	Val					
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Thr	Gly	Tyr	Lys	Phe	Phe	Glu	Asn	Gly	Leu	Gly	Pro	Trp	Thr	Asp	Glu					
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Ser	Ala	Gly	Phe	Asp	Asp	Val	Val	Tyr	Glu	Gln	Leu	Ser	Asp	Ile	Ala					
	135					140					145									
ccg	gtg	gtc	gcc	cgt	cca	gcg	gga	aca	gct	gca	tac	gca	gta	gct	cg	595				
Pro	Val	Val	Ala	Arg	Pro	Ala	Gly	Thr	Ala	Ala	Tyr	Ala	Val	Ala	Arg					
150				155					160						165					
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Glu	Glu	Ala	Thr	Asn	Leu	Val	Ala	Arg	Ala	Met	Gly	Gln	Ser	Glu	Lys					
				170				175						180						
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Gly	Gln	Glu	Leu	Asn	Glu	Glu	Thr	Asp	Ala	Leu	Ile	Gln	Ala	Ala	Arg					
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gat	gaa	aat	cct	tct	ttt	gac	ggt	aaa	aca	gga	acc	gtc	atc	ttg	cca	739				
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Tyr	Gln	Gly	Lys	Tyr	Gly	Ala	Tyr	Leu	Pro	Gly	Asp	Ala	Arg	Gly	Gln					
	215					220					225									
ttc	ctc	gat	tca	ctt	ggc	att	tcg	ctg	ccg	gaa	gca	gtt	ctt	tcg	cga	835				
Phe	Leu	Asp	Ser	Leu	Gly	Ile	Ser	Leu	Pro	Glu	Ala	Val	Leu	Ser	Arg					
230					235				240						245					
gac	acc	ggc	gac	agc	ttc	ttt	gtc	gat	gtc	ccc	gct	gaa	agc	gtc	aaa	883				
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gac gta gac ggt gat gtt ctc ctc gtg ctt tcc aac gac gaa aat ctg 931
 Asp Val Asp Gly Asp Val Leu Leu Val Leu Ser Asn Asp Glu Asn Leu
 265 270 275

 gat atc aca gca gag aat cca ctg ttt gaa aca ctc aac gtt gtg caa 979
 Asp Ile Thr Ala Glu Asn Pro Leu Phe Glu Thr Leu Asn Val Val Gln
 280 285 290

 aaa gac gca gta att gtg gca aca acc gaa gaa cgc ggg gcg att acc 1027
 Lys Asp Ala Val Ile Val Ala Thr Thr Glu Glu Arg Gly Ala Ile Thr
 295 300 305

 tac aac tca gtg ctg tct gtt cct ttt gcg ttg gaa cat ctc gca cca 1075
 Tyr Asn Ser Val Leu Ser Val Pro Phe Ala Leu Glu His Leu Ala Pro
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<211> 332

<212> PRT

<213> Corynebacterium glutamicum

<400> 224

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 35 40 45

 Glu His Glu Phe Gly Thr Thr Thr Ile Asp Asp Val Pro Glu Arg Val
 50 55 60

 Val Thr Leu Gly Val Thr Asp Ala Asp Ile Val Leu Ala Leu Gly Thr
 65 70 75 80

 Val Pro Val Gly Asn Thr Gly Tyr Lys Phe Phe Glu Asn Gly Leu Gly
 85 90 95

 Pro Trp Thr Asp Glu Leu Val Glu Gly Lys Glu Leu Thr Leu Leu Asp
 100 105 110

 Ser Asp Ser Thr Pro Asp Leu Glu Gln Val Ala Ala Leu Glu Pro Asp
 115 120 125

 Leu Ile Ile Gly Val Ser Ala Gly Phe Asp Asp Val Val Tyr Glu Gln
 130 135 140

 Leu Ser Asp Ile Ala Pro Val Val Ala Arg Pro Ala Gly Thr Ala Ala
 145 150 155 160

 Tyr Ala Val Ala Arg Glu Glu Ala Thr Asn Leu Val Ala Arg Ala Met
 165 170 175

Gly Gln Ser Glu Lys Gly Gln Glu Leu Asn Glu Glu Thr Asp Ala Leu
 180 185 190
 Ile Gln Ala Ala Arg Asp Glu Asn Pro Ser Phe Asp Gly Lys Thr Gly
 195 200 205
 Thr Val Ile Leu Pro Tyr Gln Gly Lys Tyr Gly Ala Tyr Leu Pro Gly
 210 215 220
 Asp Ala Arg Gly Gln Phe Leu Asp Ser Leu Gly Ile Ser Leu Pro Glu
 225 230 235 240
 Ala Val Leu Ser Arg Asp Thr Gly Asp Ser Phe Phe Val Asp Val Pro
 245 250 255
 Ala Glu Ser Val Lys Asp Val Asp Gly Asp Val Leu Leu Val Leu Ser
 260 265 270
 Asn Asp Glu Asn Leu Asp Ile Thr Ala Glu Asn Pro Leu Phe Glu Thr
 275 280 285
 Leu Asn Val Val Gln Lys Asp Ala Val Ile Val Ala Thr Thr Glu Glu
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 Arg Gly Ala Ile Thr Tyr Asn Ser Val Leu Ser Val Pro Phe Ala Leu
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<210> 225

<211> 1087

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1087)

<223> FRXA00466

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 Val Gln Ser Arg Leu
 1 5

tcc aaa atc ctg cgc agt agc gtc gta ggc gtt gct gtc cta gcc ctg 163
 Ser Lys Ile Leu Arg Ser Ser Val Val Gly Val Ala Val Leu Ala Leu
 10 15 20

tta gct ggg tgt tct aac aat gca gat gac acc gac gct gat tca aca 211
 Leu Ala Gly Cys Ser Asn Asn Ala Asp Asp Thr Asp Ala Asp Ser Thr
 25 30 35

tcc acg gga aac tcc gct ttt cct gtt tcg att gaa cac gag ttc gga 259
 Ser Thr Gly Asn Ser Ala Phe Pro Val Ser Ile Glu His Glu Phe Gly
 40 45 50

acc acc aca atc gat gat gta ccc gaa aga gtt gtc acc ctt ggc gtt 307

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Thr	Asp	Ala	Asp	Ile	Val	Leu	Ala	Leu	Gly	Thr	Val	Pro	Val	Gly	Asn		
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Thr	Gly	Tyr	Lys	Phe	Phe	Glu	Asn	Gly	Leu	Gly	Pro	Trp	Thr	Asp	Glu		
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Ser	Ala	Gly	Phe	Asp	Asp	Val	Val	Tyr	Glu	Gln	Leu	Ser	Asp	Ile	Ala		
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Pro	Val	Val	Ala	Arg	Pro	Ala	Gly	Thr	Ala	Ala	Tyr	Ala	Val	Ala	Arg		
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Asp	Glu	Asn	Pro	Ser	Phe	Asp	Gly	Lys	Thr	Gly	Thr	Val	Ile	Leu	Pro		
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	215					220					225						
ttc	ctc	gat	tca	ctt	ggc	att	tcg	ctg	ccg	gaa	gca	gtt	ctt	tcg	cga	835	
Phe	Leu	Asp	Ser	Leu	Gly	Ile	Ser	Leu	Pro	Glu	Ala	Val	Leu	Ser	Arg		
230					235					240					245		
gac	acc	ggc	gac	agc	ttc	ttt	gtc	gat	gtc	ccc	gct	gaa	agc	gtc	aaa	883	
Asp	Thr	Gly	Asp	Ser	Phe	Phe	Val	Asp	Val	Pro	Ala	Glu	Ser	Val	Lys		
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Asp	Val	Asp	Gly	Asp	Val	Leu	Leu	Val	Leu	Ser	Asn	Asp	Glu	Asn	Leu		
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gat	atc	aca	gca	gag	aat	cca	ctg	ttt	gaa	aca	ctc	aac	gtt	gtg	caa	979	
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Pro	Trp	Thr	Asp	Glu	Leu	Val	Glu	Gly	Lys	Glu	Leu	Thr	Leu	Leu	Asp	
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Tyr	Ala	Val	Ala	Arg	Glu	Glu	Ala	Thr	Asn	Leu	Val	Ala	Arg	Ala	Met	
				165					170					175		
Gly	Gln	Ser	Glu	Lys	Gly	Gln	Glu	Leu	Asn	Glu	Glu	Thr	Asp	Ala	Leu	
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Ile	Gln	Ala	Ala	Arg	Asp	Glu	Asn	Pro	Ser	Phe	Asp	Gly	Lys	Thr	Gly	
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Thr	Val	Ile	Leu	Pro	Tyr	Gln	Gly	Lys	Tyr	Gly	Ala	Tyr	Leu	Pro	Gly	
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										Met	Lys	Lys	Ser	Leu		
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atc gcc att gtt gcc agt gcg ctc gtg tta agc ggc tgc acc tct gat																163
Ile	Ala	Ile	Val	Ala	Ser	Ala	Leu	Val	Leu	Ser	Gly	Cys	Thr	Ser	Asp	
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tct tct gac tct tcc ggc act tcc gga act gtg gaa acc act tcg att																211
Ser	Ser	Asp	Ser	Ser	Gly	Thr	Ser	Gly	Thr	Val	Glu	Thr	Thr	Ser	Ile	
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Thr	Thr	Ser	Val	Ala	Ala	Ala	Asp	Gly	Ala	Phe	Pro	Arg	Thr	Val	Thr	
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ctc gac gat tcc tcc atc acc tta gaa tcc aaa cca gag cgc atc gcc																307
Leu	Asp	Asp	Ser	Ser	Ile	Thr	Leu	Glu	Ser	Lys	Pro	Glu	Arg	Ile	Ala	
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Val	Leu	Thr	Pro	Glu	Ala	Ala	Ser	Leu	Val	Leu	Pro	Ile	Thr	Gly	Ala	
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gac cgc gtc gtg atg acc gcc gaa atg gac acc gct gac gaa gaa acc																403
Asp	Arg	Val	Val	Met	Thr	Ala	Glu	Met	Asp	Thr	Ala	Asp	Glu	Glu	Thr	
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gca gct ctg gcc tcc caa gtg gaa tac caa gtc aaa aac ggt ggc agg 451
 Ala Ala Leu Ala Ser Gln Val Glu Tyr Gln Val Lys Asn Gly Gly Arg
 105 110 115

ctc gac ccc gaa caa gtt gtc gcc ggc gac cca gat ttg gtg atc gtc 499
 Leu Asp Pro Glu Gln Val Val Ala Gly Asp Pro Asp Leu Val Ile Val
 120 125 130

agt gcg cgt ttc gat acc gaa caa ggc acc atc gac att ttg gaa ggc 547
 Ser Ala Arg Phe Asp Thr Glu Gln Gly Thr Ile Asp Ile Leu Glu Gly
 135 140 145

ctc aac gtc ccg tagttaactt cgattcagac gct 582
 Leu Asn Val Pro
 150

<210> 228

<211> 153

<212> PRT

<213> Corynebacterium glutamicum

<400> 228

Met Lys Lys Ser Leu Ile Ala Ile Val Ala Ser Ala Leu Val Leu Ser
 1 5 10 15

Gly Cys Thr Ser Asp Ser Ser Asp Ser Ser Gly Thr Ser Gly Thr Val
 20 25 30

Glu Thr Thr Ser Ile Thr Thr Ser Val Ala Ala Ala Asp Gly Ala Phe
 35 40 45

Pro Arg Thr Val Thr Leu Asp Asp Ser Ser Ile Thr Leu Glu Ser Lys
 50 55 60

Pro Glu Arg Ile Ala Val Leu Thr Pro Glu Ala Ala Ser Leu Val Leu
 65 70 75 80

Pro Ile Thr Gly Ala Asp Arg Val Val Met Thr Ala Glu Met Asp Thr
 85 90 95

Ala Asp Glu Glu Thr Ala Ala Leu Ala Ser Gln Val Glu Tyr Gln Val
 100 105 110

Lys Asn Gly Gly Arg Leu Asp Pro Glu Gln Val Val Ala Gly Asp Pro
 115 120 125

Asp Leu Val Ile Val Ser Ala Arg Phe Asp Thr Glu Gln Gly Thr Ile
 130 135 140

Asp Ile Leu Glu Gly Leu Asn Val Pro
 145 150

<210> 229

<211> 1098

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1075)

<223> FRXA02863

<400> 229

acggactgcc cattgcggtg cgcgatgac ccgaaaccag ctcaacttcgc gtgatcccg 60

atccaaatcc cttttgattg aaagtttgac ttaaaaaccc atg aaa aaa tca ctc 115
 Met Lys Lys Ser Leu
 1 5

atc gcc att gtt gcc agt gcg ctc gtg tta agc ggc tgc acc tct gat 163
 Ile Ala Ile Val Ala Ser Ala Leu Val Leu Ser Gly Cys Thr Ser Asp
 10 15 20

tct tct gac tct tcc ggc act tcc gga act gtg gaa acc act tcg att 211
 Ser Ser Asp Ser Ser Gly Thr Ser Gly Thr Val Glu Thr Thr Ser Ile
 25 30 35

aca acc agc gtt gcc gca gct gac ggc gca ttc cca cgc acc gtc aca 259
 Thr Thr Ser Val Ala Ala Ala Asp Gly Ala Phe Pro Arg Thr Val Thr
 40 45 50

ctc gac gat tcc tcc atc acc tta gaa tcc aaa cca gag cgc atc gcc 307
 Leu Asp Asp Ser Ser Ile Thr Leu Glu Ser Lys Pro Glu Arg Ile Ala
 55 60 65

gta ctc acc cca gag gca gca tcc ttg gtt ctc ccc atc aca ggc gcc 355
 Val Leu Thr Pro Glu Ala Ala Ser Leu Val Leu Pro Ile Thr Gly Ala
 70 75 80 85

gac cgc gtc gtg atg acc gcc gaa atg gac acc gct gac gaa gaa acc 403
 Asp Arg Val Val Met Thr Ala Glu Met Asp Thr Ala Asp Glu Glu Thr
 90 95 100

gca gct ctg gcc tcc caa gtg gaa tac caa gtc aaa aac ggt ggc agc 451
 Ala Ala Leu Ala Ser Gln Val Glu Tyr Gln Val Lys Asn Gly Gly Ser
 105 110 115

ctc gac ccc gaa caa gtt gtc gcc ggc gac cca gat ttg gtg atc gtc 499
 Leu Asp Pro Glu Gln Val Val Ala Gly Asp Pro Asp Leu Val Ile Val
 120 125 130

agt gcg cgt ttc gat acc gaa caa ggc acc atc gac att ttg gaa ggc 547
 Ser Ala Arg Phe Asp Thr Glu Gln Gly Thr Ile Asp Ile Leu Glu Gly
 135 140 145

ctc aac gtc ccc gta gtt aac ttc gat tca gac gct tgg gga gac atc 595
 Leu Asn Val Pro Val Val Asn Phe Asp Ser Asp Ala Trp Gly Asp Ile
 150 155 160 165

gac gcc atc acc aaa cac cta gaa att gtg ggt gaa ctc gtc ggc gaa 643
 Asp Ala Ile Thr Lys His Leu Glu Ile Val Gly Glu Leu Val Gly Glu
 170 175 180

gaa gac aaa gcc gca gaa gca atc gca gaa atc gat gca aac cgc atc 691
 Glu Asp Lys Ala Ala Glu Ala Ile Ala Glu Ile Asp Ala Asn Arg Ile
 185 190 195

gac atc gac aag cct gcc acc tcc ccc act gtg ctc act ttg atg caa 739
 Asp Ile Asp Lys Pro Ala Thr Ser Pro Thr Val Leu Thr Leu Met Gln
 200 205 210

cgc gga cca cgc caa atg gtc atg cca gaa tct gcc atg ctc aac ggc 787
 Arg Gly Pro Arg Gln Met Val Met Pro Glu Ser Ala Met Leu Asn Gly
 215 220 225

 ctg atc cgc gaa gcc ggc ggc act cca gtg gta gat tct ctc ggc gcg 835
 Leu Ile Arg Glu Ala Gly Gly Thr Pro Val Val Asp Ser Leu Gly Ala
 230 235 240 245

 gta ggc acc atc act gca gac cca gaa caa gtt gtt gcg atg gca cct 883
 Val Gly Thr Ile Thr Ala Asp Pro Glu Gln Val Val Ala Met Ala Pro
 250 255 260

 gag atc atc atc att cag gac ttc caa ggt aaa ggc cga gag aac ttc 931
 Glu Ile Ile Ile Ile Gln Asp Phe Gln Gly Lys Gly Arg Glu Asn Phe
 265 270 275

 gct aat ttc ctc tcc aac cca gcg cta gcc aac gtt ccc gcc att gaa 979
 Ala Asn Phe Leu Ser Asn Pro Ala Leu Ala Asn Val Pro Ala Ile Glu
 280 285 290

 aac gac aag att ttc tac gcc gac act gtc acc act gga gtt act gca 1027
 Asn Asp Lys Ile Phe Tyr Ala Asp Thr Val Thr Thr Gly Val Thr Ala
 295 300 305

 ggt acc gat atc acc act ggt ctg cag caa gtg gca gaa atg ctg agc 1075
 Gly Thr Asp Ile Thr Thr Gly Leu Gln Gln Val Ala Glu Met Leu Ser
 310 315 320 325

 tagttttgag atgttgaaac tag 1098

<210> 230

<211> 325

<212> PRT

<213> Corynebacterium glutamicum

<400> 230

Met Lys Lys Ser Leu Ile Ala Ile Val Ala Ser Ala Leu Val Leu Ser
 1 5 10 15

Gly Cys Thr Ser Asp Ser Ser Asp Ser Ser Gly Thr Ser Gly Thr Val
 20 25 30

Glu Thr Thr Ser Ile Thr Thr Ser Val Ala Ala Ala Asp Gly Ala Phe
 35 40 45

Pro Arg Thr Val Thr Leu Asp Asp Ser Ser Ile Thr Leu Glu Ser Lys
 50 55 60

Pro Glu Arg Ile Ala Val Leu Thr Pro Glu Ala Ala Ser Leu Val Leu
 65 70 75 80

Pro Ile Thr Gly Ala Asp Arg Val Val Met Thr Ala Glu Met Asp Thr
 85 90 95

Ala Asp Glu Glu Thr Ala Ala Leu Ala Ser Gln Val Glu Tyr Gln Val
 100 105 110

Lys Asn Gly Gly Ser Leu Asp Pro Glu Gln Val Val Ala Gly Asp Pro
 115 120 125

Asp Leu Val Ile Val Ser Ala Arg Phe Asp Thr Glu Gln Gly Thr Ile
 130 135 140
 Asp Ile Leu Glu Gly Leu Asn Val Pro Val Val Asn Phe Asp Ser Asp
 145 150 155 160
 Ala Trp Gly Asp Ile Asp Ala Ile Thr Lys His Leu Glu Ile Val Gly
 165 170 175
 Glu Leu Val Gly Glu Glu Asp Lys Ala Ala Glu Ala Ile Ala Glu Ile
 180 185 190
 Asp Ala Asn Arg Ile Asp Ile Asp Lys Pro Ala Thr Ser Pro Thr Val
 195 200 205
 Leu Thr Leu Met Gln Arg Gly Pro Arg Gln Met Val Met Pro Glu Ser
 210 215 220
 Ala Met Leu Asn Gly Leu Ile Arg Glu Ala Gly Gly Thr Pro Val Val
 225 230 235 240
 Asp Ser Leu Gly Ala Val Gly Thr Ile Thr Ala Asp Pro Glu Gln Val
 245 250 255
 Val Ala Met Ala Pro Glu Ile Ile Ile Ile Gln Asp Phe Gln Gly Lys
 260 265 270
 Gly Arg Glu Asn Phe Ala Asn Phe Leu Ser Asn Pro Ala Leu Ala Asn
 275 280 285
 Val Pro Ala Ile Glu Asn Asp Lys Ile Phe Tyr Ala Asp Thr Val Thr
 290 295 300
 Thr Gly Val Thr Ala Gly Thr Asp Ile Thr Thr Gly Leu Gln Gln Val
 305 310 315 320
 Ala Glu Met Leu Ser
 325

<210> 231

<211> 776

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(775)

<223> RXS03221

<400> 231

caaaagtatt caaaaaaagt ttgttatgta cgattgacgg gacatatcgt gtctgccacg 60

attaaagaca ttggtgatgt gaatcactgc ctactacatc gtg ttt cgt gac cct 115
 Val Phe Arg Asp Pro
 1 5

gca cct cca agt aag ggc acg aca aac tta gga gac aag atg gct agt 163
 Ala Pro Pro Ser Lys Gly Thr Thr Asn Leu Gly Asp Lys Met Ala Ser
 10 15 20

acc ttc att cag gcc gac agc cct gaa aaa agt aag aag ctg ccc cca 211
 Thr Phe Ile Gln Ala Asp Ser Pro Glu Lys Ser Lys Lys Leu Pro Pro
 25 30 35

ctc aca gaa ggt ccg tat aga aag cgg cta ttc tac gtt gca cta gtt 259
 Leu Thr Glu Gly Pro Tyr Arg Lys Arg Leu Phe Tyr Val Ala Leu Val
 40 45 50

gcg acg ttt ggt ggg ctg ctc ttc gga tat gac acc gga gta atc aac 307
 Ala Thr Phe Gly Gly Leu Leu Phe Gly Tyr Asp Thr Gly Val Ile Asn
 55 60 65

ggt gca ctc aac cca atg aca cgt gag ctc gga cta acc gcg ttc acc 355
 Gly Ala Leu Asn Pro Met Thr Arg Glu Leu Gly Leu Thr Ala Phe Thr
 70 75 80 85

gag ggt gtt gta act tct tcc ctg ctg ttt ggt gca gca gct ggt gcg 403
 Glu Gly Val Val Thr Ser Ser Leu Leu Phe Gly Ala Ala Ala Gly Ala
 90 95 100

atg ttt ttc ggt cgc att tcc gac aac tgg ggt cgc cgg aaa aca atc 451
 Met Phe Phe Gly Arg Ile Ser Asp Asn Trp Gly Arg Arg Lys Thr Ile
 105 110 115

atc tca ctt gca gta gct ttc ttt gtc ggc acc atg atc tgc gtg ttt 499
 Ile Ser Leu Ala Val Ala Phe Phe Val Gly Thr Met Ile Cys Val Phe
 120 125 130

gct cca tct ttt gca gta atg gtt gtc gga cgt gtg ctt ctt gga ctc 547
 Ala Pro Ser Phe Ala Val Met Val Val Gly Arg Val Leu Leu Gly Leu
 135 140 145

gca gtt ggt ggc gct tcc act gtt gtc cct gtc tac ctg gct gaa ctt 595
 Ala Val Gly Gly Ala Ser Thr Val Val Pro Val Tyr Leu Ala Glu Leu
 150 155 160 165

gct cct ttt gaa atc cgt ggc tca ctg gct ggc cgt aat gag ttg atg 643
 Ala Pro Phe Glu Ile Arg Gly Ser Leu Ala Gly Arg Asn Glu Leu Met
 170 175 180

att gtt gtt ggt cag ctc gca gct ttt gtc atc aat gcg att att gga 691
 Ile Val Val Gly Gln Leu Ala Ala Phe Val Ile Asn Ala Ile Ile Gly
 185 190 195

aat gtt ttt gga cac cac gat ggt gtg tgg cgc tac atg ctg gca att 739
 Asn Val Phe Gly His His Asp Gly Val Trp Arg Tyr Met Leu Ala Ile
 200 205 210

gcc gca atc cca gca att gcc ctc ttc ttt gga atg c 776
 Ala Ala Ile Pro Ala Ile Ala Leu Phe Phe Gly Met
 215 220 225

<210> 232

<211> 225

<212> PRT

<213> Corynebacterium glutamicum

<400> 232

Val Phe Arg Asp Pro Ala Pro Pro Ser Lys Gly Thr Thr Asn Leu Gly

1	5	10	15
Asp Lys Met	Ala Ser Thr Phe Ile Gln	Ala Asp Ser Pro Glu	Lys Ser
	20	25	30
Lys Lys Leu	Pro Pro Leu Thr Glu Gly	Pro Tyr Arg Lys	Arg Leu Phe
	35	40	45
Tyr Val Ala	Leu Val Ala Thr Phe Gly	Gly Leu Leu Phe Gly	Tyr Asp
	50	55	60
Thr Gly Val	Ile Asn Gly Ala Leu Asn	Pro Met Thr Arg Glu	Leu Gly
	65	70	75
Leu Thr Ala	Phe Thr Glu Gly Val Val	Thr Ser Ser Leu Leu	Phe Gly
	85	90	95
Ala Ala Ala	Gly Ala Met Phe Phe Gly	Arg Ile Ser Asp Asn	Trp Gly
	100	105	110
Arg Arg Lys	Thr Ile Ile Ser Leu Ala	Val Ala Phe Phe Val	Gly Thr
	115	120	125
Met Ile Cys	Val Phe Ala Pro Ser Phe	Ala Val Met Val Val	Gly Arg
	130	135	140
Val Leu Leu	Gly Leu Ala Val Gly Gly	Ala Ser Thr Val Val	Pro Val
	145	150	155
Tyr Leu Ala	Glu Leu Ala Pro Phe Glu	Ile Arg Gly Ser Leu	Ala Gly
	165	170	175
Arg Asn Glu	Leu Met Ile Val Val Gly	Gln Leu Ala Ala Phe	Val Ile
	180	185	190
Asn Ala Ile	Ile Gly Asn Val Phe Gly	His His Asp Gly Val	Trp Arg
	195	200	205
Tyr Met Leu	Ala Ile Ala Ala Ile Pro	Ala Ile Ala Leu Phe	Phe Gly
	210	215	220
Met			
225			

<210> 233

<211> 718

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(718)

<223> FRXA01986

<400> 233

gccacgatta aagacattgg tgatgtgaat cactgcctac tacatcgtgt ttcgtgaccc 60

tgcacctcca agtaagggca cgacaaactt aggagacaag atg gct agt acc ttc 115

Met Ala Ser Thr Phe

1

5

att cag gcc gac agc cct gaa aaa agt aag aag ctg ccc cca ctc aca 163
 Ile Gln Ala Asp Ser Pro Glu Lys Ser Lys Lys Leu Pro Pro Leu Thr
 10 15 20

gaa ggt ccg tat aga aag cgg cta ttc tac gtt gca cta gtt gcg acg 211
 Glu Gly Pro Tyr Arg Lys Arg Leu Phe Tyr Val Ala Leu Val Ala Thr
 25 30 35

ttt ggt ggg ctg ctc ttc gga tat gac acc gga gta atc aac ggt gca 259
 Phe Gly Gly Leu Leu Phe Gly Tyr Asp Thr Gly Val Ile Asn Gly Ala
 40 45 50

ctc aac cca atg aca cgt gag ctc gga cta acc gcg ttc acc gag ggt 307
 Leu Asn Pro Met Thr Arg Glu Leu Gly Leu Thr Ala Phe Thr Glu Gly
 55 60 65

gtt gta act tct tcc ctg ctg ttt ggt gca gca gct ggt gcg atg ttt 355
 Val Val Thr Ser Ser Leu Leu Phe Gly Ala Ala Ala Gly Ala Met Phe
 70 75 80 85

ttc ggt cgc att tcc gac aac tgg ggt cgc cgg aaa aca atc atc tca 403
 Phe Gly Arg Ile Ser Asp Asn Trp Gly Arg Arg Lys Thr Ile Ile Ser
 90 95 100

ctt gca gta gct ttc ttt gtc ggc acc atg atc tgc gtg ttt gct cca 451
 Leu Ala Val Ala Phe Phe Val Gly Thr Met Ile Cys Val Phe Ala Pro
 105 110 115

tct ttt gca gta atg gtt gtc gga cgt gtg ctt ctt gga ctc gca gtt 499
 Ser Phe Ala Val Met Val Val Gly Arg Val Leu Leu Gly Leu Ala Val
 120 125 130

ggt ggc gct tcc act gtt gtc cct gtc tac ctg gct gaa ctt gct cct 547
 Gly Gly Ala Ser Thr Val Val Pro Val Tyr Leu Ala Glu Leu Ala Pro
 135 140 145

ttt gaa atc cgt ggc tca ctg gct ggc cgt aat gag ttg atg att gtt 595
 Phe Glu Ile Arg Gly Ser Leu Ala Gly Arg Asn Glu Leu Met Ile Val
 150 155 160 165

gtt ggt cag ctc gca gct ttt gtc atc aat gcg att att gga aat gtt 643
 Val Gly Gln Leu Ala Ala Phe Val Ile Asn Ala Ile Ile Gly Asn Val
 170 175 180

ttt gga cac cac gat ggt gtg tgg cgc tac atg ctg gca att gcc gca 691
 Phe Gly His His Asp Gly Val Trp Arg Tyr Met Leu Ala Ile Ala Ala
 185 190 195

atc cca gca att gcc ctc ttc ttt gga 718
 Ile Pro Ala Ile Ala Leu Phe Phe Gly
 200 205

<210> 234

<211> 206

<212> PRT

<213> Corynebacterium glutamicum

<400> 234

Met Ala Ser Thr Phe Ile Gln Ala Asp Ser Pro Glu Lys Ser Lys Lys

1	5	10	15
Leu Pro Pro Leu Thr Glu Gly Pro Tyr Arg Lys Arg Leu Phe Tyr Val	20	25	30
Ala Leu Val Ala Thr Phe Gly Gly Leu Leu Phe Gly Tyr Asp Thr Gly	35	40	45
Val Ile Asn Gly Ala Leu Asn Pro Met Thr Arg Glu Leu Gly Leu Thr	50	55	60
Ala Phe Thr Glu Gly Val Val Thr Ser Ser Leu Leu Phe Gly Ala Ala	65	70	75
Ala Gly Ala Met Phe Phe Gly Arg Ile Ser Asp Asn Trp Gly Arg Arg	85	90	95
Lys Thr Ile Ile Ser Leu Ala Val Ala Phe Phe Val Gly Thr Met Ile	100	105	110
Cys Val Phe Ala Pro Ser Phe Ala Val Met Val Val Gly Arg Val Leu	115	120	125
Leu Gly Leu Ala Val Gly Gly Ala Ser Thr Val Val Pro Val Tyr Leu	130	135	140
Ala Glu Leu Ala Pro Phe Glu Ile Arg Gly Ser Leu Ala Gly Arg Asn	145	150	155
Glu Leu Met Ile Val Val Gly Gln Leu Ala Phe Val Ile Asn Ala	165	170	175
Ile Ile Gly Asn Val Phe Gly His His Asp Gly Val Trp Arg Tyr Met	180	185	190
Leu Ala Ile Ala Ala Ile Pro Ala Ile Ala Leu Phe Phe Gly	195	200	205

<210> 235

<211> 1118

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1095)

<223> RXN02447

<400> 235

aca gta gtt ccg gtg tac ctc gct gaa ctc gca cca cta gaa atc cgc	48
Thr Val Val Pro Val Tyr Leu Ala Glu Leu Ala Pro Leu Glu Ile Arg	
1 5 10 15	

ggc tcc ctg acc ggc cga aac gag ctt gct atc gtc acc ggc cag ctg	96
Gly Ser Leu Thr Gly Arg Asn Glu Leu Ala Ile Val Thr Gly Gln Leu	
20 25 30	

ctt gcc ttc gtg atc aac gcg ctt atc gcc gtc acc cta cac gga gtt	144
Leu Ala Phe Val Ile Asn Ala Leu Ile Ala Val Thr Leu His Gly Val	
35 40 45	

att gat gga atc tgg cgc atc atg ttc gcc gtc tgt gcc ctc cct gcc	192
Ile Asp Gly Ile Trp Arg Ile Met Phe Ala Val Cys Ala Leu Pro Ala	
50 55 60	
gtc gcc ctc ttc ctc ggc atg ctg cgg atg ccg gaa tca cca cgc tgg	240
Val Ala Leu Phe Leu Gly Met Leu Arg Met Pro Glu Ser Pro Arg Trp	
65 70 75 80	
ctg gtc aac cag ggg cgt tac gac gac gcc cgc cgc gtc atg gag acc	288
Leu Val Asn Gln Gly Arg Tyr Asp Asp Ala Arg Arg Val Met Glu Thr	
85 90 95	
gtc cgt acc cct gag cgt gcg aaa gcc gaa atg gat gaa atc atc gcg	336
Val Arg Thr Pro Glu Arg Ala Lys Ala Glu Met Asp Glu Ile Ile Ala	
100 105 110	
gtg cac tct gaa aac aat gcg gca ctt cct ggt gtt aag cag tct tcg	384
Val His Ser Glu Asn Asn Ala Ala Leu Pro Gly Val Lys Gln Ser Ser	
115 120 125	
ggc cag gct tca ggc cag gtt tct agc aag cac acc cac atg tcc atc	432
Gly Gln Ala Ser Gly Gln Val Ser Ser Lys His Thr His Met Ser Ile	
130 135 140	
ggc gaa gtc ctc agc aac aaa tgg ctg gtt cgt ctg ctc atc gcc gcc	480
Gly Glu Val Leu Ser Asn Lys Trp Leu Val Arg Leu Leu Ile Ala Gly	
145 150 155 160	
atc ggt gtt gca gtt gcc cag cag ctc acc gcc atc aac gcc atc atg	528
Ile Gly Val Ala Val Ala Gln Gln Leu Thr Gly Ile Asn Ala Ile Met	
165 170 175	
tac tac gga acc cgc gtc ctc gag gaa tcc gcc atg agc gca gaa atg	576
Tyr Tyr Gly Thr Arg Val Leu Glu Glu Ser Gly Met Ser Ala Glu Met	
180 185 190	
gct gtg gtt gcc aac att gct ttc ggt gcc gtt gcc gtc atc ggt gga	624
Ala Val Val Ala Asn Ile Ala Phe Gly Ala Val Ala Val Ile Gly Gly	
195 200 205	
ctg atc gca ctg cgc aac atg gac cgc ctg gat cgc cgc acc acc ttc	672
Leu Ile Ala Leu Arg Asn Met Asp Arg Leu Asp Arg Arg Thr Thr Phe	
210 215 220	
atc atc ggc ctg tca ctg acc acc acc ttc cac ctt ttg atc gca gct	720
Ile Ile Gly Leu Ser Leu Thr Thr Thr Phe His Leu Leu Ile Ala Ala	
225 230 235 240	
gcc gcc act ctc ctt cca gaa ggt aac tcc att cga cca ttc gcc atc	768
Ala Gly Thr Leu Leu Pro Glu Gly Asn Ser Ile Arg Pro Phe Ala Ile	
245 250 255	
atg atc ctt gtt gtt ggg ttc gtg ctc tcc atg cag act ttc ctc aac	816
Met Ile Leu Val Val Gly Phe Val Leu Ser Met Gln Thr Phe Leu Asn	
260 265 270	
gtt gca gtg tgg gtg tgg ctg gcg gaa atc ttc cca gtc cga atg aag	864
Val Ala Val Trp Val Trp Leu Ala Glu Ile Phe Pro Val Arg Met Lys	
275 280 285	

ggt atc ggc acc ggt att tcg gta ttc tgc ggt tgg ggc atc aat ggc 912
 Gly Ile Gly Thr Gly Ile Ser Val Phe Cys Gly Trp Gly Ile Asn Gly
 290 295 300

 gtc cta gcg ttg ttc ttc cca gca ctg gtc tcc ggc gtg ggt atc acc 960
 Val Leu Ala Leu Phe Phe Pro Ala Leu Val Ser Gly Val Gly Ile Thr
 305 310 315 320

 ttc tcc ttc ctt atc ttc gca gtc gtc gga gtc att gcc ctg gcg ttc 1008
 Phe Ser Phe Leu Ile Phe Ala Val Val Gly Val Ile Ala Leu Ala Phe
 325 330 335

 gtc acc aag ttt gtt cct gaa acc cgt ggc cgc tca ctt gaa gaa ctc 1056
 Val Thr Lys Phe Val Pro Glu Thr Arg Gly Arg Ser Leu Glu Glu Leu
 340 345 350

 gat cac gca gca ttc acc ggc cag atc ttc aag aag gct taaacccct 1105
 Asp His Ala Ala Phe Thr Gly Gln Ile Phe Lys Lys Ala
 355 360 365

 ccgatctctt tgg 1118

<210> 236

<211> 365

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 236

Thr Val Val Pro Val Tyr Leu Ala Glu Leu Ala Pro Leu Glu Ile Arg
 1 5 10 15

 Gly Ser Leu Thr Gly Arg Asn Glu Leu Ala Ile Val Thr Gly Gln Leu
 20 25 30

 Leu Ala Phe Val Ile Asn Ala Leu Ile Ala Val Thr Leu His Gly Val
 35 40 45

 Ile Asp Gly Ile Trp Arg Ile Met Phe Ala Val Cys Ala Leu Pro Ala
 50 55 60

 Val Ala Leu Phe Leu Gly Met Leu Arg Met Pro Glu Ser Pro Arg Trp
 65 70 75 80

 Leu Val Asn Gln Gly Arg Tyr Asp Asp Ala Arg Arg Val Met Glu Thr
 85 90 95

 Val Arg Thr Pro Glu Arg Ala Lys Ala Glu Met Asp Glu Ile Ile Ala
 100 105 110

 Val His Ser Glu Asn Asn Ala Ala Leu Pro Gly Val Lys Gln Ser Ser
 115 120 125

 Gly Gln Ala Ser Gly Gln Val Ser Ser Lys His Thr His Met Ser Ile
 130 135 140

 Gly Glu Val Leu Ser Asn Lys Trp Leu Val Arg Leu Leu Ile Ala Gly
 145 150 155 160

 Ile Gly Val Ala Val Ala Gln Gln Leu Thr Gly Ile Asn Ala Ile Met
 165 170 175

Tyr Tyr Gly Thr Arg Val Leu Glu Glu Ser Gly Met Ser Ala Glu Met
 180 185 190
 Ala Val Val Ala Asn Ile Ala Phe Gly Ala Val Ala Val Ile Gly Gly
 195 200 205
 Leu Ile Ala Leu Arg Asn Met Asp Arg Leu Asp Arg Arg Thr Thr Phe
 210 215 220
 Ile Ile Gly Leu Ser Leu Thr Thr Thr Phe His Leu Leu Ile Ala Ala
 225 230 235 240
 Ala Gly Thr Leu Leu Pro Glu Gly Asn Ser Ile Arg Pro Phe Ala Ile
 245 250 255
 Met Ile Leu Val Val Gly Phe Val Leu Ser Met Gln Thr Phe Leu Asn
 260 265 270
 Val Ala Val Trp Val Trp Leu Ala Glu Ile Phe Pro Val Arg Met Lys
 275 280 285
 Gly Ile Gly Thr Gly Ile Ser Val Phe Cys Gly Trp Gly Ile Asn Gly
 290 295 300
 Val Leu Ala Leu Phe Phe Pro Ala Leu Val Ser Gly Val Gly Ile Thr
 305 310 315 320
 Phe Ser Phe Leu Ile Phe Ala Val Val Gly Val Ile Ala Leu Ala Phe
 325 330 335
 Val Thr Lys Phe Val Pro Glu Thr Arg Gly Arg Ser Leu Glu Glu Leu
 340 345 350
 Asp His Ala Ala Phe Thr Gly Gln Ile Phe Lys Lys Ala
 355 360 365

<210> 237

<211> 293

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(270)

<223> FRXA02447

<400> 237

tgg gtg tgg ctg gcg gaa atc ttc cca gtc cga atg aag ggt atc ggc 48
 Trp Val Trp Leu Ala Glu Ile Phe Pro Val Arg Met Lys Gly Ile Gly
 1 5 10 15

acc ggt att tcg gta ttc tgc ggt tgg ggc atc aat ggc gtc cta gcg 96
 Thr Gly Ile Ser Val Phe Cys Gly Trp Gly Ile Asn Gly Val Leu Ala
 20 25 30

ttg ttc ttc cca gca ctg gtc tcc ggc gtg ggt atc acc ttc tcc ttc 144
 Leu Phe Phe Pro Ala Leu Val Ser Gly Val Gly Ile Thr Phe Ser Phe
 35 40 45

ctt atc ttc gca gtc gtc gga gtc att gcc ctg gcg ttc gtc acc aag 192
 Leu Ile Phe Ala Val Val Gly Val Ile Ala Leu Ala Phe Val Thr Lys
 50 55 60

ttt gtt cct gaa acc cgt ggc cgc tca ctt gaa gaa ctc gat cac gca 240
 Phe Val Pro Glu Thr Arg Gly Arg Ser Leu Glu Glu Leu Asp His Ala
 65 70 75 80

gca ttc acc ggc cag atc ttc aag aag gct taaacccct ccgatctctt 290
 Ala Phe Thr Gly Gln Ile Phe Lys Lys Ala
 85 90

tgg 293

<210> 238

<211> 90

<212> PRT

<213> Corynebacterium glutamicum

<400> 238

Trp Val Trp Leu Ala Glu Ile Phe Pro Val Arg Met Lys Gly Ile Gly
 1 5 10 15

Thr Gly Ile Ser Val Phe Cys Gly Trp Gly Ile Asn Gly Val Leu Ala
 20 25 30

Leu Phe Phe Pro Ala Leu Val Ser Gly Val Gly Ile Thr Phe Ser Phe
 35 40 45

Leu Ile Phe Ala Val Val Gly Val Ile Ala Leu Ala Phe Val Thr Lys
 50 55 60

Phe Val Pro Glu Thr Arg Gly Arg Ser Leu Glu Glu Leu Asp His Ala
 65 70 75 80

Ala Phe Thr Gly Gln Ile Phe Lys Lys Ala
 85 90

<210> 239

<211> 711

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(711)

<223> FRXA02769

<400> 239

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 Thr Val Val Pro Val Tyr Leu Ala Glu Leu Ala Pro Leu Glu Ile Arg
 1 5 10 15

ggc tcc ctg acc ggc cga aac gag ctt gct atc gtc acc ggc cag ctg 96
 Gly Ser Leu Thr Gly Arg Asn Glu Leu Ala Ile Val Thr Gly Gln Leu
 20 25 30

ctt gcc ttc gtg atc aac gcg ctt atc gcc gtc acc cta cac gga gtt 144
 Leu Ala Phe Val Ile Asn Ala Leu Ile Ala Val Thr Leu His Gly Val

35	40	45	
att gat gga atc tgg cgc atc atg ttc gcc gtc tgt gcc ctc cct gcc			192
Ile Asp Gly Ile Trp Arg Ile Met Phe Ala Val Cys Ala Leu Pro Ala			
50	55	60	
gtc gcc ctc ttc ctc ggc atg ctg cgg atg ccg gaa tca cca cgc tgg			240
Val Ala Leu Phe Leu Gly Met Leu Arg Met Pro Glu Ser Pro Arg Trp			
65	70	75	80
ctg gtc aac cag ggg cgt tac gac gac gcc cgc cgc gtc atg gag acc			288
Leu Val Asn Gln Gly Arg Tyr Asp Asp Ala Arg Arg Val Met Glu Thr			
	85	90	95
gtc cgt acc cct gag cgt gcg aaa gcc gaa atg gat gaa atc atc gcg			336
Val Arg Thr Pro Glu Arg Ala Lys Ala Glu Met Asp Glu Ile Ile Ala			
	100	105	110
gtg cac tct gaa aac aat gcg gca ctt cct ggt gtt aag cag tct tcg			384
Val His Ser Glu Asn Asn Ala Ala Leu Pro Gly Val Lys Gln Ser Ser			
	115	120	125
ggc cag gct tca ggc cag gtt tct agc aag cac acc cac atg tcc atc			432
Gly Gln Ala Ser Gly Gln Val Ser Ser Lys His Thr His Met Ser Ile			
	130	135	140
ggc gaa gtc ctc agc aac aaa tgg ctg gtt cgt ctg ctc atc gcc ggc			480
Gly Glu Val Leu Ser Asn Lys Trp Leu Val Arg Leu Leu Ile Ala Gly			
145	150	155	160
atc ggt gtt gca gtt gcc cag cag ctc acc ggc atc aac gcc atc atg			528
Ile Gly Val Ala Val Ala Gln Gln Leu Thr Gly Ile Asn Ala Ile Met			
	165	170	175
tac tac gga acc cgc gtc ctc gag gaa tcc ggc atg agc gca gaa atg			576
Tyr Tyr Gly Thr Arg Val Leu Glu Glu Ser Gly Met Ser Ala Glu Met			
	180	185	190
gct gtg gtt gcc aac att gct ttc ggt gcc gtt gcc gtc atc ggt gga			624
Ala Val Val Ala Asn Ile Ala Phe Gly Ala Val Ala Val Ile Gly Gly			
	195	200	205
ctg atc gca ctg cgc aac atg gac cgc ctg gat cgc cgc acc acc ttc			672
Leu Ile Ala Leu Arg Asn Met Asp Arg Leu Asp Arg Arg Thr Thr Phe			
	210	215	220
atc atc ggc ctg tca ctg acc acc acc ttc cac ctt ttg			711
Ile Ile Gly Leu Ser Leu Thr Thr Thr Phe His Leu Leu			
225	230	235	

<210> 240

<211> 237

<212> PRT

<213> Corynebacterium glutamicum

<400> 240

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Gly Ser Leu Thr Gly Arg Asn Glu Leu Ala Ile Val Thr Gly Gln Leu

20					25					30					
Leu	Ala	Phe	Val	Ile	Asn	Ala	Leu	Ile	Ala	Val	Thr	Leu	His	Gly	Val
	35						40					45			
Ile	Asp	Gly	Ile	Trp	Arg	Ile	Met	Phe	Ala	Val	Cys	Ala	Leu	Pro	Ala
	50					55					60				
Val	Ala	Leu	Phe	Leu	Gly	Met	Leu	Arg	Met	Pro	Glu	Ser	Pro	Arg	Trp
	65					70					75				80
Leu	Val	Asn	Gln	Gly	Arg	Tyr	Asp	Asp	Ala	Arg	Arg	Val	Met	Glu	Thr
			85						90					95	
Val	Arg	Thr	Pro	Glu	Arg	Ala	Lys	Ala	Glu	Met	Asp	Glu	Ile	Ile	Ala
			100					105					110		
Val	His	Ser	Glu	Asn	Asn	Ala	Ala	Leu	Pro	Gly	Val	Lys	Gln	Ser	Ser
		115					120					125			
Gly	Gln	Ala	Ser	Gly	Gln	Val	Ser	Ser	Lys	His	Thr	His	Met	Ser	Ile
	130					135					140				
Gly	Glu	Val	Leu	Ser	Asn	Lys	Trp	Leu	Val	Arg	Leu	Leu	Ile	Ala	Gly
	145					150					155				160
Ile	Gly	Val	Ala	Val	Ala	Gln	Gln	Leu	Thr	Gly	Ile	Asn	Ala	Ile	Met
				165					170					175	
Tyr	Tyr	Gly	Thr	Arg	Val	Leu	Glu	Glu	Ser	Gly	Met	Ser	Ala	Glu	Met
			180					185					190		
Ala	Val	Val	Ala	Asn	Ile	Ala	Phe	Gly	Ala	Val	Ala	Val	Ile	Gly	Gly
		195					200					205			
Leu	Ile	Ala	Leu	Arg	Asn	Met	Asp	Arg	Leu	Asp	Arg	Arg	Thr	Thr	Phe
	210					215					220				
Ile	Ile	Gly	Leu	Ser	Leu	Thr	Thr	Thr	Phe	His	Leu	Leu			
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<210> 241

<211> 725

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (3)..(695)

<223> RXS03220

<400> 241

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 Met Gly Leu Arg Glu Ile Leu Ser Ser Lys Trp Leu Val Arg Ile Leu
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ctg gta ggt atc gga ttg ggt gtc gca cag cag ctg acc ggc atc aac 98
 Leu Val Gly Ile Gly Leu Gly Val Ala Gln Gln Leu Thr Gly Ile Asn
 20 25 30

tcc atc atg tac tac ggc cag gtt gtt ctc att gag gct ggt ttc tcc 146
 Ser Ile Met Tyr Tyr Gly Gln Val Val Leu Ile Glu Ala Gly Phe Ser
 35 40 45
 gag aat gca gct ctg atc gcc aac gtg gcg cca gga gtg atc gca gtt 194
 Glu Asn Ala Ala Leu Ile Ala Asn Val Ala Pro Gly Val Ile Ala Val
 50 55 60
 gtc ggt gca ttc atc gca ctg tgg atg atg gat ggt atc aac cgc cgt 242
 Val Gly Ala Phe Ile Ala Leu Trp Met Met Asp Gly Ile Asn Arg Arg
 65 70 75 80
 acc acc ctc att acc ggt tat tct ctc acc acc att agc cac gta ttg 290
 Thr Thr Leu Ile Thr Gly Tyr Ser Leu Thr Thr Ile Ser His Val Leu
 85 90 95
 atc ggt atc gca tcc gta gca ttc cca gtc ggc gat cct ctt cgc ccc 338
 Ile Gly Ile Ala Ser Val Ala Phe Pro Val Gly Asp Pro Leu Arg Pro
 100 105 110
 tac gtt atc ttg act ctg gtt gtg gtc ttc gtg gga tcc atg cag acc 386
 Tyr Val Ile Leu Thr Leu Val Val Phe Val Gly Ser Met Gln Thr
 115 120 125
 ttc ctc aac gta gct acc tgg gtt atg ctc tct gag ctc ttc ccg ctg 434
 Phe Leu Asn Val Ala Thr Trp Val Met Leu Ser Glu Leu Phe Pro Leu
 130 135 140
 gca atg cgc ggt ttc gca atc ggt atc tca gtg ttc ttc ctc tgg atc 482
 Ala Met Arg Gly Phe Ala Ile Gly Ile Ser Val Phe Phe Leu Trp Ile
 145 150 155 160
 gca aac gcg ttc ctc gga ttg ttc ttc cca acc atc atg gaa gca gta 530
 Ala Asn Ala Phe Leu Gly Leu Phe Phe Pro Thr Ile Met Glu Ala Val
 165 170 175
 gga cta acc gga acc ttc ttc atg ttc gcc gga atc ggt gtg gtt gcc 578
 Gly Leu Thr Gly Thr Phe Phe Met Phe Ala Gly Ile Gly Val Val Ala
 180 185 190
 ttg atc ttc atc tac acc cag gtt cct gaa act cgt gga cgt acc ttg 626
 Leu Ile Phe Ile Tyr Thr Gln Val Pro Glu Thr Arg Gly Arg Thr Leu
 195 200 205
 gag gag att gat gag gat gtt act tcc ggt gtc att ttc aac aag gac 674
 Glu Glu Ile Asp Glu Asp Val Thr Ser Gly Val Ile Phe Asn Lys Asp
 210 215 220
 atc cga aaa gga aag gtg cac taaaaaccca gacactgcat agataacacg 725
 Ile Arg Lys Gly Lys Val His
 225 230

<210> 242

<211> 231

<212> PRT

<213> Corynebacterium glutamicum

<400> 242

Met Gly Leu Arg Glu Ile Leu Ser Ser Lys Trp Leu Val Arg Ile Leu
 1 5 10 15

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<210> 243
<211> 408
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS
<222> (101)..(385)
<223> FRXA02762
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ggatccatgc agaccttcct caacggtagc tacctggggt atg ctc tct gag ctc 115
                               Met Leu Ser Glu Leu
                               1       5
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ttc ccg ctg gca atg cgc ggt ttc gca atc ggt atc tca gtg ttc ttc 163
 Phe Pro Leu Ala Met Arg Gly Phe Ala Ile Gly Ile Ser Val Phe Phe
 10 15 20

 ctc tgg atc gca aac gcg ttc ctc gga ttg ttc ttc cca acc atc atg 211
 Leu Trp Ile Ala Asn Ala Phe Leu Gly Leu Phe Phe Pro Thr Ile Met
 25 30 35

 gaa gca gta gga cta acc gga acc ttc ttc atg ttc gcc gga atc ggt 259
 Glu Ala Val Gly Leu Thr Gly Thr Phe Phe Met Phe Ala Gly Ile Gly
 40 45 50

 gtg gtt gcc ttg atc ttc atc tac acc cag gtt cct gaa act cgt gga 307
 Val Val Ala Leu Ile Phe Ile Tyr Thr Gln Val Pro Glu Thr Arg Gly
 55 60 65

 cgt acc ttg gag gag att gat gag gat gtt act tcc ggt gtc att ttc 355
 Arg Thr Leu Glu Glu Ile Asp Glu Asp Val Thr Ser Gly Val Ile Phe
 70 75 80 85

 aac aag gac atc cga aaa gga aag gtg cac taaaaaccga gacactgcat 405
 Asn Lys Asp Ile Arg Lys Gly Lys Val His
 90 95

 aga 408

<210> 244
 <211> 95
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 244
 Met Leu Ser Glu Leu Phe Pro Leu Ala Met Arg Gly Phe Ala Ile Gly
 1 5 10 15

 Ile Ser Val Phe Phe Leu Trp Ile Ala Asn Ala Phe Leu Gly Leu Phe
 20 25 30

 Phe Pro Thr Ile Met Glu Ala Val Gly Leu Thr Gly Thr Phe Phe Met
 35 40 45

 Phe Ala Gly Ile Gly Val Val Ala Leu Ile Phe Ile Tyr Thr Gln Val
 50 55 60

 Pro Glu Thr Arg Gly Arg Thr Leu Glu Glu Ile Asp Glu Asp Val Thr
 65 70 75 80

 Ser Gly Val Ile Phe Asn Lys Asp Ile Arg Lys Gly Lys Val His
 85 90 95

<210> 245
 <211> 324
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(301)
 <223> FRXA02761

<400> 245

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cagaagtgat cgcagttgtc gggcattcat cgcactgtgg atg atg gat ggt atc 115
 Met Met Asp Gly Ile
 1 5

aac cgc cgt acc acc ctc att acc ggt tat tct ctc acc acc att agc 163
 Asn Arg Arg Thr Thr Leu Ile Thr Gly Tyr Ser Leu Thr Thr Ile Ser
 10 15 20

cac gta ttg atc ggt atc gca tcc gta gca ttc cca gtc ggc gat cct 211
 His Val Leu Ile Gly Ile Ala Ser Val Ala Phe Pro Val Gly Asp Pro
 25 30 35

ctt cgc ccc tac gtt atc ttg act ctg gtt gtg gtc ttc gtg gga tcc 259
 Leu Arg Pro Tyr Val Ile Leu Thr Leu Val Val Val Phe Val Gly Ser
 40 45 50

atg cag acc ttc ctc aac ggt agc tac ctg ggt tat gct ctc 301
 Met Gln Thr Phe Leu Asn Gly Ser Tyr Leu Gly Tyr Ala Leu
 55 60 65

tgagctcttc ccgctggcaa tgc 324

<210> 246

<211> 67

<212> PRT

<213> Corynebacterium glutamicum

<400> 246

Met Met Asp Gly Ile Asn Arg Arg Thr Thr Leu Ile Thr Gly Tyr Ser
 1 5 10 15

Leu Thr Thr Ile Ser His Val Leu Ile Gly Ile Ala Ser Val Ala Phe
 20 25 30

Pro Val Gly Asp Pro Leu Arg Pro Tyr Val Ile Leu Thr Leu Val Val
 35 40 45

Val Phe Val Gly Ser Met Gln Thr Phe Leu Asn Gly Ser Tyr Leu Gly
 50 55 60

Tyr Ala Leu
 65

<210> 247

<211> 1242

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1219)

<223> RXA00123

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tagtagaaat tgctgtccag aactgttgaa ggagttgaaa atg cca aag aat tac	115
Met Pro Lys Asn Tyr	
1 5	
gac atc aac ggg gcg atc cgc aga cgg gat atg ctc aga cgt cgg tac	163
Asp Ile Asn Gly Ala Ile Arg Arg Arg Asp Met Leu Arg Arg Arg Tyr	
10 15 20	
ctt cct gat tcg gca aat tca act cct gta cct gaa gag gtt tct ccg	211
Leu Pro Asp Ser Ala Asn Ser Thr Pro Val Pro Glu Glu Val Ser Pro	
25 30 35	
ctg acc cgc tat gtc acc gac ggc atc ccg aag cgc cca ccg ctg ggt	259
Leu Thr Arg Tyr Val Thr Asp Gly Ile Pro Lys Arg Pro Pro Leu Gly	
40 45 50	
gcc act gtt gct gac ggt tta aaa ttc gcc gaa ggc gcc tcc aac cgc	307
Ala Thr Val Ala Asp Gly Leu Lys Phe Ala Glu Gly Ala Ser Asn Arg	
55 60 65	
atg gtc atg tcg ctg tac cct gcg cca tcc aag ccc gca atc gag gaa	355
Met Val Met Ser Leu Tyr Pro Ala Pro Ser Lys Pro Ala Ile Glu Glu	
70 75 80 85	
ttg gca gag gcc tgg gac ctc cac ccc acc atc gta gaa gac ttg ctc	403
Leu Ala Glu Ala Trp Asp Leu His Pro Thr Ile Val Glu Asp Leu Leu	
90 95 100	
ctt ggt cag cag cgc cca aaa cta gac cgc tac gaa gac atc att ttt	451
Leu Gly Gln Gln Arg Pro Lys Leu Asp Arg Tyr Glu Asp Ile Ile Phe	
105 110 115	
atc gcg atc cgc tcc gcg cgc tac atc gac tcc cgc gaa gag gtg gac	499
Ile Ala Ile Arg Ser Ala Arg Tyr Ile Asp Ser Arg Glu Glu Val Asp	
120 125 130	
ttc tcc gaa ttc cac atc ctc atg aag cct cag gcc ata gcc att ttg	547
Phe Ser Glu Phe His Ile Leu Met Lys Pro Gln Ala Ile Ala Ile Leu	
135 140 145	
tgc cag gat aac caa tgg att gac ggc acc agc gcc gcc agc ttc agc	595
Cys Gln Asp Asn Gln Trp Ile Asp Gly Thr Ser Ala Ala Ser Phe Ser	
150 155 160 165	
aac ccc gag gag atc gat aag cgc ata aaa aca ttg ctt gcc gac gcc	643
Asn Pro Glu Glu Ile Asp Lys Arg Ile Lys Thr Leu Leu Ala Asp Ala	
170 175 180	
gag tta ctc tcg tcc ggc ccc cgc gcc gcg gcc tat agg ctt ctc gac	691
Glu Leu Leu Ser Ser Gly Pro Arg Ala Ala Ala Tyr Arg Leu Leu Asp	
185 190 195	
gcc atc gtc gac ggc ttc tcc ccc gtt ctt aga ggc atc gcc atc gac	739
Ala Ile Val Asp Gly Phe Ser Pro Val Leu Arg Gly Ile Ala Ile Asp	
200 205 210	
cag gaa cag att gag cgc cag gtg ttc tcc ggc gac gcc gcc gtc gcc	787
Gln Glu Gln Ile Glu Arg Gln Val Phe Ser Gly Asp Ala Ala Val Ala	
215 220 225	

gaa cgt att tac aac ctg tcc caa gaa atc atc gac atg cag cac acc 835
 Glu Arg Ile Tyr Asn Leu Ser Gln Glu Ile Ile Asp Met Gln His Thr
 230 235 240 245

 acc agc tca gtt acc gaa gtg gtg caa cgc ctc aac aaa gac ttc atc 883
 Thr Ser Ser Val Thr Glu Val Val Gln Arg Leu Asn Lys Asp Phe Ile
 250 255 260

 cga agt ggc atg tcc gaa gaa ctc cgc gcc tac ctc gac gac gtc gcc 931
 Arg Ser Gly Met Ser Glu Glu Leu Arg Ala Tyr Leu Asp Asp Val Ala
 265 270 275

 gac cac ctc acc cgc gac aac acc cgc gtc tcc gaa tac cgc gaa tcc 979
 Asp His Leu Thr Arg Asp Asn Thr Arg Val Ser Glu Tyr Arg Glu Ser
 280 285 290

 cta tcc caa att ttg aac gtc aac gcc acc ctt gta gcc caa cgc caa 1027
 Leu Ser Gln Ile Leu Asn Val Asn Ala Thr Leu Val Ala Gln Arg Gln
 295 300 305

 aac gaa gac atg aag aaa atc tcc gga tgg gcc gcc atc atc ttc gcc 1075
 Asn Glu Asp Met Lys Lys Ile Ser Gly Trp Ala Ala Ile Ile Phe Ala
 310 315 320 325

 cca acc ctc gtg tcc tcc atc tac ggc atg aac ttc gac atc atg cca 1123
 Pro Thr Leu Val Ser Ser Ile Tyr Gly Met Asn Phe Asp Ile Met Pro
 330 335 340

 gaa ctt cac tgg gcg ttt ggc tac ccg ttg gct ctc tta gca atg ctc 1171
 Glu Leu His Trp Ala Phe Gly Tyr Pro Leu Ala Leu Leu Ala Met Leu
 345 350 355

 gga ttc acc ctc ctt ttg tac tgg atc ttc aaa cgc agt aag tgg atg 1219
 Gly Phe Thr Leu Leu Leu Tyr Trp Ile Phe Lys Arg Ser Lys Trp Met
 360 365 370

 tgagacaaaa accgaaaaac caa 1242

<210> 248

<211> 373

<212> PRT

<213> Corynebacterium glutamicum

<400> 248

Met Pro Lys Asn Tyr Asp Ile Asn Gly Ala Ile Arg Arg Arg Asp Met
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Leu Arg Arg Arg Tyr Leu Pro Asp Ser Ala Asn Ser Thr Pro Val Pro
 20 25 30

Glu Glu Val Ser Pro Leu Thr Arg Tyr Val Thr Asp Gly Ile Pro Lys
 35 40 45

Arg Pro Pro Leu Gly Ala Thr Val Ala Asp Gly Leu Lys Phe Ala Glu
 50 55 60

Gly Ala Ser Asn Arg Met Val Met Ser Leu Tyr Pro Ala Pro Ser Lys
 65 70 75 80

Pro Ala Ile Glu Glu Leu Ala Glu Ala Trp Asp Leu His Pro Thr Ile

85					90					95					
Val	Glu	Asp	Leu	Leu	Leu	Gly	Gln	Gln	Arg	Pro	Lys	Leu	Asp	Arg	Tyr
			100					105					110		
Glu	Asp	Ile	Ile	Phe	Ile	Ala	Ile	Arg	Ser	Ala	Arg	Tyr	Ile	Asp	Ser
		115					120					125			
Arg	Glu	Glu	Val	Asp	Phe	Ser	Glu	Phe	His	Ile	Leu	Met	Lys	Pro	Gln
	130					135					140				
Ala	Ile	Ala	Ile	Leu	Cys	Gln	Asp	Asn	Gln	Trp	Ile	Asp	Gly	Thr	Ser
145					150					155					160
Ala	Ala	Ser	Phe	Ser	Asn	Pro	Glu	Glu	Ile	Asp	Lys	Arg	Ile	Lys	Thr
				165					170					175	
Leu	Leu	Ala	Asp	Ala	Glu	Leu	Leu	Ser	Ser	Gly	Pro	Arg	Ala	Ala	Ala
			180					185					190		
Tyr	Arg	Leu	Leu	Asp	Ala	Ile	Val	Asp	Gly	Phe	Ser	Pro	Val	Leu	Arg
		195					200					205			
Gly	Ile	Ala	Ile	Asp	Gln	Glu	Gln	Ile	Glu	Arg	Gln	Val	Phe	Ser	Gly
	210					215					220				
Asp	Ala	Ala	Val	Ala	Glu	Arg	Ile	Tyr	Asn	Leu	Ser	Gln	Glu	Ile	Ile
225					230					235					240
Asp	Met	Gln	His	Thr	Thr	Ser	Ser	Val	Thr	Glu	Val	Val	Gln	Arg	Leu
				245					250					255	
Asn	Lys	Asp	Phe	Ile	Arg	Ser	Gly	Met	Ser	Glu	Glu	Leu	Arg	Ala	Tyr
			260					265					270		
Leu	Asp	Asp	Val	Ala	Asp	His	Leu	Thr	Arg	Asp	Asn	Thr	Arg	Val	Ser
		275					280					285			
Glu	Tyr	Arg	Glu	Ser	Leu	Ser	Gln	Ile	Leu	Asn	Val	Asn	Ala	Thr	Leu
	290					295					300				
Val	Ala	Gln	Arg	Gln	Asn	Glu	Asp	Met	Lys	Lys	Ile	Ser	Gly	Trp	Ala
305					310					315					320
Ala	Ile	Ile	Phe	Ala	Pro	Thr	Leu	Val	Ser	Ser	Ile	Tyr	Gly	Met	Asn
				325					330					335	
Phe	Asp	Ile	Met	Pro	Glu	Leu	His	Trp	Ala	Phe	Gly	Tyr	Pro	Leu	Ala
			340					345					350		
Leu	Leu	Ala	Met	Leu	Gly	Phe	Thr	Leu	Leu	Leu	Tyr	Trp	Ile	Phe	Lys
		355					360					365			
Arg	Ser	Lys	Trp	Met											
	370														

<210> 249

<211> 780

<212> DNA

<213> Corynebacterium glutamicum

<223> RXA02441

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gtc cgg aat ctc aca tgc aca tac ggc aat cac atc gcg ctc aac aac 163
Val Arg Asn Leu Thr Cys Thr Tyr Gly Asn His Ile Ala Leu Asn Asn
10 15 20

atc acg gca cgc ttc cca acc gga aaa ata act gcc ctc atc ggc agc 211
Ile Thr Ala Arg Phe Pro Thr Gly Lys Ile Thr Ala Leu Ile Gly Ser
25 30 35

aac ggc tcc gga aaa tcc aca ctg ttg gaa act ttg gcg ggc atg ctg 259
Asn Gly Ser Gly Lys Ser Thr Leu Leu Glu Thr Leu Ala Gly Met Leu
40 45 50

gca ccc cgc agc gga agc att aac aac ctt gtg cca gaa atc gcg ttc 307
Ala Pro Arg Ser Gly Ser Ile Asn Asn Leu Val Pro Glu Ile Ala Phe
55 60 65

gtc ccc caa cgc agc cac gtc tcc cat aat ttg ccc atc acg atc aga 355
Val Pro Gln Arg Ser His Val Ser His Asn Leu Pro Ile Thr Ile Arg
70 75 80 85

caa aca gtc agc atg ggg cga tgg tca gcc aag aaa aac tgg caa cga 403
Gln Thr Val Ser Met Gly Arg Trp Ser Ala Lys Lys Asn Trp Gln Arg
90 95 100

ctc act gcc gca gat tgc aac atc gtg gac agc tgc ctc gac cgg ctc 451
Leu Thr Ala Ala Asp Cys Asn Ile Val Asp Ser Cys Leu Asp Arg Leu
105 110 115

gaa atc tcc ggc ctc gcc gac cgc ccc ctc ggc gaa gta tca ggc ggg 499
Glu Ile Ser Gly Leu Ala Asp Arg Pro Leu Gly Glu Val Ser Gly Gly
120 125 130

cag cgc caa cgc gcc ctc ata gcg caa ggt tta gcg caa cag gcg ccc 547
Gln Arg Gln Arg Ala Leu Ile Ala Gln Gly Leu Ala Gln Gln Ala Pro
135 140 145

tta ttg ctt ctc gac gaa ccc ctc gcc gcc gtg gac tcc cac gcg gca	595
Leu Leu Leu Leu Asp Glu Pro Leu Ala Ala Val Asp Ser His Ala Ala	
150	155 160 165

agt ctt atc gaa gat gtc att aac caa caa cgc aac caa gga acc aca 643
 Ser Leu Ile Glu Asp Val Ile Asn Gln Gln Arg Asn Gln Gly Thr Thr
 170 175 180

att att ctt gcg act cac gat ctt gat caa gca cat caa gca gat cag 691
Ile Ile Leu Ala Thr His Asp Leu Asp Gln Ala His Gln Ala Asp Gln
185 190 195

att atc gcc ttg gaa aaa gga atc ata aag cca cag cgc aaa gcc act 739
 Ile Ile Ala Leu Glu Lys Gly Ile Ile Lys Pro Gln Arg Lys Ala Thr
 200 210

gaa tca ata aag aag cgt taataaaagtt tgacttgtgc ctc 780
 Glu Ser Ile Lys Lys Arg
 215

<210> 250

<211> 219

<212> PRT

<213> Corynebacterium glutamicum

<400> 250

Met Ala Glu Leu Ser Val Arg Asn Leu Thr Cys Thr Tyr Gly Asn His
 1 10 15

Ile Ala Leu Asn Asn Ile Thr Ala Arg Phe Pro Thr Gly Lys Ile Thr
 20 25 30

Ala Leu Ile Gly Ser Asn Gly Ser Gly Lys Ser Thr Leu Leu Glu Thr
 35 40 45

Leu Ala Gly Met Leu Ala Pro Arg Ser Gly Ser Ile Asn Asn Leu Val
 50 55 60

Pro Glu Ile Ala Phe Val Pro Gln Arg Ser His Val Ser His Asn Leu
 65 70 75 80

Pro Ile Thr Ile Arg Gln Thr Val Ser Met Gly Arg Trp Ser Ala Lys
 85 90 95

Lys Asn Trp Gln Arg Leu Thr Ala Ala Asp Cys Asn Ile Val Asp Ser
 100 105 110

Cys Leu Asp Arg Leu Glu Ile Ser Gly Leu Ala Asp Arg Pro Leu Gly
 115 120 125

Glu Val Ser Gly Gly Gln Arg Gln Arg Ala Leu Ile Ala Gln Gly Leu
 130 135 140

Ala Gln Gln Ala Pro Leu Leu Leu Leu Asp Glu Pro Leu Ala Ala Val
 145 150 155 160

Asp Ser His Ala Ala Ser Leu Ile Glu Asp Val Ile Asn Gln Gln Arg
 165 170 175

Asn Gln Gly Thr Thr Ile Ile Leu Ala Thr His Asp Leu Asp Gln Ala
 180 185 190

His Gln Ala Asp Gln Ile Ile Ala Leu Glu Lys Gly Ile Ile Lys Pro
 195 200 205

Gln Arg Lys Ala Thr Glu Ser Ile Lys Lys Arg
 210 215

<210> 251

<211> 972

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(949)

<223> RXN02442

<400> 251

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agttctgccca ttccttaatg ataacggtta tcattttcaa atg aag ttt ttt act 115
                                         Met Lys Phe Phe Thr
                                         1           5

gac gcc ctc ata gtg cct ttt gac gtt tca ttc atc tcc cgc gcc ctg 163
Asp Ala Leu Ile Val Pro Phe Asp Val Ser Phe Ile Ser Arg Ala Leu
                        10                15                20

gtc gcc gga tgc ctg gcc gca att tta tgc tca ctc att gga acg tgg 211
Val Ala Gly Cys Leu Ala Ala Ile Leu Cys Ser Leu Ile Gly Thr Trp
                        25                30                35

gtt att ttg cgc agg cta acc ttt ttc ggc gac gct atg tgc cac ggc 259
Val Ile Leu Arg Arg Leu Thr Phe Phe Gly Asp Ala Met Ser His Gly
                        40                45                50

ttg ctc ccc gga gta gcc acg gca tca cta ttg ggc gga aat ctc atg 307
Leu Leu Pro Gly Val Ala Thr Ala Ser Leu Leu Gly Gly Asn Leu Met
                        55                60                65

ttc ggc gca gca atc agc gca tta atc atg tca gcc gga gtg gtg tgg 355
Phe Gly Ala Ala Ile Ser Ala Leu Ile Met Ser Ala Gly Val Val Trp
                        70                75                80                85

acc agc aga aaa tcc agc ctc tcc caa gac gtc agc att ggc ctg caa 403
Thr Ser Arg Lys Ser Ser Leu Ser Gln Asp Val Ser Ile Gly Leu Gln
                        90                95                100

ttt att acc atg ctt tcc ctc ggc gtg gtt att gtg tcc cac tcc gat 451
Phe Ile Thr Met Leu Ser Leu Gly Val Val Ile Val Ser His Ser Asp
                        105                110                115

tcc cac gcc gta gac ctc acc agt ttc ctt ttt gga gac att ctt ggc 499
Ser His Ala Val Asp Leu Thr Ser Phe Leu Phe Gly Asp Ile Leu Gly
                        120                125                130

gtg cga ccc tcg gat ata ttc atc atc gcc att gca aca gtg ttg ggt 547
Val Arg Pro Ser Asp Ile Phe Ile Ile Ala Ile Ala Thr Val Leu Gly
                        135                140                145

gga ttg act att ttt ctc ttc cac cga cag ttc act gca ctc gct ttc 595
Gly Leu Thr Ile Phe Leu Phe His Arg Gln Phe Thr Ala Leu Ala Phe
                        150                155                160                165

gac gag cgt aaa gct cac acc tta gga ctc aat ccc cgc ttt gca cac 643
Asp Glu Arg Lys Ala His Thr Leu Gly Leu Asn Pro Arg Phe Ala His
                        170                175                180

cta ctc atg ctg gca ctg atc gca tta gct acg gtg gtg tcg ttt cag 691
Leu Leu Met Leu Ala Leu Ile Ala Leu Ala Thr Val Val Ser Phe Gln
                        185                190                195

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<210> 252
<211> 283
<212> PRT
<213> Corvnebacterium glutamicum
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Met	Lys	Phe	Phe	Thr	Asp	Ala	Leu	Ile	Val	Pro	Phe	Asp	Val	Ser	Phe
1				5					10					15	
Ile	Ser	Arg	Ala	Leu	Val	Ala	Gly	Cys	Leu	Ala	Ala	Ile	Leu	Cys	Ser
			20					25					30		
Leu	Ile	Gly	Thr	Trp	Val	Ile	Leu	Arg	Arg	Leu	Thr	Phe	Phe	Gly	Asp
		35					40					45			
Ala	Met	Ser	His	Gly	Leu	Leu	Pro	Gly	Val	Ala	Thr	Ala	Ser	Leu	Leu
	50					55					60				
Gly	Gly	Asn	Leu	Met	Phe	Gly	Ala	Ala	Ile	Ser	Ala	Leu	Ile	Met	Ser
65					70					75					80
Ala	Gly	Val	Val	Trp	Thr	Ser	Arg	Lys	Ser	Ser	Leu	Ser	Gln	Asp	Val
				85					90					95	
Ser	Ile	Gly	Leu	Gln	Phe	Ile	Thr	Met	Leu	Ser	Leu	Gly	Val	Val	Ile
			100					105					110		
Val	Ser	His	Ser	Asp	Ser	His	Ala	Val	Asp	Leu	Thr	Ser	Phe	Leu	Phe
		115					120					125			
Gly	Asp	Ile	Leu	Gly	Val	Arg	Pro	Ser	Asp	Ile	Phe	Ile	Ile	Ala	Ile
	130					135					140				
Ala	Thr	Val	Leu	Gly	Gly	Leu	Thr	Ile	Phe	Leu	Phe	His	Arg	Gln	Phe
145					150					155					160

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<210> 253
<211> 972
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(949)
<223> FRXA02442
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<400> 253															60
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agttctgccca ttctttaatg ataacgggta tcattttcaa															115
Met Lys Phe Phe Thr															
1 5															
gac gcc ctc ata gtg cct ttt gac gtt tca ttc atc tcc cgc gcc ctg															163
Asp Ala Leu Ile Val Pro Phe Asp Val Ser Phe Ile Ser Arg Ala Leu															
10 15 20															
gtc gcc gga tgc ctg gcc gca att tta tgc tca ctc att gga acg tgg															211
Val Ala Gly Cys Leu Ala Ala Ile Leu Cys Ser Leu Ile Gly Thr Trp															
25 30 35															
gtt att ttg cgc agg cta acc ttt ttc ggc gac gct atg tgc cac ggc															259
Val Ile Leu Arg Arg Leu Thr Phe Phe Gly Asp Ala Met Ser His Gly															
40 45 50															
ttg ctc ccc gga gta gcc acg gca tca cta ttg ggc gga aat ctc atg															307
Leu Leu Pro Gly Val Ala Thr Ala Ser Leu Leu Gly Gly Asn Leu Met															
55 60 65															
ttc ggc gca gca atc agc gca tta atc atg tca gcc gga gtg gtg tgg															355
Phe Gly Ala Ala Ile Ser Ala Leu Ile Met Ser Ala Gly Val Val Trp															

70	75	80	85	
acc agc aga aaa tcc agc ctc tcc caa gac gtc agc att ggc ctg caa				403
Thr Ser Arg Lys Ser Ser Leu Ser Gln Asp Val Ser Ile Gly Leu Gln	90	95	100	
ttt att acc atg ctt tcc ctc ggc gtg gtt att gtg tcc cac tcc gat				451
Phe Ile Thr Met Leu Ser Leu Gly Val Val Ile Val Ser His Ser Asp	105	110	115	
tcc cac gcc gta gac ctc acc agt ttc ctt ttt gga gac att ctt ggc				499
Ser His Ala Val Asp Leu Thr Ser Phe Leu Phe Gly Asp Ile Leu Gly	120	125	130	
gtg cga ccc tcg gat ata ttc atc atc gcc att gca aca gtg ttg ggt				547
Val Arg Pro Ser Asp Ile Phe Ile Ile Ala Ile Ala Thr Val Leu Gly	135	140	145	
gga ttg act att ttt ctc ttc cac cga cag ttc act gca ctc gct ttc				595
Gly Leu Thr Ile Phe Leu Phe His Arg Gln Phe Thr Ala Leu Ala Phe	150	155	160	165
gac gag cgt aaa gct cac acc tta gga ctc aat ccc cgc ttt gca cac				643
Asp Glu Arg Lys Ala His Thr Leu Gly Leu Asn Pro Arg Phe Ala His	170	175	180	
cta ctc atg ctg gca ctg atc gca tta gct acg gtg gtg tcg ttt cag				691
Leu Leu Met Leu Ala Leu Ile Ala Leu Ala Thr Val Val Ser Phe Gln	185	190	195	
gtg gtg gga acg ctt tta gtg ttt gga ctt ctc att ggt ccg ccc gcc				739
Val Val Gly Thr Leu Leu Val Phe Gly Leu Leu Ile Gly Pro Pro Ala	200	205	210	
acg gct gca ctt tta gtg caa gac aaa gca agt att tca ctg atc atg				787
Thr Ala Ala Leu Leu Val Gln Asp Lys Ala Ser Ile Ser Leu Ile Met	215	220	225	
atc gtc gcg tcg ctt ctt gga tgc gcg gaa att tac ctc ggg ctt tta				835
Ile Val Ala Ser Leu Leu Gly Cys Ala Glu Ile Tyr Leu Gly Leu Leu	230	235	240	245
atc agc tgg cac gca agc act gcc gcg gga gcc act atc act ttg tta				883
Ile Ser Trp His Ala Ser Thr Ala Ala Gly Ala Thr Ile Thr Leu Leu	250	255	260	
agt gct gcg ata ttt ttt gcc acc tta ttg aca aag agt gcc att agt				931
Ser Ala Ala Ile Phe Phe Ala Thr Leu Leu Thr Lys Ser Ala Ile Ser	265	270	275	
agg tta aac ttc acc gcg tgatactgaa agacattttc aat				972
Arg Leu Asn Phe Thr Ala	280			

<210> 254

<211> 283

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 254

Met Lys Phe Phe Thr Asp Ala Leu Ile Val Pro Phe Asp Val Ser Phe
 1 5 10 15
 Ile Ser Arg Ala Leu Val Ala Gly Cys Leu Ala Ala Ile Leu Cys Ser
 20 25 30
 Leu Ile Gly Thr Trp Val Ile Leu Arg Arg Leu Thr Phe Phe Gly Asp
 35 40 45
 Ala Met Ser His Gly Leu Leu Pro Gly Val Ala Thr Ala Ser Leu Leu
 50 55 60
 Gly Gly Asn Leu Met Phe Gly Ala Ala Ile Ser Ala Leu Ile Met Ser
 65 70 75 80
 Ala Gly Val Val Trp Thr Ser Arg Lys Ser Ser Leu Ser Gln Asp Val
 85 90 95
 Ser Ile Gly Leu Gln Phe Ile Thr Met Leu Ser Leu Gly Val Val Ile
 100 105 110
 Val Ser His Ser Asp Ser His Ala Val Asp Leu Thr Ser Phe Leu Phe
 115 120 125
 Gly Asp Ile Leu Gly Val Arg Pro Ser Asp Ile Phe Ile Ile Ala Ile
 130 135 140
 Ala Thr Val Leu Gly Gly Leu Thr Ile Phe Leu Phe His Arg Gln Phe
 145 150 155 160
 Thr Ala Leu Ala Phe Asp Glu Arg Lys Ala His Thr Leu Gly Leu Asn
 165 170 175
 Pro Arg Phe Ala His Leu Leu Met Leu Ala Leu Ile Ala Leu Ala Thr
 180 185 190
 Val Val Ser Phe Gln Val Val Gly Thr Leu Leu Val Phe Gly Leu Leu
 195 200 205
 Ile Gly Pro Pro Ala Thr Ala Ala Leu Leu Val Gln Asp Lys Ala Ser
 210 215 220
 Ile Ser Leu Ile Met Ile Val Ala Ser Leu Leu Gly Cys Ala Glu Ile
 225 230 235 240
 Tyr Leu Gly Leu Leu Ile Ser Trp His Ala Ser Thr Ala Ala Gly Ala
 245 250 255
 Thr Ile Thr Leu Leu Ser Ala Ala Ile Phe Phe Ala Thr Leu Leu Thr
 260 265 270
 Lys Ser Ala Ile Ser Arg Leu Asn Phe Thr Ala
 275 280

<210> 255

<211> 1431

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS
 <222> (101)..(1408)
 <223> RXA01756

<400> 255

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gcgcctgaaa tcgggcttgt tgaggggaga ggtgtgtgac atg aaa gag ttg gaa 115
               Met Lys Glu Leu Glu
               1               5

ctg ggc gag gcg agg gac gtc gct gca acg ttg gaa gcg atg ccg atc 163
Leu Gly Glu Ala Arg Asp Val Ala Ala Thr Leu Glu Ala Met Pro Ile
               10               15               20

cag gag gtt att gat cag gtt gag cga act tct ata act aaa ggt gcg 211
Gln Glu Val Ile Asp Gln Val Glu Arg Thr Ser Ile Thr Lys Gly Ala
               25               30               35

gta ctg ctg cgt ctg ctc agt aaa gat cga tcg ttg ttg gtc ttc gat 259
Val Leu Leu Arg Leu Leu Ser Lys Asp Arg Ser Leu Leu Val Phe Asp
               40               45               50

gct ctt ggt ccg cga ctc cag gct gat ctc att ggt gct ttt cag gat 307
Ala Leu Gly Pro Arg Leu Gln Ala Asp Leu Ile Gly Ala Phe Gln Asp
               55               60               65

gcg gaa gtg ctg gat tat ttc gct gac ctt gac cct gat gac cgc gtt 355
Ala Glu Val Leu Asp Tyr Phe Ala Asp Leu Asp Pro Asp Asp Arg Val
               70               75               80               85

tca ctg ctt gat gag ctg ccg gcg tcg atc gct gac gag ttg ctt cgc 403
Ser Leu Leu Asp Glu Leu Pro Ala Ser Ile Ala Asp Glu Leu Leu Arg
               90               95               100

agt ctc gat ccg cag gaa aag cag gtc acg gag ctg gtc ttg ggt tac 451
Ser Leu Asp Pro Gln Glu Lys Gln Val Thr Glu Leu Val Leu Gly Tyr
               105               110               115

gca aag ggg tcg gtt gga cgt tgg atg tcg ccc cag gtt tta ttg ctt 499
Ala Lys Gly Ser Val Gly Arg Trp Met Ser Pro Gln Val Leu Leu Leu
               120               125               130

ttc gac gac atg tcc gtc gcc gaa gtc tta gat ttt gtg cgc aat cat 547
Phe Asp Asp Met Ser Val Ala Glu Val Leu Asp Phe Val Arg Asn His
               135               140               145

gct gct gag gct gag acg att tat gcc tta cct att gtg aac cgt gct 595
Ala Ala Glu Ala Glu Thr Ile Tyr Ala Leu Pro Ile Val Asn Arg Ala
               150               155               160               165

cgc caa gtg atg ggc gtg gtg tcg ttg cga aag ctg ttc atc gca gat 643
Arg Gln Val Met Gly Val Val Ser Leu Arg Lys Leu Phe Ile Ala Asp
               170               175               180

ccc act cta aaa gtc tcg gaa atc atg gtg cgt cct gtt tcg gtg ttg 691
Pro Thr Leu Lys Val Ser Glu Ile Met Val Arg Pro Val Ser Val Leu
               185               190               195

gcg tcc gcg gat att gaa gaa acc gcc cgc tgg ttc cta cag ttg gac 739
Ala Ser Ala Asp Ile Glu Glu Thr Ala Arg Trp Phe Leu Gln Leu Asp

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200	205	210	
ctc gtt gcg atg ccc gtt gtg gat gaa tcg aac atg ctc tta gga gtg Leu Val Ala Met Pro Val Val Asp Glu Ser Asn Met Leu Leu Gly Val 215 220 225			787
ctg acc ttc gat gat gcg caa gac atc gtg gag caa gcc gac tct gag Leu Thr Phe Asp Asp Ala Gln Asp Ile Val Glu Gln Ala Asp Ser Glu 230 235 240 245			835
gac tcc gct cgc agt ggt ggt tcg gaa cct ctc cag cag ccg tat cta Asp Ser Ala Arg Ser Gly Gly Ser Glu Pro Leu Gln Gln Pro Tyr Leu 250 255 260			883
tcc acg ccg att cgg aaa ctg gtg aag tcc cgc atc gta tgg ctt ctg Ser Thr Pro Ile Arg Lys Leu Val Lys Ser Arg Ile Val Trp Leu Leu 265 270 275			931
gtt ttg gca gtg tca gca att ttg acg gtt caa gtt ctt gat att ttc Val Leu Ala Val Ser Ala Ile Leu Thr Val Gln Val Leu Asp Ile Phe 280 285 290			979
gaa gcc acc ttg gtt gaa gcc gtg gta ctg gca ttg ttc att cct ttg Glu Ala Thr Leu Val Glu Ala Val Val Leu Ala Leu Phe Ile Pro Leu 295 300 305			1027
ctc act ggt act ggc gga aac acc gga aac caa gct gca aca acc gtg Leu Thr Gly Thr Gly Gly Asn Thr Gly Asn Gln Ala Ala Thr Thr Val 310 315 320 325			1075
acc cgt gcg ctc gca ttg ggt gac gtc cga aaa tca gat gtc ttc cgc Thr Arg Ala Leu Ala Leu Gly Asp Val Arg Lys Ser Asp Val Phe Arg 330 335 340			1123
gtc ttg ggc aga gaa atc cga gtc ggc ctc atg ctc ggg gca ttg ttg Val Leu Gly Arg Glu Ile Arg Val Gly Leu Met Leu Gly Ala Leu Leu 345 350 355			1171
ggt gcc gtt gga ttt gtg atc gca tcg ctt gtt tac ggc atg ccc gta Gly Ala Val Gly Phe Val Ile Ala Ser Leu Val Tyr Gly Met Pro Val 360 365 370			1219
ggc act gtc atc ggt ctg aca ttg ttg gcg gtg tgc acg atg gcc gca Gly Thr Val Ile Gly Leu Thr Leu Leu Ala Val Cys Thr Met Ala Ala 375 380 385			1267
tca gtt ggc gga gta atg cca att att gcc aag gcg atc gga gcg gac Ser Val Gly Gly Val Met Pro Ile Ile Ala Lys Ala Ile Gly Ala Asp 390 395 400 405			1315
cca gcg gtg ttc tct aat cct ttt att tca acc ttc tgt gat gca aca Pro Ala Val Phe Ser Asn Pro Phe Ile Ser Thr Phe Cys Asp Ala Thr 410 415 420			1363
ggt ttg atc atc tac ttt gca att gcc aag ttg gtg ctc gga atc Gly Leu Ile Ile Tyr Phe Ala Ile Ala Lys Leu Val Leu Gly Ile 425 430 435			1408
taaaagattt ttgcttttcg acg			1431

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<211> 436

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 256

Met Lys Glu Leu Glu Leu Gly Glu Ala Arg Asp Val Ala Ala Thr Leu
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Glu Ala Met Pro Ile Gln Glu Val Ile Asp Gln Val Glu Arg Thr Ser
 20 25 30

Ile Thr Lys Gly Ala Val Leu Leu Arg Leu Leu Ser Lys Asp Arg Ser
 35 40 45

Leu Leu Val Phe Asp Ala Leu Gly Pro Arg Leu Gln Ala Asp Leu Ile
 50 55 60

Gly Ala Phe Gln Asp Ala Glu Val Leu Asp Tyr Phe Ala Asp Leu Asp
 65 70 75 80

Pro Asp Asp Arg Val Ser Leu Leu Asp Glu Leu Pro Ala Ser Ile Ala
 85 90 95

Asp Glu Leu Leu Arg Ser Leu Asp Pro Gln Glu Lys Gln Val Thr Glu
 100 105 110

Leu Val Leu Gly Tyr Ala Lys Gly Ser Val Gly Arg Trp Met Ser Pro
 115 120 125

Gln Val Leu Leu Leu Phe Asp Asp Met Ser Val Ala Glu Val Leu Asp
 130 135 140

Phe Val Arg Asn His Ala Ala Glu Ala Glu Thr Ile Tyr Ala Leu Pro
 145 150 155 160

Ile Val Asn Arg Ala Arg Gln Val Met Gly Val Val Ser Leu Arg Lys
 165 170 175

Leu Phe Ile Ala Asp Pro Thr Leu Lys Val Ser Glu Ile Met Val Arg
 180 185 190

Pro Val Ser Val Leu Ala Ser Ala Asp Ile Glu Glu Thr Ala Arg Trp
 195 200 205

Phe Leu Gln Leu Asp Leu Val Ala Met Pro Val Val Asp Glu Ser Asn
 210 215 220

Met Leu Leu Gly Val Leu Thr Phe Asp Asp Ala Gln Asp Ile Val Glu
 225 230 235 240

Gln Ala Asp Ser Glu Asp Ser Ala Arg Ser Gly Gly Ser Glu Pro Leu
 245 250 255

Gln Gln Pro Tyr Leu Ser Thr Pro Ile Arg Lys Leu Val Lys Ser Arg
 260 265 270

Ile Val Trp Leu Leu Val Leu Ala Val Ser Ala Ile Leu Thr Val Gln
 275 280 285

Val Leu Asp Ile Phe Glu Ala Thr Leu Val Glu Ala Val Val Leu Ala

290 295 300
 Leu Phe Ile Pro Leu Leu Thr Gly Thr Gly Gly Asn Thr Gly Asn Gln
 305 310 315 320
 Ala Ala Thr Thr Val Thr Arg Ala Leu Ala Leu Gly Asp Val Arg Lys
 325 330 335
 Ser Asp Val Phe Arg Val Leu Gly Arg Glu Ile Arg Val Gly Leu Met
 340 345 350
 Leu Gly Ala Leu Leu Gly Ala Val Gly Phe Val Ile Ala Ser Leu Val
 355 360 365
 Tyr Gly Met Pro Val Gly Thr Val Ile Gly Leu Thr Leu Leu Ala Val
 370 375 380
 Cys Thr Met Ala Ala Ser Val Gly Gly Val Met Pro Ile Ile Ala Lys
 385 390 395 400
 Ala Ile Gly Ala Asp Pro Ala Val Phe Ser Asn Pro Phe Ile Ser Thr
 405 410 415
 Phe Cys Asp Ala Thr Gly Leu Ile Ile Tyr Phe Ala Ile Ala Lys Leu
 420 425 430
 Val Leu Gly Ile
 435

<210> 257
 <211> 1142
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1119)
 <223> RXA02068

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 act ttg gtt acc ggt tct gta tca ctt cga acc ttt cgc gtg cgc acc 96
 thr leu val thr gly ser val ser leu arg thr phe arg val arg thr
 20 25 30
 ggt gaa ttg cag gtc atg ggc gat att gtg ggt gca aaa gta cat acc 144
 gly glu leu gln val met gly asp ile val gly ala lys val his thr
 35 40 45
 gat gat cca gag ctg caa caa ttc cac ggt cgc gcg gta gaa atc gcc 192
 asp asp pro glu leu gln gln phe his gly arg ala val glu ile ala
 50 55 60
 gat gtg gag ctg gag tta tcg cgc act cgc gat tgg atc atc acg cgc 240
 asp val glu leu glu leu ser arg thr arg asp trp ile ile thr arg
 65 70 75 80

gtg gcg gtg ctg ggt gag cgc cct aaa ttt ggc cgg cgc cca gtg ctg	288
Val Ala Val Leu Gly Glu Arg Pro Lys Phe Gly Arg Arg Pro Val Leu	
85 90 95	
cac aca gtg ccg tgg agt cat atc cac ggc atc acc gca ggt ggt gtc	336
His Thr Val Pro Trp Ser His Ile His Gly Ile Thr Ala Gly Gly Val	
100 105 110	
ggc gag tcc aat cac acc gcc gaa ctc atc gca ggg ttt gag gat atg	384
Gly Glu Ser Asn His Thr Ala Glu Leu Ile Ala Gly Phe Glu Asp Met	
115 120 125	
agg cct gcg gac gtc gca aag cag ctt tat cag ctg cct acg gct cag	432
Arg Pro Ala Asp Val Ala Lys Gln Leu Tyr Gln Leu Pro Thr Ala Gln	
130 135 140	
cgt acc gaa gtg acg gaa gag ctt gac gac gaa aag ctg gcg gat atc	480
Arg Thr Glu Val Thr Glu Glu Leu Asp Asp Glu Lys Leu Ala Asp Ile	
145 150 155 160	
ctg cag gaa ttg tcc gag gac cgc caa gcc gag ttg att gaa gaa tta	528
Leu Gln Glu Leu Ser Glu Asp Arg Gln Ala Glu Leu Ile Glu Glu Leu	
165 170 175	
gac atc gaa cgt gcc gcg gac att ctg gag gaa atg gat cca gat gat	576
Asp Ile Glu Arg Ala Ala Asp Ile Leu Glu Glu Met Asp Pro Asp Asp	
180 185 190	
gct gca gac ttg ttg ggt gag ctg cct gat gac aaa gct gat gtg ttg	624
Ala Ala Asp Leu Leu Gly Glu Leu Pro Asp Asp Lys Ala Asp Val Leu	
195 200 205	
ttg gat ctg atg gac cct gag gaa tct gcg ccg gtg cgt cgt ttg atg	672
Leu Asp Leu Met Asp Pro Glu Glu Ser Ala Pro Val Arg Arg Leu Met	
210 215 220	
gat ttc tcc ccg gac acc gtt ggt gcg ctg atg act cct gag cca tta	720
Asp Phe Ser Pro Asp Thr Val Gly Ala Leu Met Thr Pro Glu Pro Leu	
225 230 235 240	
att atg gat cct tcc acc aca gtc gct gaa gcg ttg gcg atg gcc aga	768
Ile Met Asp Pro Ser Thr Thr Val Ala Glu Ala Leu Ala Met Ala Arg	
245 250 255	
aac ccc gac ctt cct act tct ttg gca tcg ttg atc ttt gtg gtg cgc	816
Asn Pro Asp Leu Pro Thr Ser Leu Ala Ser Leu Ile Phe Val Val Arg	
260 265 270	
cca ccc acg gcc acg cct act gga aaa tac ctc ggc tgc gtg cat ctg	864
Pro Pro Thr Ala Thr Pro Thr Gly Lys Tyr Leu Gly Cys Val His Leu	
275 280 285	
cag aaa ctg ctt ccg gag cct cca tca agt ttg att ggt ggc atc ctc	912
Gln Lys Leu Leu Arg Glu Pro Pro Ser Ser Leu Ile Gly Gly Ile Leu	
290 295 300	
gac ccc gat ctg cca ccg ctc tac gct gat gat tct caa gaa acc gca	960
Asp Pro Asp Leu Pro Pro Leu Tyr Ala Asp Asp Ser Gln Glu Thr Ala	
305 310 315 320	
gct cga ttc ttt gcc acc tac aac ttg gtg tgc ggc ccc gtc ttg gat	1008

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<210> 258
<211> 373
<212> PRT
<213> Corynebacterium glutamicum
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			20					25					30		
Gly	Glu	Leu	Gln	Val	Met	Gly	Asp	Ile	Val	Gly	Ala	Lys	Val	His	Thr
		35					40					45			
Asp	Asp	Pro	Glu	Leu	Gln	Gln	Phe	His	Gly	Arg	Ala	Val	Glu	Ile	Ala
	50					55					60				
Asp	Val	Glu	Leu	Glu	Leu	Ser	Arg	Thr	Arg	Asp	Trp	Ile	Ile	Thr	Arg
65					70					75					80
Val	Ala	Val	Leu	Gly	Glu	Arg	Pro	Lys	Phe	Gly	Arg	Arg	Pro	Val	Leu
				85					90					95	
His	Thr	Val	Pro	Trp	Ser	His	Ile	His	Gly	Ile	Thr	Ala	Gly	Gly	Val
			100					105					110		
Gly	Glu	Ser	Asn	His	Thr	Ala	Glu	Leu	Ile	Ala	Gly	Phe	Glu	Asp	Met
		115					120					125			
Arg	Pro	Ala	Asp	Val	Ala	Lys	Gln	Leu	Tyr	Gln	Leu	Pro	Thr	Ala	Gln
	130					135					140				
Arg	Thr	Glu	Val	Thr	Glu	Glu	Leu	Asp	Asp	Glu	Lys	Leu	Ala	Asp	Ile
145					150					155					160
Leu	Gln	Glu	Leu	Ser	Glu	Asp	Arg	Gln	Ala	Glu	Leu	Ile	Glu	Glu	Leu
				165					170					175	
Asp	Ile	Glu	Arg	Ala	Ala	Asp	Ile	Leu	Glu	Glu	Met	Asp	Pro	Asp	Asp
			180					185					190		
Ala	Ala	Asp	Leu	Leu	Gly	Glu	Leu	Pro	Asp	Asp	Lys	Ala	Asp	Val	Leu
		195					200					205			

Leu Asp Leu Met Asp Pro Glu Glu Ser Ala Pro Val Arg Arg Leu Met
 210 215 220
 Asp Phe Ser Pro Asp Thr Val Gly Ala Leu Met Thr Pro Glu Pro Leu
 225 230 235 240
 Ile Met Asp Pro Ser Thr Thr Val Ala Glu Ala Leu Ala Met Ala Arg
 245 250 255
 Asn Pro Asp Leu Pro Thr Ser Leu Ala Ser Leu Ile Phe Val Val Arg
 260 265 270
 Pro Pro Thr Ala Thr Pro Thr Gly Lys Tyr Leu Gly Cys Val His Leu
 275 280 285
 Gln Lys Leu Leu Arg Glu Pro Pro Ser Ser Leu Ile Gly Gly Ile Leu
 290 295 300
 Asp Pro Asp Leu Pro Pro Leu Tyr Ala Asp Asp Ser Gln Glu Thr Ala
 305 310 315 320
 Ala Arg Phe Phe Ala Thr Tyr Asn Leu Val Cys Gly Pro Val Leu Asp
 325 330 335
 Glu Asn Arg His Leu Leu Gly Ala Val Ala Val Asp Asp Leu Leu Asp
 340 345 350
 His Met Leu Pro Glu Asp Trp Arg Asp Ala Gly Ile Arg Pro Gly Lys
 355 360 365
 Glu His Thr His Gly
 370

<210> 259
 <211> 538
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(538)
 <223> RXA00665

<400> 259
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 Met Ser Ser Ser Thr
 1 5
 ctt ctc ctg gct tca gga caa gtc acg gca tta gcc gct gac tac acg 163
 Leu Leu Leu Ala Ser Gly Gln Val Thr Ala Leu Ala Ala Asp Tyr Thr
 10 15 20
 ctc agc cac acc ccc tca gat ggc atc ctg gta gtc ctt ggc ttc gcc 211
 Leu Ser His Thr Pro Ser Asp Gly Ile Leu Val Val Leu Gly Phe Ala
 25 30 35
 atg atc ctc acc ttc atg acc ctg atc atg ctg ggt cga ctc acc cca 259
 Met Ile Leu Thr Phe Met Thr Leu Ile Met Leu Gly Arg Leu Thr Pro

40	45	50	
atg gtg gcc atg ctg ttg gtc ccc acc atc ttc ggt ctc atc gcc ggc			307
Met Val Ala Met Leu Leu Val Pro Thr Ile Phe Gly Leu Ile Ala Gly			
55	60	65	
gca gga ctc ggc ctt ggt gac atg gcg ctt gac gcc atc aag gac atg			355
Ala Gly Leu Gly Leu Gly Asp Met Ala Leu Asp Ala Ile Lys Asp Met			
70	75	80	85
gcg cct acc gcg gca ctc ctg atg ttc gcg att atg ttc ttc gga atc			403
Ala Pro Thr Ala Ala Leu Leu Met Phe Ala Ile Met Phe Phe Gly Ile			
	90	95	100
atg atc gac gtc gga ctc ttc gac ccc ctg atc cgc gtg atc acc cgc			451
Met Ile Asp Val Gly Leu Phe Asp Pro Leu Ile Arg Val Ile Thr Arg			
	105	110	115
gtt ctt cac gat gac ccc gca aag gtc gtc atc ggc acc gca gta ctt			499
Val Leu His Asp Asp Pro Ala Lys Val Val Ile Gly Thr Ala Val Leu			
	120	125	130
gca ggt gtt gtc tcc ctc gac ggc gac ggc tcc acc acc			538
Ala Gly Val Val Ser Leu Asp Gly Asp Gly Ser Thr Thr			
135	140	145	

<210> 260

<211> 146

<212> PRT

<213> Corynebacterium glutamicum

<400> 260

Met Ser Ser Ser Thr Leu Leu Leu Ala Ser Gly Gln Val Thr Ala Leu
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Ala Ala Asp Tyr Thr Leu Ser His Thr Pro Ser Asp Gly Ile Leu Val
20 25 30

Val Leu Gly Phe Ala Met Ile Leu Thr Phe Met Thr Leu Ile Met Leu
35 40 45

Gly Arg Leu Thr Pro Met Val Ala Met Leu Leu Val Pro Thr Ile Phe
50 55 60

Gly Leu Ile Ala Gly Ala Gly Leu Gly Leu Gly Asp Met Ala Leu Asp
65 70 75 80

Ala Ile Lys Asp Met Ala Pro Thr Ala Ala Leu Leu Met Phe Ala Ile
85 90 95

Met Phe Phe Gly Ile Met Ile Asp Val Gly Leu Phe Asp Pro Leu Ile
100 105 110

Arg Val Ile Thr Arg Val Leu His Asp Asp Pro Ala Lys Val Val Ile
115 120 125

Gly Thr Ala Val Leu Ala Gly Val Val Ser Leu Asp Gly Asp Gly Ser
130 135 140

Thr Thr

145

<210> 261
 <211> 281
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(258)
 <223> RXA02808

<400> 261
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 Phe Tyr Phe Gly Ile Leu Pro Val Leu Ala Glu Ser Ala Ser His Phe
 1 5 10 15
 ggc atc gag cct gtg gaa atg gcc cgc gca tcc atc act ggc cag ccc 96
 Gly Ile Glu Pro Val Glu Met Ala Arg Ala Ser Ile Thr Gly Gln Pro
 20 25 30
 gtt cac atg caa agc ccg ctg gtc cca gcg atc ctc ctg ctg gtt tcc 144
 Val His Met Gln Ser Pro Leu Val Pro Ala Ile Leu Leu Leu Val Ser
 35 40 45
 ctc gcc aac gtc aac ctt ggc gac cac cac aag aag gtt ctg tgg cgc 192
 Leu Ala Asn Val Asn Leu Gly Asp His His Lys Lys Val Leu Trp Arg
 50 55 60
 gcc tgc atc gtg tcc atc gcg atg ctc gcc gta gcc ctc ttc atc ggc 240
 Ala Cys Ile Val Ser Ile Ala Met Leu Ala Val Ala Leu Phe Ile Gly
 65 70 75 80
 gtc gtg cca ctc agc gca taaaatagct tttcgacgcc aaa 281
 Val Val Pro Leu Ser Ala
 85

<210> 262
 <211> 86
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 262
 Phe Tyr Phe Gly Ile Leu Pro Val Leu Ala Glu Ser Ala Ser His Phe
 1 5 10 15
 Gly Ile Glu Pro Val Glu Met Ala Arg Ala Ser Ile Thr Gly Gln Pro
 20 25 30
 Val His Met Gln Ser Pro Leu Val Pro Ala Ile Leu Leu Leu Val Ser
 35 40 45
 Leu Ala Asn Val Asn Leu Gly Asp His His Lys Lys Val Leu Trp Arg
 50 55 60
 Ala Cys Ile Val Ser Ile Ala Met Leu Ala Val Ala Leu Phe Ile Gly
 65 70 75 80
 Val Val Pro Leu Ser Ala

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<210> 263
<211> 960
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(937)  
<223> RXN00444
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ttcctcagca	gcgatcgtgc	caaggagatc		cttgccagct		atg	ggt	ttg	gca	caa	115					
						Met	Val	Leu	Ala	Gln	5					
							1									
act	aaa	aag	gct	cgt	cga	agc	gag	aat	cat	atc	ctc	cca	ggg	tgg	ttg	163
Thr	Lys	Lys	Ala	Arg	Arg	Ser	Glu	Asn	His	Ile	Leu	Pro	Gly	Trp	Leu	
				10					15					20		
ctc	atc	cca	gcc	acc	ctg	gcc	atg	ctg	ctg	atc	att	gga	cct	att	ttt	211
Leu	Ile	Pro	Ala	Thr	Leu	Ala	Met	Leu	Leu	Ile	Ile	Gly	Pro	Ile	Phe	
			25					30					35			
gct	ttg	ctg	ttg	cag	atc	ccc	tgg	gat	cgg	tct	tgg	gag	ttg	ctt	acc	259
Ala	Leu	Leu	Leu	Gln	Ile	Pro	Trp	Asp	Arg	Ser	Trp	Glu	Leu	Leu	Thr	
		40					45					50				
gcg	ccg	gaa	tct	tta	gga	acc	gca	cgg	tta	tct	atc	gga	act	gct	ctg	307
Ala	Pro	Glu	Ser	Leu	Gly	Thr	Ala	Arg	Leu	Ser	Ile	Gly	Thr	Ala	Leu	
	55					60					65					
ttt	tct	acc	gcg	cta	tgc	gca	att	gtg	ggt	ttc	ccg	cta	gcg	ttg	gcg	355
Phe	Ser	Thr	Ala	Leu	Cys	Ala	Ile	Val	Gly	Phe	Pro	Leu	Ala	Leu	Ala	
	70				75					80					85	
ctg	cat	tta	tat	gag	cgt	tcg	cac	ccc	agg	gtg	aca	tca	gtt	ttg	acg	403
Leu	His	Leu	Tyr	Glu	Arg	Ser	His	Pro	Arg	Val	Thr	Ser	Val	Leu	Thr	
				90					95					100		
gtg	ctg	gtt	tat	gcg	cct	ttg	gtg	ttg	tcg	ccg	gtg	gtg	tct	ggt	ttg	451
Val	Leu	Val	Tyr	Ala	Pro	Leu	Val	Leu	Ser	Pro	Val	Val	Ser	Gly	Leu	
			105					110					115			
gcg	ctg	act	ttt	ctg	tgg	ggc	agg	cgt	ggt	ttt	tta	ggt	tct	tgg	ctt	499
Ala	Leu	Thr	Phe	Leu	Trp	Gly	Arg	Arg	Gly	Phe	Leu	Gly	Ser	Trp	Leu	
		120					125					130				
gat	cag	gtt	gga	ttg	ccg	att	gca	ttt	acc	acc	acg	gct	gtg	gtg	ttt	547
Asp	Gln	Val	Gly	Leu	Pro	Ile	Ala	Phe	Thr	Thr	Thr	Ala	Val	Val	Phe	
		135				140					145					
gcc	cag	gtg	ttt	gta	gcg	ttg	cca	ttt	ttc	att	tcc	act	gtg	act	act	595
Ala	Gln	Val	Phe	Val	Ala	Leu	Pro	Phe	Phe	Ile	Ser	Thr	Val	Thr	Thr	
	150				155					160					165	
gca	ctg	cgt	ggc	att	cca	aaa	cag	ttt	gag	gaa	atc	gca	gct	act	gaa	643

Ala Leu Arg Gly Ile Pro Lys Gln Phe Glu Glu Ile Ala Ala Thr Glu
 170 175 180

ggc gca acc cgc tgg gag atc atg cac aag atg atc att ccg ctg gcg 691
 Gly Ala Thr Arg Trp Glu Ile Met His Lys Met Ile Ile Pro Leu Ala
 185 190 195

atg cct gga att ttc acc ggt atg att ttg gga ttc gcc agg gcc ttg 739
 Met Pro Gly Ile Phe Thr Gly Met Ile Leu Gly Phe Ala Arg Ala Leu
 200 205 210

ggc gag tat ggt gcg aca ctg act ttt gct gga aat att gca ggt gtt 787
 Gly Glu Tyr Gly Ala Thr Leu Thr Phe Ala Gly Asn Ile Ala Gly Val
 215 220 225

acc cgc acc att ccg ttg cat att gag ctt ggt ttg agt tcc aat gac 835
 Thr Arg Thr Ile Pro Leu His Ile Glu Leu Gly Leu Ser Ser Asn Asp
 230 235 240 245

atg gat aaa gcc ttg gga gcg gtg att atg ctt ttg gct gtc tat gtc 883
 Met Asp Lys Ala Leu Gly Ala Val Ile Met Leu Leu Ala Val Tyr Val
 250 255 260

ctc atc att gga gcc atc gga gcg tta cga ttg ttt tcc aag gtg aga 931
 Leu Ile Ile Gly Ala Ile Gly Ala Leu Arg Leu Phe Ser Lys Val Arg
 265 270 275

aag gtt taattgatgt ctggttcgcc gga 960
 Lys Val

<210> 264

<211> 279

<212> PRT

<213> Corynebacterium glutamicum

<400> 264

Met Val Leu Ala Gln Thr Lys Lys Ala Arg Arg Ser Glu Asn His Ile
 1 5 10 15

Leu Pro Gly Trp Leu Leu Ile Pro Ala Thr Leu Ala Met Leu Leu Ile
 20 25 30

Ile Gly Pro Ile Phe Ala Leu Leu Gln Ile Pro Trp Asp Arg Ser
 35 40 45

Trp Glu Leu Leu Thr Ala Pro Glu Ser Leu Gly Thr Ala Arg Leu Ser
 50 55 60

Ile Gly Thr Ala Leu Phe Ser Thr Ala Leu Cys Ala Ile Val Gly Phe
 65 70 75 80

Pro Leu Ala Leu Ala Leu His Leu Tyr Glu Arg Ser His Pro Arg Val
 85 90 95

Thr Ser Val Leu Thr Val Leu Val Tyr Ala Pro Leu Val Leu Ser Pro
 100 105 110

Val Val Ser Gly Leu Ala Leu Thr Phe Leu Trp Gly Arg Arg Gly Phe
 115 120 125

Leu Gly Ser Trp Leu Asp Gln Val Gly Leu Pro Ile Ala Phe Thr Thr
 130 135 140
 Thr Ala Val Val Phe Ala Gln Val Phe Val Ala Leu Pro Phe Phe Ile
 145 150 155 160
 Ser Thr Val Thr Thr Ala Leu Arg Gly Ile Pro Lys Gln Phe Glu Glu
 165 170 175
 Ile Ala Ala Thr Glu Gly Ala Thr Arg Trp Glu Ile Met His Lys Met
 180 185 190
 Ile Ile Pro Leu Ala Met Pro Gly Ile Phe Thr Gly Met Ile Leu Gly
 195 200 205
 Phe Ala Arg Ala Leu Gly Glu Tyr Gly Ala Thr Leu Thr Phe Ala Gly
 210 215 220
 Asn Ile Ala Gly Val Thr Arg Thr Ile Pro Leu His Ile Glu Leu Gly
 225 230 235 240
 Leu Ser Ser Asn Asp Met Asp Lys Ala Leu Gly Ala Val Ile Met Leu
 245 250 255
 Leu Ala Val Tyr Val Leu Ile Ile Gly Ala Ile Gly Ala Leu Arg Leu
 260 265 270
 Phe Ser Lys Val Arg Lys Val
 275

<210> 265

<211> 900

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(877)

<223> FRXA00444

<220>

<223> All occurrences of n = any nucleotide

<400> 265

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aaaggctcgt cgaagcgaga atcatatcct cccaggggtg ttg ctc atc cca gcc 115
 Leu Leu Ile Pro Ala
 1 5

acc ctg gcc atg ctg ctg atc att gga cct att ttt gct ttg ctg ttg 163
 Thr Leu Ala Met Leu Leu Ile Ile Gly Pro Ile Phe Ala Leu Leu Leu
 10 15 20

cag atc ccc tgg gat cgg tct tgg gag ttg ctt acc gcg ccg gaa tct 211
 Gln Ile Pro Trp Asp Arg Ser Trp Glu Leu Leu Thr Ala Pro Glu Ser
 25 30 35

tta gga acc gca cgg tta tct atc gga act gct ctg ttt tct acc gcg 259

Leu Gly Thr Ala Arg Leu Ser Ile Gly Thr Ala Leu Phe Ser Thr Ala
 40 45 50
 cta tgc gca att gtg ggt ttc ccg cta gcg ttg gcg ctg cat tta tat 307
 Leu Cys Ala Ile Val Gly Phe Pro Leu Ala Leu Ala Leu His Leu Tyr
 55 60 65
 gag cgt tcg cac ccc agg gtg aca tca gtt ttg acg gtg ctg gtt tat 355
 Glu Arg Ser His Pro Arg Val Thr Ser Val Leu Thr Val Leu Val Tyr
 70 75 80 85
 gcg cct ttg gtg ttg tcg ccg gtg gtg tct ggt ttg gcg ctg act ttt 403
 Ala Pro Leu Val Leu Ser Pro Val Val Ser Gly Leu Ala Leu Thr Phe
 90 95 100
 ctg tgg ggc agg cgt ggt ttt tta ggt tct tgg ctt gat cag gtt gga 451
 Leu Trp Gly Arg Arg Gly Phe Leu Gly Ser Trp Leu Asp Gln Val Gly
 105 110 115
 ttg ccg att gca ttt acc acc acg gct gtg gtg ttt gcc cag gtg ttt 499
 Leu Pro Ile Ala Phe Thr Thr Thr Ala Val Val Phe Ala Gln Val Phe
 120 125 130
 gta gcg ttg cca ttt ttc att tcc act gtg act act gca ctg cgt ggc 547
 Val Ala Leu Pro Phe Phe Ile Ser Thr Val Thr Thr Ala Leu Arg Gly
 135 140 145
 att cca aaa cag ttt gag gaa atc gca gct act gaa ggc gca acc cgc 595
 Ile Pro Lys Gln Phe Glu Glu Ile Ala Ala Thr Glu Gly Ala Thr Arg
 150 155 160 165
 tgg gag atc atg cac aag atg atc att ccg ctg gcg atg cct gga att 643
 Trp Glu Ile Met His Lys Met Ile Ile Pro Leu Ala Met Pro Gly Ile
 170 175 180
 ttc acc ggt atg att ttg gga ttc gcc agg gcc ttg ggc gag tat ggt 691
 Phe Thr Gly Met Ile Leu Gly Phe Ala Arg Ala Leu Gly Glu Tyr Gly
 185 190 195
 gcg aca ctg act ttt gct gga aat att gca ggt gtt acc cgc acc att 739
 Ala Thr Leu Thr Phe Ala Gly Asn Ile Ala Gly Val Thr Arg Thr Ile
 200 205 210
 ccg ttg cat att gag ctt ggt ttg agt tcc aat gac atg gat aaa gcc 787
 Pro Leu His Ile Glu Leu Gly Leu Ser Ser Asn Asp Met Asp Lys Ala
 215 220 225
 ttg gga gcg gtg att atg ctt ttg gct gtc tat gtc ctc atc att gga 835
 Leu Gly Ala Val Ile Met Leu Leu Ala Val Tyr Val Leu Ile Ile Gly
 230 235 240 245
 gcc atc gga gcg tta cga ttg ttt tcc aag gtg aga aag gtt 877
 Ala Ile Gly Ala Leu Arg Leu Phe Ser Lys Val Arg Lys Val
 250 255
 taattgatgt ctggttcgcc gga 900

<210> 266

<211> 259

<212> PRT

<213> Corynebacterium glutamicum

<400> 266

Leu Leu Ile Pro Ala Thr Leu Ala Met Leu Leu Ile Ile Gly Pro Ile
1 5 10 15

Phe Ala Leu Leu Leu Gln Ile Pro Trp Asp Arg Ser Trp Glu Leu Leu
20 25 30

Thr Ala Pro Glu Ser Leu Gly Thr Ala Arg Leu Ser Ile Gly Thr Ala
35 40 45

Leu Phe Ser Thr Ala Leu Cys Ala Ile Val Gly Phe Pro Leu Ala Leu
50 55 60

Ala Leu His Leu Tyr Glu Arg Ser His Pro Arg Val Thr Ser Val Leu
65 70 75 80

Thr Val Leu Val Tyr Ala Pro Leu Val Leu Ser Pro Val Val Ser Gly
85 90 95

Leu Ala Leu Thr Phe Leu Trp Gly Arg Arg Gly Phe Leu Gly Ser Trp
100 105 110

Leu Asp Gln Val Gly Leu Pro Ile Ala Phe Thr Thr Thr Ala Val Val
115 120 125

Phe Ala Gln Val Phe Val Ala Leu Pro Phe Phe Ile Ser Thr Val Thr
130 135 140

Thr Ala Leu Arg Gly Ile Pro Lys Gln Phe Glu Glu Ile Ala Ala Thr
145 150 155 160

Glu Gly Ala Thr Arg Trp Glu Ile Met His Lys Met Ile Ile Pro Leu
165 170 175

Ala Met Pro Gly Ile Phe Thr Gly Met Ile Leu Gly Phe Ala Arg Ala
180 185 190

Leu Gly Glu Tyr Gly Ala Thr Leu Thr Phe Ala Gly Asn Ile Ala Gly
195 200 205

Val Thr Arg Thr Ile Pro Leu His Ile Glu Leu Gly Leu Ser Ser Asn
210 215 220

Asp Met Asp Lys Ala Leu Gly Ala Val Ile Met Leu Leu Ala Val Tyr
225 230 235 240

Val Leu Ile Ile Gly Ala Ile Gly Ala Leu Arg Leu Phe Ser Lys Val
245 250 255

Arg Lys Val

<210> 267

<211> 852

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(829)

<223> RXN02614

<400> 267

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acaccttccg ctaccgaaac gcataagaaa gttgctcgcc atg act gcc aca ttg 115
                               Met Thr Ala Thr Leu
                               1 5

tca ctc aaa ccc gca gcc act gtc cgt gga ttg cgc aaa tca tac gga 163
Ser Leu Lys Pro Ala Ala Thr Val Arg Gly Leu Arg Lys Ser Tyr Gly
          10          15          20

act aaa gaa gtc ctc caa gga atc gac ctc acc atc aac tgc ggc gaa 211
Thr Lys Glu Val Leu Gln Gly Ile Asp Leu Thr Ile Asn Cys Gly Glu
          25          30          35

gta acc gcg ctg atc gga cgc tca ggt tca gga aaa tcc acc atc ctg 259
Val Thr Ala Leu Ile Gly Arg Ser Gly Ser Gly Lys Ser Thr Ile Leu
          40          45          50

cgc gtg ttg gcg ggc cta tct aaa gag cat tcc ggc tct gta gaa att 307
Arg Val Leu Ala Gly Leu Ser Lys Glu His Ser Gly Ser Val Glu Ile
          55          60          65

tcc gga aac ccg gcc gtt gcc ttc caa gag cct cgc ctg ttg ccg tgg 355
Ser Gly Asn Pro Ala Val Ala Phe Gln Glu Pro Arg Leu Leu Pro Trp
          70          75          80          85

aaa acg gtg ctc gat aat gtg acc ttt ggc ctc aac cgc act gat att 403
Lys Thr Val Leu Asp Asn Val Thr Phe Gly Leu Asn Arg Thr Asp Ile
          90          95          100

tcc tgg tca gaa gca caa gaa cgc gcc tgc gca ctg ctt gca gaa gtc 451
Ser Trp Ser Glu Ala Gln Glu Arg Ala Ser Ala Leu Leu Ala Glu Val
          105          110          115

aaa ctt ccc gac tcc gac gcc gcc tgg ccc ctc acg ctc tcc ggc ggc 499
Lys Leu Pro Asp Ser Asp Ala Ala Trp Pro Leu Thr Leu Ser Gly Gly
          120          125          130

caa gcc cag cgc gtc tcc ctt gcg cga gcg ctc atc tcc gag cca gag 547
Gln Ala Gln Arg Val Ser Leu Ala Arg Ala Leu Ile Ser Glu Pro Glu
          135          140          145

ctt ttg ctt ctc gac gaa ccc ttc ggc gcc ctc gat gct ctg aca aga 595
Leu Leu Leu Leu Asp Glu Pro Phe Gly Ala Leu Asp Ala Leu Thr Arg
          150          155          160          165

ctg aca gcc caa gac ctg ctg ctc aaa acc gtg aac acc cga aac ttg 643
Leu Thr Ala Gln Asp Leu Leu Leu Lys Thr Val Asn Thr Arg Asn Leu
          170          175          180

gga gtt ctg ctg gtc acc cat gat gtt tcc gag gcc atc gcc ctg gcc 691
Gly Val Leu Leu Val Thr His Asp Val Ser Glu Ala Ile Ala Leu Ala
          185          190          195

gac cac gtc ctt ctt ctt gac gac ggc gcc atc aca cac agt ttg act 739
Asp His Val Leu Leu Leu Asp Asp Gly Ala Ile Thr His Ser Leu Thr

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200	205	210	
gta gat atc ccc ggc gat cgc cgc acc cac ccc tcc ttt gcc tcc tac			787
Val Asp Ile Pro Gly Asp Arg Arg Thr His Pro Ser Phe Ala Ser Tyr			
215	220	225	
acc gct caa ctc ctt gag tgg ctc gaa atc acc aca cct gcc			829
Thr Ala Gln Leu Leu Glu Trp Leu Glu Ile Thr Thr Pro Ala			
230	235	240	
tagaaagaaa tcatgaaatt taa			852
<210> 268			
<211> 243			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 268			
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1	5	10	15
Arg Lys Ser Tyr Gly Thr Lys Glu Val Leu Gln Gly Ile Asp Leu Thr			
	20	25	30
Ile Asn Cys Gly Glu Val Thr Ala Leu Ile Gly Arg Ser Gly Ser Gly			
	35	40	45
Lys Ser Thr Ile Leu Arg Val Leu Ala Gly Leu Ser Lys Glu His Ser			
	50	55	60
Gly Ser Val Glu Ile Ser Gly Asn Pro Ala Val Ala Phe Gln Glu Pro			
	65	70	75
Arg Leu Leu Pro Trp Lys Thr Val Leu Asp Asn Val Thr Phe Gly Leu			
	85	90	95
Asn Arg Thr Asp Ile Ser Trp Ser Glu Ala Gln Glu Arg Ala Ser Ala			
	100	105	110
Leu Leu Ala Glu Val Lys Leu Pro Asp Ser Asp Ala Ala Trp Pro Leu			
	115	120	125
Thr Leu Ser Gly Gly Gln Ala Gln Arg Val Ser Leu Ala Arg Ala Leu			
	130	135	140
Ile Ser Glu Pro Glu Leu Leu Leu Leu Asp Glu Pro Phe Gly Ala Leu			
	145	150	155
Asp Ala Leu Thr Arg Leu Thr Ala Gln Asp Leu Leu Leu Lys Thr Val			
	165	170	175
Asn Thr Arg Asn Leu Gly Val Leu Leu Val Thr His Asp Val Ser Glu			
	180	185	190
Ala Ile Ala Leu Ala Asp His Val Leu Leu Leu Asp Asp Gly Ala Ile			
	195	200	205
Thr His Ser Leu Thr Val Asp Ile Pro Gly Asp Arg Arg Thr His Pro			
	210	215	220

Ser Phe Ala Ser Tyr Thr Ala Gln Leu Leu Glu Trp Leu Glu Ile Thr
 225 230 235 240

Thr Pro Ala

<210> 269

<211> 852

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(829)

<223> FRXA02614

<400> 269

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acaccttccg ctaccgaaac gcataagaaa gttgctcgcc atg act gcc aca ttg 115
 Met Thr Ala Thr Leu
 1 5

tca ctc aaa ccc gca gcc act gtc cgt gga ttg cgc aaa tca tac gga 163
 Ser Leu Lys Pro Ala Ala Thr Val Arg Gly Leu Arg Lys Ser Tyr Gly
 10 15 20

act aaa gaa gtc ctc caa gga atc gac ctc acc atc aac tgc ggc gaa 211
 Thr Lys Glu Val Leu Gln Gly Ile Asp Leu Thr Ile Asn Cys Gly Glu
 25 30 35

gta acc gcg ctg atc gga cgc tca ggt tca gga aaa tcc acc atc ctg 259
 Val Thr Ala Leu Ile Gly Arg Ser Gly Ser Gly Lys Ser Thr Ile Leu
 40 45 50

cgc gtg ttg gcg ggc cta tct aaa gag cat tcc ggc tot gta gaa att 307
 Arg Val Leu Ala Gly Leu Ser Lys Glu His Ser Gly Ser Val Glu Ile
 55 60 65

tcc gga aac ccg gcc gtt gcc ttc caa gag cct cgc ctg ttg ccg tgg 355
 Ser Gly Asn Pro Ala Val Ala Phe Gln Glu Pro Arg Leu Leu Pro Trp
 70 75 80 85

aaa acg gtg ctc gat aat gtg acc ttt ggc ctc aac cgc act gat att 403
 Lys Thr Val Leu Asp Asn Val Thr Phe Gly Leu Asn Arg Thr Asp Ile
 90 95 100

tcc tgg tca gaa gca caa gaa cgc gcc tcg gca ctg ctt gca gaa gtc 451
 Ser Trp Ser Glu Ala Gln Glu Arg Ala Ser Ala Leu Leu Ala Glu Val
 105 110 115

aaa ctt ccc gac tcc gac gcc gcc tgg ccc ctc acg ctc tcc ggc ggc 499
 Lys Leu Pro Asp Ser Asp Ala Ala Trp Pro Leu Thr Leu Ser Gly Gly
 120 125 130

caa gcc cag cgc gtc tcc ctt gcg cga gcg ctc atc tcc gag cca gag 547
 Gln Ala Gln Arg Val Ser Leu Ala Arg Ala Leu Ile Ser Glu Pro Glu
 135 140 145

ctt ttg ctt ctc gac gaa ccc ttc ggc gcc ctc gat gct ctg aca aga 595

Leu Leu Leu Leu Asp Glu Pro Phe Gly Ala Leu Asp Ala Leu Thr Arg
 150 155 160 165
 ctg aca gcc caa gac ctg ctg ctc aaa acc gtg aac acc cga aac ttg 643
 Leu Thr Ala Gln Asp Leu Leu Leu Lys Thr Val Asn Thr Arg Asn Leu
 170 175 180
 gga gtt ctg ctg gtc acc cat gat gtt tcc gag gcc atc gcc ctg gcc 691
 Gly Val Leu Leu Val Thr His Asp Val Ser Glu Ala Ile Ala Leu Ala
 185 190 195
 gac cac gtc ctt ctt ctt gac gac ggc gcc atc aca cac agt ttg act 739
 Asp His Val Leu Leu Leu Asp Asp Gly Ala Ile Thr His Ser Leu Thr
 200 205 210
 gta gat atc ccc ggc gat cgc cgc acc cac ccc tcc ttt gcc tcc tac 787
 Val Asp Ile Pro Gly Asp Arg Arg Thr His Pro Ser Phe Ala Ser Tyr
 215 220 225
 acc gct caa ctc ctt gag tgg ctc gaa atc acc aca cct gcc 829
 Thr Ala Gln Leu Leu Glu Trp Leu Glu Ile Thr Thr Pro Ala
 230 235 240
 tagaaagaaa tcatgaaatt taa 852

<210> 270
 <211> 243
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 270
 Met Thr Ala Thr Leu Ser Leu Lys Pro Ala Ala Thr Val Arg Gly Leu
 1 5 10 15
 Arg Lys Ser Tyr Gly Thr Lys Glu Val Leu Gln Gly Ile Asp Leu Thr
 20 25 30
 Ile Asn Cys Gly Glu Val Thr Ala Leu Ile Gly Arg Ser Gly Ser Gly
 35 40 45
 Lys Ser Thr Ile Leu Arg Val Leu Ala Gly Leu Ser Lys Glu His Ser
 50 55 60
 Gly Ser Val Glu Ile Ser Gly Asn Pro Ala Val Ala Phe Gln Glu Pro
 65 70 75 80
 Arg Leu Leu Pro Trp Lys Thr Val Leu Asp Asn Val Thr Phe Gly Leu
 85 90 95
 Asn Arg Thr Asp Ile Ser Trp Ser Glu Ala Gln Glu Arg Ala Ser Ala
 100 105 110
 Leu Leu Ala Glu Val Lys Leu Pro Asp Ser Asp Ala Ala Trp Pro Leu
 115 120 125
 Thr Leu Ser Gly Gly Gln Ala Gln Arg Val Ser Leu Ala Arg Ala Leu
 130 135 140
 Ile Ser Glu Pro Glu Leu Leu Leu Leu Asp Glu Pro Phe Gly Ala Leu
 145 150 155 160

[illegible]

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<210> 271
<211> 621
<212> DNA
<213> Corvnebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(598)
<223> RXN01142
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 Met Val Thr His Asp Val Asp Glu Ala Ile Leu Leu Ser Asp Arg Val
 105 110 115

 ctc gtg atg tcc aag agc ccc gaa gcc acc atc atc acc gat att cca 499
 Leu Val Met Ser Lys Ser Pro Glu Ala Thr Ile Ile Thr Asp Ile Pro
 120 125 130

 gtg aat ctt ccc cgc ccc aga cac gag ctg agt gaa gac gct tct gtt 547
 Val Asn Leu Pro Arg Pro Arg His Glu Leu Ser Glu Asp Ala Ser Val
 135 140 145

 gaa gcc gag acc aca gcc ctg cgt aag cgg atg ctg cat ctg ctg gag 595
 Glu Ala Glu Thr Thr Ala Leu Arg Lys Arg Met Leu His Leu Leu Glu
 150 155 160 165

 cac tagttttctaa cacgtctttt aaa 621
 His

<210> 272

<211> 166

<212> PRT

<213> Corynebacterium glutamicum

<400> 272

Leu Thr Ala Arg Gly Asn Ile Asp Phe Gly Leu Arg Ser Ala Arg Pro
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 Ser Leu Ser Lys Thr Glu Arg Ala Asp Ile Thr Arg Thr His Leu Glu
 20 25 30

 Gln Val Gly Leu Thr Asp Ala Ala Glu Arg Arg Pro Ala Arg Leu Ser
 35 40 45

 Gly Gly Met Gln Gln Arg Val Gly Ile Ala Arg Ala Phe Ala Ile Asp
 50 55 60

 Pro Pro Ile Met Leu Leu Asp Glu Pro Phe Gly Ala Leu Asp Ala Leu
 65 70 75 80

 Thr Arg Arg Glu Leu Gln Leu Gln Leu Leu Asn Ile Trp Glu Ala Ser
 85 90 95

 Arg Arg Thr Val Val Met Val Thr His Asp Val Asp Glu Ala Ile Leu
 100 105 110

 Leu Ser Asp Arg Val Leu Val Met Ser Lys Ser Pro Glu Ala Thr Ile
 115 120 125

 Ile Thr Asp Ile Pro Val Asn Leu Pro Arg Pro Arg His Glu Leu Ser
 130 135 140

 Glu Asp Ala Ser Val Glu Ala Glu Thr Thr Ala Leu Arg Lys Arg Met
 145 150 155 160

 Leu His Leu Leu Glu His
 165

<210> 273
 <211> 443
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(420)
 <223> FRXA01142

<400> 273
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 Thr Arg Thr His Leu Glu Gln Val Gly Leu Thr Asp Ala Ala Glu Arg
 1 5 10 15
 cgc ccc gcc cgc ctc tcc ggc ggc atg caa cag cga gtc ggc atc gca 96
 Arg Pro Ala Arg Leu Ser Gly Gly Met Gln Gln Arg Val Gly Ile Ala
 20 25 30
 cgc gcc ttc gcc atc gac cca cca atc atg ctt ctc gac gaa ccc ttc 144
 Arg Ala Phe Ala Ile Asp Pro Ile Met Leu Leu Asp Glu Pro Phe
 35 40 45
 gga gcc ctc gac gcc ctc acc cgc cgc gaa ctc cag ctc caa cta ctc 192
 Gly Ala Leu Asp Ala Leu Thr Arg Arg Glu Leu Gln Leu Gln Leu Leu
 50 55 60
 aac att tgg gaa gcc tcc cgc cgc acc gtc gtc atg gtc acc cac gac 240
 Asn Ile Trp Glu Ala Ser Arg Arg Thr Val Val Met Val Thr His Asp
 65 70 75 80
 gtc gac gag gcc atc ctg ctc tcc gac cga gtt ctc gtg atg tcc aag 288
 Val Asp Glu Ala Ile Leu Leu Ser Asp Arg Val Leu Val Met Ser Lys
 85 90 95
 agc ccc gaa gcc acc atc atc acc gat att cca gtg aat ctt ccc cgc 336
 Ser Pro Glu Ala Thr Ile Ile Thr Asp Ile Pro Val Asn Leu Pro Arg
 100 105 110
 ccc aga cac gag ctg agt gaa gac gct tct gtt gaa gcc gag acc aca 384
 Pro Arg His Glu Leu Ser Glu Asp Ala Ser Val Glu Ala Glu Thr Thr
 115 120 125
 gcc ctg cgt aag cgg atg ctg cat ctg ctg gag cac tagttttctaa 430
 Ala Leu Arg Lys Arg Met Leu His Leu Leu Glu His
 130 135 140
 cacgtctttt aaa 443

<210> 274
 <211> 140
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 274
 Thr Arg Thr His Leu Glu Gln Val Gly Leu Thr Asp Ala Ala Glu Arg
 1 5 10 15
 Arg Pro Ala Arg Leu Ser Gly Gly Met Gln Gln Arg Val Gly Ile Ala
 20 25 30

Arg Ala Phe Ala Ile Asp Pro Pro Ile Met Leu Leu Asp Glu Pro Phe
 35 40 45

Gly Ala Leu Asp Ala Leu Thr Arg Arg Glu Leu Gln Leu Gln Leu Leu
 50 55 60

Asn Ile Trp Glu Ala Ser Arg Arg Thr Val Val Met Val Thr His Asp
 65 70 75 80

Val Asp Glu Ala Ile Leu Leu Ser Asp Arg Val Leu Val Met Ser Lys
 85 90 95

Ser Pro Glu Ala Thr Ile Ile Thr Asp Ile Pro Val Asn Leu Pro Arg
 100 105 110

Pro Arg His Glu Leu Ser Glu Asp Ala Ser Val Glu Ala Glu Thr Thr
 115 120 125

Ala Leu Arg Lys Arg Met Leu His Leu Leu Glu His
 130 135 140

<210> 275

<211> 948

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(925)

<223> RXN01141

<400> 275

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cgacagcagg cgttttctgc aactgggcgc ttttgcgtcc ttg agc acc gca ttg 115
 Leu Ser Thr Ala Leu
 1 5

gcc gga gcg gcc cgc tac gtg acg tcg aca agc aat aat gaa cct gcg 163
 Ala Gly Ala Ala Arg Tyr Val Thr Ser Thr Ser Asn Asn Glu Pro Ala
 10 15 20

gat aac act ccc ctg acc att ggc tac gtg cct att gcg ggc tcg gcg 211
 Asp Asn Thr Pro Leu Thr Ile Gly Tyr Val Pro Ile Ala Gly Ser Ala
 25 30 35

ccg att gct atc gca gat gcg cta ggg ctg ttt aag aaa cac ggc gtg 259
 Pro Ile Ala Ile Ala Asp Ala Leu Gly Leu Phe Lys Lys His Gly Val
 40 45 50

aat gtc acg ttg aag aag tac tca ggc tgg tcc gac ctg tgg acc gcc 307
 Asn Val Thr Leu Lys Lys Tyr Ser Gly Trp Ser Asp Leu Trp Thr Ala
 55 60 65

tat gca aca gag cag ctt gat gtt gcg cac atg ctg tcg ccg atg act 355
 Tyr Ala Thr Glu Gln Leu Asp Val Ala His Met Leu Ser Pro Met Thr
 70 75 80 85

gtg gcg att aat gct gga gtg acc aac gcg tcg cgc ccg acg gag ctg 403

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<400> 276
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 1          5          10          15

Asn Asn Glu Pro Ala Asp Asn Thr Pro Leu Thr Ile Gly Tyr Val Pro
      20          25          30

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Ile Ala Gly Ser Ala Pro Ile Ala Ile Ala Asp Ala Leu Gly Leu Phe
 35 40 45
 Lys Lys His Gly Val Asn Val Thr Leu Lys Lys Tyr Ser Gly Trp Ser
 50 55 60
 Asp Leu Trp Thr Ala Tyr Ala Thr Glu Gln Leu Asp Val Ala His Met
 65 70 75 80
 Leu Ser Pro Met Thr Val Ala Ile Asn Ala Gly Val Thr Asn Ala Ser
 85 90 95
 Arg Pro Thr Glu Leu Ser Phe Thr Gln Asn Thr Asn Gly Gln Ala Ile
 100 105 110
 Thr Leu Ala Ser Lys His Tyr Gly Ser Val Asn Ser Ala Ala Asp Leu
 115 120 125
 Lys Gly Met Val Leu Gly Ile Pro Phe Glu Tyr Ser Val His Ala Leu
 130 135 140
 Leu Leu Arg Asp Tyr Leu Val Ser Asn Ala Val Asp Pro Ile Ala Asp
 145 150 155 160
 Leu Glu Leu Arg Leu Leu Arg Pro Ala Asp Met Val Ala Gln Leu Thr
 165 170 175
 Val Glu Gly Ile Asp Gly Phe Ile Gly Pro Gly Pro Phe Asn Glu Arg
 180 185 190
 Ala Ile Ser Asn Gly Ser Gly Arg Ile Trp Leu Leu Thr Lys Gln Leu
 195 200 205
 Trp Asp Lys His Pro Cys Cys Ala Val Ala Met Ala Lys Glu Trp Lys
 210 215 220
 Ala Glu His Pro Thr Ala Ala Gln Gly Val Leu Asn Ala Leu Glu Glu
 225 230 235 240
 Ala Ser Ala Ile Leu Ser Asn Pro Ala Gln Phe Asp Ser Ser Ala Arg
 245 250 255
 Thr Leu Ser Gln Glu Lys Tyr Leu Asn Gln Pro Ala Thr Leu Leu Asp
 260 265 270
 Gly Pro Ser
 275

<210> 277

<211> 424

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(424)

<223> FRXA01135

<400> 277

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gaacactcgg tatggcacct gatttaagga tgctgcaatc gtg aca cat atc ctc 115
 Val Thr His Ile Leu
 1 5

ttc gac agc agg cgt ttt ctg caa ctg ggc gct ttt gcg tcc ttg agc 163
 Phe Asp Ser Arg Arg Phe Leu Gln Leu Gly Ala Phe Ala Ser Leu Ser
 10 15 20

acc gca ttg gcc gga gcg gcc cgc tac gtg acg tcg aca agc aat aat 211
 Thr Ala Leu Ala Gly Ala Ala Arg Tyr Val Thr Ser Thr Ser Asn Asn
 25 30 35

gaa cct gcg gat aac act ccc ctg acc att ggc tac gtg cct att gcg 259
 Glu Pro Ala Asp Asn Thr Pro Leu Thr Ile Gly Tyr Val Pro Ile Ala
 40 45 50

ggc tcg gcg ccg att gct atc gca gat gcg cta ggg ctg ttt aag aaa 307
 Gly Ser Ala Pro Ile Ala Ile Ala Asp Ala Leu Gly Leu Phe Lys Lys
 55 60 65

cac ggc gtg aat gtc acg ttg aag aag tac tca ggc tgg tcc gac ctg 355
 His Gly Val Asn Val Thr Leu Lys Lys Tyr Ser Gly Trp Ser Asp Leu
 70 75 80 85

tgg acc gcc tat gca aca gag cag ctt gat gtt gcg cac atg ctg tcg 403
 Trp Thr Ala Tyr Ala Thr Glu Gln Leu Asp Val Ala His Met Leu Ser
 90 95 100

ccg atg act gtg gcg att aat 424
 Pro Met Thr Val Ala Ile Asn
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<210> 278

<211> 108

<212> PRT

<213> Corynebacterium glutamicum

<400> 278

Val Thr His Ile Leu Phe Asp Ser Arg Arg Phe Leu Gln Leu Gly Ala
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Phe Ala Ser Leu Ser Thr Ala Leu Ala Gly Ala Ala Arg Tyr Val Thr
 20 25 30

Ser Thr Ser Asn Asn Glu Pro Ala Asp Asn Thr Pro Leu Thr Ile Gly
 35 40 45

Tyr Val Pro Ile Ala Gly Ser Ala Pro Ile Ala Ile Ala Asp Ala Leu
 50 55 60

Gly Leu Phe Lys Lys His Gly Val Asn Val Thr Leu Lys Lys Tyr Ser
 65 70 75 80

Gly Trp Ser Asp Leu Trp Thr Ala Tyr Ala Thr Glu Gln Leu Asp Val
 85 90 95

Ala His Met Leu Ser Pro Met Thr Val Ala Ile Asn
 100 105

<210> 279
 <211> 485
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(462)
 <223> FRXA01141

<400> 279
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 Val Asn Ser Ala Ala Asp Leu Lys Gly Met Val Leu Gly Ile Pro Phe
 1 5 10 15
 gaa tat tca gtc cat gcg ctg ctc ctg cgc gat tat ctc gtc tca aac 96
 Glu Tyr Ser Val His Ala Leu Leu Leu Arg Asp Tyr Leu Val Ser Asn
 20 25 30
 gca gtt gat ccc atc gcc gat ctt gag ctt cgc ctg ctc cga cct gcc 144
 Ala Val Asp Pro Ile Ala Asp Leu Glu Leu Arg Leu Leu Arg Pro Ala
 35 40 45
 gat atg gtc gca caa ttg aca gtt gag ggc atc gat gga ttc att ggg 192
 Asp Met Val Ala Gln Leu Thr Val Glu Gly Ile Asp Gly Phe Ile Gly
 50 55 60
 cct ggg ccg ttt aat gaa cgc gcc atc agc aat ggc tcc ggc cgg att 240
 Pro Gly Pro Phe Asn Glu Arg Ala Ile Ser Asn Gly Ser Gly Arg Ile
 65 70 75 80
 tgg ctg ctg acc aaa caa ctg tgg gac aaa cat cca tgc tgc gcc gtg 288
 Trp Leu Leu Thr Lys Gln Leu Trp Asp Lys His Pro Cys Cys Ala Val
 85 90 95
 gcg atg gcc aaa gag tgg aaa gct gaa cac ccc acg gcg gct cag ggt 336
 Ala Met Ala Lys Glu Trp Lys Ala Glu His Pro Thr Ala Ala Gln Gly
 100 105 110
 gtg ctt aat gcg ctg gag gaa gcc tcc gca att ttg agc aat ccg gca 384
 Val Leu Asn Ala Leu Glu Glu Ala Ser Ala Ile Leu Ser Asn Pro Ala
 115 120 125
 caa ttt gat tcc tcg gca cgc acg ctg tcg cag gaa aaa tac ctc aac 432
 Gln Phe Asp Ser Ser Ala Arg Thr Leu Ser Gln Glu Lys Tyr Leu Asn
 130 135 140
 cag cct gcc acg ttg ctg gat gga ccg tcg taatcatcgg catcaccggc 482
 Gln Pro Ala Thr Leu Leu Asp Gly Pro Ser
 145 150
 tta 485

<210> 280
 <211> 154
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 280

Val Asn Ser Ala Ala Asp Leu Lys Gly Met Val Leu Gly Ile Pro Phe
 1 5 10 15

Glu Tyr Ser Val His Ala Leu Leu Leu Arg Asp Tyr Leu Val Ser Asn
 20 25 30

Ala Val Asp Pro Ile Ala Asp Leu Glu Leu Arg Leu Leu Arg Pro Ala
 35 40 45

Asp Met Val Ala Gln Leu Thr Val Glu Gly Ile Asp Gly Phe Ile Gly
 50 55 60

Pro Gly Pro Phe Asn Glu Arg Ala Ile Ser Asn Gly Ser Gly Arg Ile
 65 70 75 80

Trp Leu Leu Thr Lys Gln Leu Trp Asp Lys His Pro Cys Cys Ala Val
 85 90 95

Ala Met Ala Lys Glu Trp Lys Ala Glu His Pro Thr Ala Ala Gln Gly
 100 105 110

Val Leu Asn Ala Leu Glu Glu Ala Ser Ala Ile Leu Ser Asn Pro Ala
 115 120 125

Gln Phe Asp Ser Ser Ala Arg Thr Leu Ser Gln Glu Lys Tyr Leu Asn
 130 135 140

Gln Pro Ala Thr Leu Leu Asp Gly Pro Ser
 145 150

<210> 281

<211> 892

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(892)

<223> RXA00728

<400> 281

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accgattgaa gccaaagccac tacgccaccc tggccggtgg gtg gca gcc gct atc 115
 Val Ala Ala Ala Ile
 1 5

atc gtg gca ctg ctc gca tgg ttt atc atc agc gcg ctc aac aat gag 163
 Ile Val Ala Leu Leu Ala Trp Phe Ile Ile Ser Ala Leu Asn Asn Glu
 10 15 20

gcc tac ggt tgg gat acc tac cgc tcg tat ctt ttt gac acc cgc att 211
 Ala Tyr Gly Trp Asp Thr Tyr Arg Ser Tyr Leu Phe Asp Thr Arg Ile
 25 30 35

gcc acc gcg gca ctt cac acc att gcg ctg acc ttg ctg tcc atg atc 259
 Ala Thr Ala Ala Leu His Thr Ile Ala Leu Thr Leu Leu Ser Met Ile
 40 45 50

ttg ggt gtg gtt ctc ggc gca atc ttg gcc gtc atg cgt atg tcc ggc	307
Leu Gly Val Val Leu Gly Ala Ile Leu Ala Val Met Arg Met Ser Gly	
55 60 65	
aac cct gtc atg cag ggc gta gcg tgg ctg tac ctg tgg att ttc cgc	355
Asn Pro Val Met Gln Gly Val Ala Trp Leu Tyr Leu Trp Ile Phe Arg	
70 75 80 85	
ggc acc cca att tat gtg cag ttg gtg ttc tgg ggc ctg ctg ggt tcc	403
Gly Thr Pro Ile Tyr Val Gln Leu Val Phe Trp Gly Leu Leu Gly Ser	
90 95 100	
ttg tac cag tcg atc aac ctc ggt ttc gca gag atc gat ctg caa agc	451
Leu Tyr Gln Ser Ile Asn Leu Gly Phe Ala Glu Ile Asp Leu Gln Ser	
105 110 115	
ttg ctg tct aat atg ttc ctg ctc gcg gtg atc ggt ctg ggt ctc aac	499
Leu Leu Ser Asn Met Phe Leu Leu Ala Val Ile Gly Leu Gly Leu Asn	
120 125 130	
gag gct gcg tac atg gcg gaa atc gtg cgc tcg ggc atc caa gcg gtg	547
Glu Ala Ala Tyr Met Ala Glu Ile Val Arg Ser Gly Ile Gln Ala Val	
135 140 145	
cct gag ggc cag atg gag gcg tcg aaa gct ttg ggt atg aac tgg tca	595
Pro Glu Gly Gln Met Glu Ala Ser Lys Ala Leu Gly Met Asn Trp Ser	
150 155 160 165	
atg acc atg cgt cgc acc atc ttg ccg cag gcc atg cgc atc atc att	643
Met Thr Met Arg Arg Thr Ile Leu Pro Gln Ala Met Arg Ile Ile Ile	
170 175 180	
ccg cca acc ggc aat gaa ctg atc tcc atg ctc aag acc acc tct ctg	691
Pro Pro Thr Gly Asn Glu Leu Ile Ser Met Leu Lys Thr Thr Ser Leu	
185 190 195	
gtt gtt gcg att cct tat tct ctc gag ctg tac ggc cgc agc atg gat	739
Val Val Ala Ile Pro Tyr Ser Leu Glu Leu Tyr Gly Arg Ser Met Asp	
200 205 210	
att gcg tac tcc ctc ttc gag cca gtt cca atg ctt ctg gtt gct gcg	787
Ile Ala Tyr Ser Leu Phe Glu Pro Val Pro Met Leu Leu Val Ala Ala	
215 220 225	
agc tgg tac ttg gtc atc acc tct att ctt atg gtt ggt cag tac tac	835
Ser Trp Tyr Leu Val Ile Thr Ser Ile Leu Met Val Gly Gln Tyr Tyr	
230 235 240 245	
ctg gag aag cac ttc gaa aag ggc agc acc cgc acc ctg acc gca cgt	883
Leu Glu Lys His Phe Glu Lys Gly Ser Thr Arg Thr Leu Thr Ala Arg	
250 255 260	
cag ctc gct	892
Gln Leu Ala	

<210> 282

<211> 264

<212> PRT

<213> Corynebacterium glutamicum

<400> 282

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 Phe Asp Thr Arg Ile Ala Thr Ala Ala Leu His Thr Ile Ala Leu Thr
 35 40 45
 Leu Leu Ser Met Ile Leu Gly Val Val Leu Gly Ala Ile Leu Ala Val
 50 55 60
 Met Arg Met Ser Gly Asn Pro Val Met Gln Gly Val Ala Trp Leu Tyr
 65 70 75 80
 Leu Trp Ile Phe Arg Gly Thr Pro Ile Tyr Val Gln Leu Val Phe Trp
 85 90 95
 Gly Leu Leu Gly Ser Leu Tyr Gln Ser Ile Asn Leu Gly Phe Ala Glu
 100 105 110
 Ile Asp Leu Gln Ser Leu Leu Ser Asn Met Phe Leu Leu Ala Val Ile
 115 120 125
 Gly Leu Gly Leu Asn Glu Ala Ala Tyr Met Ala Glu Ile Val Arg Ser
 130 135 140
 Gly Ile Gln Ala Val Pro Glu Gly Gln Met Glu Ala Ser Lys Ala Leu
 145 150 155 160
 Gly Met Asn Trp Ser Met Thr Met Arg Arg Thr Ile Leu Pro Gln Ala
 165 170 175
 Met Arg Ile Ile Ile Pro Pro Thr Gly Asn Glu Leu Ile Ser Met Leu
 180 185 190
 Lys Thr Thr Ser Leu Val Val Ala Ile Pro Tyr Ser Leu Glu Leu Tyr
 195 200 205
 Gly Arg Ser Met Asp Ile Ala Tyr Ser Leu Phe Glu Pro Val Pro Met
 210 215 220
 Leu Leu Val Ala Ala Ser Trp Tyr Leu Val Ile Thr Ser Ile Leu Met
 225 230 235 240
 Val Gly Gln Tyr Tyr Leu Glu Lys His Phe Glu Lys Gly Ser Thr Arg
 245 250 255
 Thr Leu Thr Ala Arg Gln Leu Ala
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<210> 283

<211> 1518

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1495)

<223> RXA02663

<400> 283

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aaccgctcac atcttgatca agcacgttgc ccgaaactgc atg gct ccg att ctg 115
Met Ala Pro Ile Leu
1 5

gtg ttc gcc acc gtc ctg gtc gcc gat gcg att gtc ttc gaa gca tcc 163
Val Phe Ala Thr Val Leu Val Ala Asp Ala Ile Val Phe Glu Ala Ser
10 15 20

ctg tcc ttc atc aac gct ggt gtg aaa cca cca tca cct tca tgg ggc 211
Leu Ser Phe Ile Asn Ala Gly Val Lys Pro Pro Ser Pro Ser Trp Gly
25 30 35

aac atc ctt gcc gat ggt aaa gcc ctg ctg ctt agc ggc gca tgg tgg 259
Asn Ile Leu Ala Asp Gly Lys Ala Leu Leu Leu Ser Gly Ala Trp Trp
40 45 50

cca acc ttc ttc cca ggt ttg atg atc ctg ctg acc gtt ctc tgc ttg 307
Pro Thr Phe Phe Pro Gly Leu Met Ile Leu Leu Thr Val Leu Cys Leu
55 60 65

aac atc ctt tct gaa ggc ctc acc gac acc ctg gcc agc cct aag cca 355
Asn Ile Leu Ser Glu Gly Leu Thr Asp Thr Leu Ala Ser Pro Lys Pro
70 75 80 85

aag cct gtt tca gct tct gca aag aag gca ctg aag aag gaa gaa tcc 403
Lys Pro Val Ser Ala Ser Ala Lys Lys Ala Leu Lys Lys Glu Glu Ser
90 95 100

ggt gaa aag gaa ggc tcc gga atc gtg ctt ggg cac acc aca cgt gaa 451
Gly Glu Lys Glu Gly Ser Gly Ile Val Leu Gly His Thr Thr Arg Glu
105 110 115

gaa gcc aac gcc tca ctg ctc gca tca ctt gct gcg cta tcc acc agc 499
Glu Ala Asn Ala Ser Leu Leu Ala Ser Leu Ala Ala Leu Ser Thr Ser
120 125 130

gaa aac aat tcc aat aac cgg ctt ata ttt gat ggc aac ccc act cct 547
Glu Asn Asn Ser Asn Asn Arg Leu Ile Phe Asp Gly Asn Pro Thr Pro
135 140 145

ctg ttg gaa gtt cgc gat cta aag atc tcc ttc ccc aat gct cac gga 595
Leu Leu Glu Val Arg Asp Leu Lys Ile Ser Phe Pro Asn Ala His Gly
150 155 160 165

gat atc aat att gtc gac ggc gtg aac ttc acc gtc gcc cca ggc caa 643
Asp Ile Asn Ile Val Asp Gly Val Asn Phe Thr Val Ala Pro Gly Gln
170 175 180

acc atg ggt ctt gtc ggt gaa tcc ggc tgt ggt aaa tcg att acc gca 691
Thr Met Gly Leu Val Gly Glu Ser Gly Cys Gly Lys Ser Ile Thr Ala
185 190 195

atg tcg atc atg ggt ctg ctg cct cca aca gca aag atc gaa ggc gag 739
Met Ser Ile Met Gly Leu Leu Pro Pro Thr Ala Lys Ile Glu Gly Glu
200 205 210

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atc ctt ttc gac gga aag aac ctc ctt gat ctg aaa cca gac gag ctc Ile Leu Phe Asp Gly Lys Asn Leu Leu Asp Leu Lys Pro Asp Glu Leu 215 220 225	787
aat gca ctg cgt gga cat gaa atc gcc atg atc tac caa gat gca ctc Asn Ala Leu Arg Gly His Glu Ile Ala Met Ile Tyr Gln Asp Ala Leu 230 235 240 245	835
tcc tca ctc aac cca tcc atg ctg atc agc gcc caa atg aag cag ctg Ser Ser Leu Asn Pro Ser Met Leu Ile Ser Ala Gln Met Lys Gln Leu 250 255 260	883
acc cgc cgc ggt gga aag cgc agt gcc gaa gaa ctc ctg gaa ctt gta Thr Arg Arg Gly Lys Arg Ser Ala Glu Glu Leu Leu Glu Leu Val 265 270 275	931
ggc ctt gat cca aag cgc acc ctg cag tcc tac ccg cat gag ctt tca Gly Leu Asp Pro Lys Arg Thr Leu Gln Ser Tyr Pro His Glu Leu Ser 280 285 290	979
ggt ggc cag cgc cag cga gtt ctc atc gca atg gca ctg acc aga aac Gly Gly Gln Arg Gln Arg Val Leu Ile Ala Met Ala Leu Thr Arg Asn 295 300 305	1027
cca cgc ctc ctc atc gcc gac gag cca acc acc gcg cta gac gtc act Pro Arg Leu Leu Ile Ala Asp Glu Pro Thr Thr Ala Leu Asp Val Thr 310 315 320 325	1075
gtt cag cag cag gtt gtc gat ctg ctt aat gaa ctg cgt gaa aag ctc Val Gln Gln Gln Val Val Asp Leu Leu Asn Glu Leu Arg Glu Lys Leu 330 335 340	1123
gga ttc gcc atg atc ttt gta tcc cac gac ttg gct ctt gtc gcc cgc Gly Phe Ala Met Ile Phe Val Ser His Asp Leu Ala Leu Val Ala Arg 345 350 355	1171
ctg gtg cac aag ctc acc gtc atg tac gca ggt cag gtt gtt gag caa Leu Val His Lys Leu Thr Val Met Tyr Ala Gly Gln Val Val Glu Gln 360 365 370	1219
gga acc acc cgc gaa atc ctt atc gat cct cga cac gaa tac acc cgc Gly Thr Thr Arg Glu Ile Leu Ile Asp Pro Arg His Glu Tyr Thr Arg 375 380 385	1267
ggt ttg ctc gga tcc gtg ctc tcc atc gaa gct ggt gtg gac cgc ctc Gly Leu Leu Gly Ser Val Leu Ser Ile Glu Ala Gly Val Asp Arg Leu 390 395 400 405	1315
tac cag gtc cca ggc act gtt cca tca cca aag gaa ttc gtg gca ggc Tyr Gln Val Pro Gly Thr Val Pro Ser Pro Lys Glu Phe Val Ala Gly 410 415 420	1363
gac cgc ttt gca cca cga tca gaa ttc cca gaa ctt ggc ctt gac caa Asp Arg Phe Ala Pro Arg Ser Glu Phe Pro Glu Leu Gly Leu Asp Gln 425 430 435	1411
aag cca gta ctt cgc ccc atc acg ggc aca gag cat gca tac gca gca Lys Pro Val Leu Arg Pro Ile Thr Gly Thr Glu His Ala Tyr Ala Ala 440 445 450	1459

acc gat gaa ctt ctt gcc gca aag gga gaa caa cga tgacctcgac 1505
 Thr Asp Glu Leu Leu Ala Ala Lys Gly Glu Gln Arg
 455 460 465

aatcgacacc agg 1518

<210> 284

<211> 465

<212> PRT

<213> Corynebacterium glutamicum

<400> 284

Met Ala Pro Ile Leu Val Phe Ala Thr Val Leu Val Ala Asp Ala Ile
 1 5 10 15

Val Phe Glu Ala Ser Leu Ser Phe Ile Asn Ala Gly Val Lys Pro Pro
 20 25 30

Ser Pro Ser Trp Gly Asn Ile Leu Ala Asp Gly Lys Ala Leu Leu Leu
 35 40 45

Ser Gly Ala Trp Trp Pro Thr Phe Phe Pro Gly Leu Met Ile Leu Leu
 50 55 60

Thr Val Leu Cys Leu Asn Ile Leu Ser Glu Gly Leu Thr Asp Thr Leu
 65 70 75 80

Ala Ser Pro Lys Pro Lys Pro Val Ser Ala Ser Ala Lys Lys Ala Leu
 85 90 95

Lys Lys Glu Glu Ser Gly Glu Lys Glu Gly Ser Gly Ile Val Leu Gly
 100 105 110

His Thr Thr Arg Glu Glu Ala Asn Ala Ser Leu Leu Ala Ser Leu Ala
 115 120 125

Ala Leu Ser Thr Ser Glu Asn Asn Ser Asn Asn Arg Leu Ile Phe Asp
 130 135 140

Gly Asn Pro Thr Pro Leu Leu Glu Val Arg Asp Leu Lys Ile Ser Phe
 145 150 155 160

Pro Asn Ala His Gly Asp Ile Asn Ile Val Asp Gly Val Asn Phe Thr
 165 170 175

Val Ala Pro Gly Gln Thr Met Gly Leu Val Gly Glu Ser Gly Cys Gly
 180 185 190

Lys Ser Ile Thr Ala Met Ser Ile Met Gly Leu Leu Pro Pro Thr Ala
 195 200 205

Lys Ile Glu Gly Glu Ile Leu Phe Asp Gly Lys Asn Leu Leu Asp Leu
 210 215 220

Lys Pro Asp Glu Leu Asn Ala Leu Arg Gly His Glu Ile Ala Met Ile
 225 230 235 240

Tyr Gln Asp Ala Leu Ser Ser Leu Asn Pro Ser Met Leu Ile Ser Ala
 245 250 255

Gln Met Lys Gln Leu Thr Arg Arg Gly Gly Lys Arg Ser Ala Glu Glu
 260 265 270
 Leu Leu Glu Leu Val Gly Leu Asp Pro Lys Arg Thr Leu Gln Ser Tyr
 275 280 285
 Pro His Glu Leu Ser Gly Gly Gln Arg Gln Arg Val Leu Ile Ala Met
 290 295 300
 Ala Leu Thr Arg Asn Pro Arg Leu Leu Ile Ala Asp Glu Pro Thr Thr
 305 310 315 320
 Ala Leu Asp Val Thr Val Gln Gln Gln Val Val Asp Leu Leu Asn Glu
 325 330 335
 Leu Arg Glu Lys Leu Gly Phe Ala Met Ile Phe Val Ser His Asp Leu
 340 345 350
 Ala Leu Val Ala Arg Leu Val His Lys Leu Thr Val Met Tyr Ala Gly
 355 360 365
 Gln Val Val Glu Gln Gly Thr Thr Arg Glu Ile Leu Ile Asp Pro Arg
 370 375 380
 His Glu Tyr Thr Arg Gly Leu Leu Gly Ser Val Leu Ser Ile Glu Ala
 385 390 395 400
 Gly Val Asp Arg Leu Tyr Gln Val Pro Gly Thr Val Pro Ser Pro Lys
 405 410 415
 Glu Phe Val Ala Gly Asp Arg Phe Ala Pro Arg Ser Glu Phe Pro Glu
 420 425 430
 Leu Gly Leu Asp Gln Lys Pro Val Leu Arg Pro Ile Thr Gly Thr Glu
 435 440 445
 His Ala Tyr Ala Ala Thr Asp Glu Leu Leu Ala Ala Lys Gly Glu Gln
 450 455 460
 Arg
 465

<210> 285
 <211> 783
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(760)
 <223> RXA02664

<400> 285
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 catcaacttc aaggcctacc gcgatgaagt aatcggcatc gtg ggt gaa tct ggt 115
 Val Gly Glu Ser Gly
 1 5
 tgc gga aaa tct acc ctt gcc cgc gtt atg gtt ggc ctg caa ccg gtc 163

Cys	Gly	Lys	Ser	Thr	Leu	Ala	Arg	Val	Met	Val	Gly	Leu	Gln	Pro	Val	
				10					15					20		
acc	tcc	ggc	gaa	gtg	ctg	ttc	aaa	ggc	aag	ccc	atg	aag	cct	cgt	ggt	211
Thr	Ser	Gly	Glu	Val	Leu	Phe	Lys	Gly	Lys	Pro	Met	Lys	Pro	Arg	Gly	
			25					30					35			
gcg	cag	cgc	aaa	gaa	ctc	ggc	agc	tca	gta	tcc	gtc	gtg	ttc	cag	gat	259
Ala	Gln	Arg	Lys	Glu	Leu	Gly	Ser	Ser	Val	Ser	Val	Val	Phe	Gln	Asp	
			40				45						50			
cct	gcc	acc	tcg	tta	aac	cca	cga	atg	acc	gtg	cgc	gaa	cag	ctc	ctc	307
Pro	Ala	Thr	Ser	Leu	Asn	Pro	Arg	Met	Thr	Val	Arg	Glu	Gln	Leu	Leu	
	55					60					65					
gat	cca	ctt	cga	gta	cac	aaa	gtt	ggc	gat	gaa	gca	tcc	cgc	aac	cag	355
Asp	Pro	Leu	Arg	Val	His	Lys	Val	Gly	Asp	Glu	Ala	Ser	Arg	Asn	Gln	
	70				75				80						85	
tgg	gtt	tca	gag	ctg	atc	tcc	atg	gtt	ggc	ctc	ccg	caa	tcc	gcg	ttg	403
Trp	Val	Ser	Glu	Leu	Ile	Ser	Met	Val	Gly	Leu	Pro	Gln	Ser	Ala	Leu	
				90					95					100		
gaa	gta	ctc	ccc	cga	cag	gtt	tcc	ggt	ggc	caa	cgc	caa	cgc	gtg	gcc	451
Glu	Val	Leu	Pro	Arg	Gln	Val	Ser	Gly	Gly	Gln	Arg	Gln	Arg	Val	Ala	
			105					110					115			
att	gct	cga	gca	ctt	gcg	ctg	aaa	cct	gac	atc	atc	gtt	gcc	gac	gaa	499
Ile	Ala	Arg	Ala	Leu	Ala	Leu	Lys	Pro	Asp	Ile	Ile	Val	Ala	Asp	Glu	
			120				125					130				
cca	acc	tcc	gcg	ctg	gat	gta	tcc	gtt	cgt	gcg	cag	gtc	ctc	aac	ctt	547
Pro	Thr	Ser	Ala	Leu	Asp	Val	Ser	Val	Arg	Ala	Gln	Val	Leu	Asn	Leu	
			135			140					145					
ctg	ctg	gat	ctg	aaa	act	gaa	ctc	ggc	ctg	gga	ttg	gta	ttc	atc	tcc	595
Leu	Leu	Asp	Leu	Lys	Thr	Glu	Leu	Gly	Leu	Gly	Leu	Val	Phe	Ile	Ser	
	150				155				160						165	
cac	gac	atc	aac	act	gtt	cgc	tac	gtt	tct	gat	cgc	atc	gca	gtc	atg	643
His	Asp	Ile	Asn	Thr	Val	Arg	Tyr	Val	Ser	Asp	Arg	Ile	Ala	Val	Met	
			170					175						180		
ctg	gct	gga	gaa	atc	att	gag	gaa	aac	acc	acc	tca	gag	atc	ttc	aac	691
Leu	Ala	Gly	Glu	Ile	Ile	Glu	Glu	Asn	Thr	Thr	Ser	Glu	Ile	Phe	Asn	
			185					190					195			
aat	gcg	cag	cag	gac	tac	acc	cgc	act	ctg	ctc	gaa	gcg	aca	cca	tcg	739
Asn	Ala	Gln	Gln	Asp	Tyr	Thr	Arg	Thr	Leu	Leu	Glu	Ala	Thr	Pro	Ser	
			200				205					210				
ctg	ctg	aac	aaa	act	cgt	ttg	tagtctccaa	ccctttattc	cct							783
Leu	Leu	Asn	Lys	Thr	Arg	Leu										
			215			220										

<210> 286

<211> 220

<212> PRT

<213> Corynebacterium glutamicum

<400> 286

Val Gly Glu Ser Gly Cys Gly Lys Ser Thr Leu Ala Arg Val Met Val
1 5 10 15

Gly Leu Gln Pro Val Thr Ser Gly Glu Val Leu Phe Lys Gly Lys Pro
20 25 30

Met Lys Pro Arg Gly Ala Gln Arg Lys Glu Leu Gly Ser Ser Val Ser
35 40 45

Val Val Phe Gln Asp Pro Ala Thr Ser Leu Asn Pro Arg Met Thr Val
50 55 60

Arg Glu Gln Leu Leu Asp Pro Leu Arg Val His Lys Val Gly Asp Glu
65 70 75 80

Ala Ser Arg Asn Gln Trp Val Ser Glu Leu Ile Ser Met Val Gly Leu
85 90 95

Pro Gln Ser Ala Leu Glu Val Leu Pro Arg Gln Val Ser Gly Gly Gln
100 105 110

Arg Gln Arg Val Ala Ile Ala Arg Ala Leu Ala Leu Lys Pro Asp Ile
115 120 125

Ile Val Ala Asp Glu Pro Thr Ser Ala Leu Asp Val Ser Val Arg Ala
130 135 140

Gln Val Leu Asn Leu Leu Leu Asp Leu Lys Thr Glu Leu Gly Leu Gly
145 150 155 160

Leu Val Phe Ile Ser His Asp Ile Asn Thr Val Arg Tyr Val Ser Asp
165 170 175

Arg Ile Ala Val Met Leu Ala Gly Glu Ile Ile Glu Glu Asn Thr Thr
180 185 190

Ser Glu Ile Phe Asn Asn Ala Gln Gln Asp Tyr Thr Arg Thr Leu Leu
195 200 205

Glu Ala Thr Pro Ser Leu Leu Asn Lys Thr Arg Leu
210 215 220

<210> 287

<211> 1155

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1132)

<223> RXA00760

<400> 287

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gtggacttga tctacgccgt tctcgatccg aggatccgct atg cct aat aat gaa 115
Met Pro Asn Asn Glu
1 5

ttc cac aca aac cac tcg ttg ggc caa gat gat caa acc cca gat cag	163
Phe His Thr Asn His Ser Leu Gly Gln Asp Asp Gln Thr Pro Asp Gln	
10 15 20	
gct cat ttc ttc cca caa gga cga ggc gag gct cta gtt cga cca ggt	211
Ala His Phe Phe Pro Gln Gly Arg Gly Glu Ala Leu Val Arg Pro Gly	
25 30 35	
caa gag cac ttc atc gca gcc act gat gaa acc gga ctt ggt gcc gtc	259
Gln Glu His Phe Ile Ala Ala Thr Asp Glu Thr Gly Leu Gly Ala Val	
40 45 50	
gat gct gtt gct gat gac tct gca cca acc tcc atg tgg ggc gaa gcg	307
Asp Ala Val Ala Asp Asp Ser Ala Pro Thr Ser Met Trp Gly Glu Ala	
55 60 65	
tgg cga gac ctt cgt cgt cga cca ctg ttc tgg gtc tct gcg gtg ttg	355
Trp Arg Asp Leu Arg Arg Arg Pro Leu Phe Trp Val Ser Ala Val Leu	
70 75 80 85	
att att ttg gcg ctt ctc ctg gcc gca gtt ccg cag ctg ttt acc tca	403
Ile Ile Leu Ala Leu Leu Leu Ala Ala Val Pro Gln Leu Phe Thr Ser	
90 95 100	
acg gat ccc cag ttc tgt gtg ctg gca aac tct ctt gat ggt cca cag	451
Thr Asp Pro Gln Phe Cys Val Leu Ala Asn Ser Leu Asp Gly Pro Gln	
105 110 115	
tct gga cat ccc ttc gga ttc gac cgt caa ggt tgc gat att ttt gct	499
Ser Gly His Pro Phe Gly Phe Asp Arg Gln Gly Cys Asp Ile Phe Ala	
120 125 130	
cgt acc gtc tac ggt gct cgt gcc tcg gtc gcc gtc ggt gtg ttg acc	547
Arg Thr Val Tyr Gly Ala Arg Ala Ser Val Ala Val Gly Val Leu Thr	
135 140 145	
acg tta ctg gtc gcc ctc atc ggt act gta ttt ggt gct ttg gct ggc	595
Thr Leu Leu Val Ala Leu Ile Gly Thr Val Phe Gly Ala Leu Ala Gly	
150 155 160 165	
ttc ttt ggt ggc atc atg gat acc atc ctc tcc cgc atc acc gac atg	643
Phe Phe Gly Gly Ile Met Asp Thr Ile Leu Ser Arg Ile Thr Asp Met	
170 175 180	
ttc ttc gcc att cca ctg gtt ctg gca gcc atc gtt gtg atg cag atg	691
Phe Phe Ala Ile Pro Leu Val Leu Ala Ala Ile Val Val Met Gln Met	
185 190 195	
ttc aag gaa cac cgc acc atc gtc acc gtg gtt ttg gtg ctt ggg ctt	739
Phe Lys Glu His Arg Thr Ile Val Thr Val Val Leu Val Leu Gly Leu	
200 205 210	
ttc ggc tgg acc aac att gcg cgt att acc cgt gga gcg gtg atg acc	787
Phe Gly Trp Thr Asn Ile Ala Arg Ile Thr Arg Gly Ala Val Met Thr	
215 220 225	
gca aag aat gaa gag tat gtc acc tcc gca cgt gcg ctt ggt gca tca	835
Ala Lys Asn Glu Glu Tyr Val Thr Ser Ala Arg Ala Leu Gly Ala Ser	
230 235 240 245	
aaa gcc aag ata ctg ctg tct cac atc atg cca aac gcc gca gca ccc	883

Lys Ala Lys Ile Leu Leu Ser His Ile Met Pro Asn Ala Ala Ala Pro
 250 255 260
 atc att gtg tat gca act gtg gca ctg gga aca ttc atc gtg gca gag 931
 Ile Ile Val Tyr Ala Thr Val Ala Leu Gly Thr Phe Ile Val Ala Glu
 265 270 275
 gcg acg ctc tcc ttc ctg ggc att ggc ctt cca cca tca att gtc tcc 979
 Ala Thr Leu Ser Phe Leu Gly Ile Gly Leu Pro Pro Ser Ile Val Ser
 280 285 290
 tgg ggt gct gat atc gcg aag gca caa acc tcc ctt cgt acc caa ccc 1027
 Trp Gly Ala Asp Ile Ala Lys Ala Gln Thr Ser Leu Arg Thr Gln Pro
 295 300 305
 atg gtg ctg ttc tac ccc gca atg gca ctt gca cta acc gtt ttg agc 1075
 Met Val Leu Phe Tyr Pro Ala Met Ala Leu Ala Leu Thr Val Leu Ser
 310 315 320 325
 ttc atc atg atg ggc gat gtc gtc cgc gac gct ctg gat cct aag tcg 1123
 Phe Ile Met Met Gly Asp Val Val Arg Asp Ala Leu Asp Pro Lys Ser
 330 335 340
 agg aag cga tgaccaccaa catcccacaa acc 1155
 Arg Lys Arg

<210> 288

<211> 344

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 288

Met Pro Asn Asn Glu Phe His Thr Asn His Ser Leu Gly Gln Asp Asp
 1 5 10 15
 Gln Thr Pro Asp Gln Ala His Phe Phe Pro Gln Gly Arg Gly Glu Ala
 20 25 30
 Leu Val Arg Pro Gly Gln Glu His Phe Ile Ala Ala Thr Asp Glu Thr
 35 40 45
 Gly Leu Gly Ala Val Asp Ala Val Ala Asp Asp Ser Ala Pro Thr Ser
 50 55 60
 Met Trp Gly Glu Ala Trp Arg Asp Leu Arg Arg Arg Pro Leu Phe Trp
 65 70 75 80
 Val Ser Ala Val Leu Ile Ile Leu Ala Leu Leu Leu Ala Ala Val Pro
 85 90 95
 Gln Leu Phe Thr Ser Thr Asp Pro Gln Phe Cys Val Leu Ala Asn Ser
 100 105 110
 Leu Asp Gly Pro Gln Ser Gly His Pro Phe Gly Phe Asp Arg Gln Gly
 115 120 125
 Cys Asp Ile Phe Ala Arg Thr Val Tyr Gly Ala Arg Ala Ser Val Ala
 130 135 140

Val Gly Val Leu Thr Thr Leu Leu Val Ala Leu Ile Gly Thr Val Phe
145 150 155 160

Gly Ala Leu Ala Gly Phe Phe Gly Gly Ile Met Asp Thr Ile Leu Ser
165 170 175

Arg Ile Thr Asp Met Phe Phe Ala Ile Pro Leu Val Leu Ala Ala Ile
180 185 190

Val Val Met Gln Met Phe Lys Glu His Arg Thr Ile Val Thr Val Val
195 200 205

Leu Val Leu Gly Leu Phe Gly Trp Thr Asn Ile Ala Arg Ile Thr Arg
210 215 220

Gly Ala Val Met Thr Ala Lys Asn Glu Glu Tyr Val Thr Ser Ala Arg
225 230 235 240

Ala Leu Gly Ala Ser Lys Ala Lys Ile Leu Leu Ser His Ile Met Pro
245 250 255

Asn Ala Ala Ala Pro Ile Ile Val Tyr Ala Thr Val Ala Leu Gly Thr
260 265 270

Phe Ile Val Ala Glu Ala Thr Leu Ser Phe Leu Gly Ile Gly Leu Pro
275 280 285

Pro Ser Ile Val Ser Trp Gly Ala Asp Ile Ala Lys Ala Gln Thr Ser
290 295 300

Leu Arg Thr Gln Pro Met Val Leu Phe Tyr Pro Ala Met Ala Leu Ala
305 310 315 320

Leu Thr Val Leu Ser Phe Ile Met Met Gly Asp Val Val Arg Asp Ala
325 330 335

Leu Asp Pro Lys Ser Arg Lys Arg
340

<210> 289

<211> 1632

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1609)

<223> RXA02035

<400> 289

ggattttcca ttggcggagg ttcatgcggc gggtatccat tgccttccat tttagttttc 60

catttagttt cccgatcac accgactaat ctcaagaagcc atg aag atc acg cgc 115
Met Lys Ile Thr Arg
1 5

gga ctc ctg cca tca ttg ctg ttg gca agc aca atc gtg gtg tcg tca 163
Gly Leu Leu Pro Ser Leu Leu Leu Ala Ser Thr Ile Val Val Ser Ser
10 15 20

tgc tct gct gga tcg act gcg tat cag cag ccc cct gct gtt gat caa	211
Cys Ser Ala Gly Ser Thr Ala Tyr Gln Gln Pro Pro Ala Val Asp Gln	
25 30 35	
tca tcc att gtc att gct acc acg gct gct gcg gcg tca ctt gat ttc	259
Ser Ser Ile Val Ile Ala Thr Thr Ala Ala Ala Ala Ser Leu Asp Phe	
40 45 50	
acc aat gct gcg ggc gct gct att ccg cag gcg atg atg tcc aat att	307
Thr Asn Ala Ala Gly Ala Ala Ile Pro Gln Ala Met Met Ser Asn Ile	
55 60 65	
tac gag ggg ctt gtg cgc atc gat gcg gag ggt gag att cag ccg ctg	355
Tyr Glu Gly Leu Val Arg Ile Asp Ala Glu Gly Glu Ile Gln Pro Leu	
70 75 80 85	
ctt gcc acg tcg tgg gat att tca gac gat cgc acc gag tac att ttc	403
Leu Ala Thr Ser Trp Asp Ile Ser Asp Asp Arg Thr Glu Tyr Ile Phe	
90 95 100	
cat ttg cgg gag ggt gtg ctg ttt tcc aac ggc gat ccc ttc aat gct	451
His Leu Arg Glu Gly Val Leu Phe Ser Asn Gly Asp Pro Phe Asn Ala	
105 110 115	
gat tct gcg aag ttt tcc att gat cgg gta aaa act gac tgg acc aat	499
Asp Ser Ala Lys Phe Ser Ile Asp Arg Val Lys Thr Asp Trp Thr Asn	
120 125 130	
ggt ttg aaa agt ggc atg gat gtg gtg gag tcc acc gag gtg att gac	547
Gly Leu Lys Ser Gly Met Asp Val Val Glu Ser Thr Glu Val Ile Asp	
135 140 145	
gat cac acg ctg aaa gtt tcg ctg gtc agg ccg tcc aac caa tgg ttg	595
Asp His Thr Leu Lys Val Ser Leu Val Arg Pro Ser Asn Gln Trp Leu	
150 155 160 165	
tgg agc atg ggt acc gcg atc ggt gcc atg atg acg gag ggg ggc gtc	643
Trp Ser Met Gly Thr Ala Ile Gly Ala Met Met Thr Glu Gly Gly Val	
170 175 180	
gat aag ctg gca act gat ccc gtt ggc acc ggc ccg tac acg gtg acg	691
Asp Lys Leu Ala Thr Asp Pro Val Gly Thr Gly Pro Tyr Thr Val Thr	
185 190 195	
cac tgg gcg ccg ggc cgc gca att ggg ttc ggc gcg ccg gcc gat tat	739
His Trp Ala Pro Gly Arg Ala Ile Gly Phe Gly Ala Arg Ala Asp Tyr	
200 205 210	
tgg ggg cag aag ccg ctt aac gac gcc gca acc atc cgc tac ttc agc	787
Trp Gly Gln Lys Pro Leu Asn Asp Ala Ala Thr Ile Arg Tyr Phe Ser	
215 220 225	
gat gcg acg gcc tcg acc aat gcg ctg caa agc ggt gac gtg gac gtg	835
Asp Ala Thr Ala Ser Thr Asn Ala Leu Gln Ser Gly Asp Val Asp Val	
230 235 240 245	
att tgg gcg atg caa gcg ccc gaa cag ctg gct acg ctg cag gaa tac	883
Ile Trp Ala Met Gln Ala Pro Glu Gln Leu Ala Thr Leu Gln Glu Tyr	
250 255 260	
acc gtg gaa gtg ggc aca acc aat ggt gag atg ttg ctg tcg atg aat	931

Thr	Val	Glu	Val	Gly	Thr	Thr	Asn	Gly	Glu	Met	Leu	Leu	Ser	Met	Asn	
			265					270					275			
aat	cag	cgt	gca	cct	ttt	gat	gat	gtg	cgt	gtg	cgc	cag	gcg	gtg	atg	979
Asn	Gln	Arg	Ala	Pro	Phe	Asp	Asp	Val	Arg	Val	Arg	Gln	Ala	Val	Met	
		280					285					290				
ttt	gcg	att	gat	cgc	caa	gcc	gtc	att	gat	acc	gcg	ttg	gaa	ggg	tac	1027
Phe	Ala	Ile	Asp	Arg	Gln	Ala	Val	Ile	Asp	Thr	Ala	Leu	Glu	Gly	Tyr	
	295					300					305					
ggc	acc	gac	act	ggg	ggc	gtg	cct	gtt	cgg	cgg	act	gat	cgg	tgg	tac	1075
Gly	Thr	Asp	Thr	Gly	Gly	Val	Pro	Val	Pro	Pro	Thr	Asp	Pro	Trp	Tyr	
310				315					320					325		
gag	aaa	tcc	acg	atg	tac	ccc	tac	gat	cgg	gac	cgc	gca	cgg	gca	ttg	1123
Glu	Lys	Ser	Thr	Met	Tyr	Pro	Tyr	Asp	Pro	Asp	Arg	Ala	Arg	Ala	Leu	
				330				335						340		
tta	gag	gag	gcc	ggc	gcc	gag	gga	acg	cgg	atc	acc	atg	tcc	att	cct	1171
Leu	Glu	Glu	Ala	Gly	Ala	Glu	Gly	Thr	Arg	Ile	Thr	Met	Ser	Ile	Pro	
			345					350					355			
tcg	ttg	cgg	tac	gct	cag	gca	gcc	tct	gaa	atc	ctg	tac	tcg	caa	ctg	1219
Ser	Leu	Pro	Tyr	Ala	Gln	Ala	Ala	Ser	Glu	Ile	Leu	Tyr	Ser	Gln	Leu	
		360				365						370				
cga	gat	gtt	ggg	ttt	gat	cct	gtg	att	gaa	tca	acc	gag	ttc	cca	gcc	1267
Arg	Asp	Val	Gly	Phe	Asp	Pro	Val	Ile	Glu	Ser	Thr	Glu	Phe	Pro	Ala	
	375					380					385					
gtc	tgg	ttg	gca	cag	gtc	atg	ggg	caa	aaa	gac	tac	gac	atg	tca	cta	1315
Val	Trp	Leu	Ala	Gln	Val	Met	Gly	Gln	Lys	Asp	Tyr	Asp	Met	Ser	Leu	
390				395					400						405	
atc	gcg	cat	gtg	gaa	ccc	cgc	gac	atc	ccc	acg	ctg	ttt	agc	ccc	aac	1363
Ile	Ala	His	Val	Glu	Pro	Arg	Asp	Ile	Pro	Thr	Leu	Phe	Ser	Pro	Asn	
			410					415					420			
tac	tat	ttg	ggc	ttt	gac	gac	acc	gaa	acc	caa	gcc	ctc	ctc	gca	gag	1411
Tyr	Tyr	Leu	Gly	Phe	Asp	Asp	Thr	Glu	Thr	Gln	Ala	Leu	Leu	Ala	Glu	
			425					430					435			
gca	gac	agt	tca	gca	aac	gaa	gtg	gaa	ttg	atg	caa	caa	gct	gtc	gat	1459
Ala	Asp	Ser	Ser	Ala	Asn	Glu	Val	Glu	Leu	Met	Gln	Gln	Ala	Val	Asp	
		440				445						450				
cga	atc	atg	gaa	caa	gcc	gtc	gcc	gac	aac	ctc	atg	aac	gtg	gcc	aac	1507
Arg	Ile	Met	Glu	Gln	Ala	Val	Ala	Asp	Asn	Leu	Met	Asn	Val	Ala	Asn	
	455					460					465					
atc	gtg	gtg	atg	tca	cca	gag	atc	acc	ggc	att	gat	ccc	aac			

<210> 290

<211> 503

<212> PRT

<213> Corynebacterium glutamicum

<400> 290

Met	Lys	Ile	Thr	Arg	Gly	Leu	Leu	Pro	Ser	Leu	Leu	Leu	Ala	Ser	Thr
1				5					10					15	

Ile	Val	Val	Ser	Ser	Cys	Ser	Ala	Gly	Ser	Thr	Ala	Tyr	Gln	Gln	Pro
			20					25					30		

Pro	Ala	Val	Asp	Gln	Ser	Ser	Ile	Val	Ile	Ala	Thr	Thr	Ala	Ala	Ala
		35					40					45			

Ala	Ser	Leu	Asp	Phe	Thr	Asn	Ala	Ala	Gly	Ala	Ala	Ile	Pro	Gln	Ala
50						55					60				

Met	Met	Ser	Asn	Ile	Tyr	Glu	Gly	Leu	Val	Arg	Ile	Asp	Ala	Glu	Gly
65					70					75				80	

Glu	Ile	Gln	Pro	Leu	Leu	Ala	Thr	Ser	Trp	Asp	Ile	Ser	Asp	Asp	Arg
				85					90					95	

Thr	Glu	Tyr	Ile	Phe	His	Leu	Arg	Glu	Gly	Val	Leu	Phe	Ser	Asn	Gly
			100					105						110	

Asp	Pro	Phe	Asn	Ala	Asp	Ser	Ala	Lys	Phe	Ser	Ile	Asp	Arg	Val	Lys
		115					120					125			

Thr	Asp	Trp	Thr	Asn	Gly	Leu	Lys	Ser	Gly	Met	Asp	Val	Val	Glu	Ser
130						135					140				

Thr	Glu	Val	Ile	Asp	Asp	His	Thr	Leu	Lys	Val	Ser	Leu	Val	Arg	Pro
145					150					155					160

Ser	Asn	Gln	Trp	Leu	Trp	Ser	Met	Gly	Thr	Ala	Ile	Gly	Ala	Met	Met
				165					170					175	

Thr	Glu	Gly	Gly	Val	Asp	Lys	Leu	Ala	Thr	Asp	Pro	Val	Gly	Thr	Gly
			180					185					190		

Pro	Tyr	Thr	Val	Thr	His	Trp	Ala	Pro	Gly	Arg	Ala	Ile	Gly	Phe	Gly
			195				200					205			

Ala	Arg	Ala	Asp	Tyr	Trp	Gly	Gln	Lys	Pro	Leu	Asn	Asp	Ala	Ala	Thr
		210				215					220				

Ile	Arg	Tyr	Phe	Ser	Asp	Ala	Thr	Ala	Ser	Thr	Asn	Ala	Leu	Gln	Ser
225					230					235					240

Gly	Asp	Val	Asp	Val	Ile	Trp	Ala	Met	Gln	Ala	Pro	Glu	Gln	Leu	Ala
				245					250					255	

Thr	Leu	Gln	Glu	Tyr	Thr	Val	Glu	Val	Gly	Thr	Thr	Asn	Gly	Glu	Met
			260					265					270		

Leu	Leu	Ser	Met	Asn	Asn	Gln	Arg	Ala	Pro	Phe	Asp	Asp	Val	Arg	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

275 280 285
 Arg Gln Ala Val Met Phe Ala Ile Asp Arg Gln Ala Val Ile Asp Thr
 290 295 300
 Ala Leu Glu Gly Tyr Gly Thr Asp Thr Gly Gly Val Pro Val Pro Pro
 305 310 315 320
 Thr Asp Pro Trp Tyr Glu Lys Ser Thr Met Tyr Pro Tyr Asp Pro Asp
 325 330 335
 Arg Ala Arg Ala Leu Leu Glu Glu Ala Gly Ala Glu Gly Thr Arg Ile
 340 345 350
 Thr Met Ser Ile Pro Ser Leu Pro Tyr Ala Gln Ala Ala Ser Glu Ile
 355 360 365
 Leu Tyr Ser Gln Leu Arg Asp Val Gly Phe Asp Pro Val Ile Glu Ser
 370 375 380
 Thr Glu Phe Pro Ala Val Trp Leu Ala Gln Val Met Gly Gln Lys Asp
 385 390 395 400
 Tyr Asp Met Ser Leu Ile Ala His Val Glu Pro Arg Asp Ile Pro Thr
 405 410 415
 Leu Phe Ser Pro Asn Tyr Tyr Leu Gly Phe Asp Asp Thr Glu Thr Gln
 420 425 430
 Ala Leu Leu Ala Glu Ala Asp Ser Ser Ala Asn Glu Val Glu Leu Met
 435 440 445
 Gln Gln Ala Val Asp Arg Ile Met Glu Gln Ala Val Ala Asp Asn Leu
 450 455 460
 Met Asn Val Ala Asn Ile Val Val Met Ser Pro Glu Ile Thr Gly Ile
 465 470 475 480
 Asp Pro Asn Val Val Ser Gly Ala Leu Glu Leu Ser Leu Ile Gly Arg
 485 490 495
 Lys Glu Ser Gly Val Ala Gln
 500

<210> 291
 <211> 927
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(904)
 <223> RXN01002

<400> 291
 gactgctgat accgcacagg atgaaatcac tcgttacggc gagatcctga agaagttctc 60

caactaattt ccoctgtttcc aataactcaag gtgtgcgcat atg aat tct gat gct 115
 Met Asn Ser Asp Ala

tcg gct acc acc aac tcc tgg gct atc aac ttc gac cat gtg tcg gtg	163
Ser Ala Thr Thr Asn Ser Trp Ala Ile Asn Phe Asp His Val Ser Val	
10 15 20	
acg tat ccc aat ggg acg aaa gcc ctc gat gat gtt tcc ctc acc atc	211
Thr Tyr Pro Asn Gly Thr Lys Ala Leu Asp Asp Val Ser Leu Thr Ile	
25 30 35	
aat ccc ggt gag atg gtt gcc atc gtg ggt ctg tca gga tcg ggt aaa	259
Asn Pro Gly Glu Met Val Ala Ile Val Gly Leu Ser Gly Ser Gly Lys	
40 45 50	
tcc acg ctg att cgc acg atc aac ggt ctt gtc cgc gct acg gaa ggc	307
Ser Thr Leu Ile Arg Thr Ile Asn Gly Leu Val Arg Ala Thr Glu Gly	
55 60 65	
acc gtg acg gtg ggg ccg cat cag atc aac acc ttg aag ggg aaa gca	355
Thr Val Thr Val Gly Pro His Gln Ile Asn Thr Leu Lys Gly Lys Ala	
70 75 80 85	
ctg cgt gat gcc cgt ggg cag atc ggc atg att ttc cag ggg ttc aac	403
Leu Arg Asp Ala Arg Gly Gln Ile Gly Met Ile Phe Gln Gly Phe Asn	
90 95 100	
ctg tcg gaa cgc agc agt gtg ttc cag aat gtt ttg gtg ggc cgc ttc	451
Leu Ser Glu Arg Ser Ser Val Phe Gln Asn Val Leu Val Gly Arg Phe	
105 110 115	
gcg cac aca gcg tgg tgg cgt aac ctc ctc ggg ttt ccc acg gag cac	499
Ala His Thr Ala Trp Trp Arg Asn Leu Leu Gly Phe Pro Thr Glu His	
120 125 130	
gac aag cag att gct ttt cac gcg ttg gag tcc gtg ggc att ttg cac	547
Asp Lys Gln Ile Ala Phe His Ala Leu Glu Ser Val Gly Ile Leu His	
135 140 145	
aaa gtg tgg acc cga gct ggt gct ttg tcg ggt gga cag aaa cag cgc	595
Lys Val Trp Thr Arg Ala Gly Ala Leu Ser Gly Gly Gln Lys Gln Arg	
150 155 160 165	
gtt gct att gcg cgc gcc tta tcg caa gat ccg tct gtc atg ctg gca	643
Val Ala Ile Ala Arg Ala Leu Ser Gln Asp Pro Ser Val Met Leu Ala	
170 175 180	
gat gag cct gtg gca agc ctt gat ccg cca acc gcg cat tcc gtg atg	691
Asp Glu Pro Val Ala Ser Leu Asp Pro Pro Thr Ala His Ser Val Met	
185 190 195	
cgc gat cta gaa aac atc aac aac gtg gaa ggc ctc acc gtg ttg gtg	739
Arg Asp Leu Glu Asn Ile Asn Asn Val Glu Gly Leu Thr Val Leu Val	
200 205 210	
aac ttg cac ttg att gat ttg gct cgt caa tac acc aca agg ctt gtg	787
Asn Leu His Leu Ile Asp Leu Ala Arg Gln Tyr Thr Thr Arg Leu Val	
215 220 225	
ggg ttg cgt gcc ggc aag ctg gtc tat gac ggt cct atc tct gag gcc	835
Gly Leu Arg Ala Gly Lys Leu Val Tyr Asp Gly Pro Ile Ser Glu Ala	
230 235 240 245	

acc gat aaa gac ttt gaa gct atc tat ggt cgc ccc atc cag gct aaa 883
 Thr Asp Lys Asp Phe Glu Ala Ile Tyr Gly Arg Pro Ile Gln Ala Lys
 250 255 260

gac ctg cta ggt gat cgc gca tgaccacgcc ttcttctaca ctt 927
 Asp Leu Leu Gly Asp Arg Ala
 265

<210> 292

<211> 268

<212> PRT

<213> Corynebacterium glutamicum

<400> 292

Met Asn Ser Asp Ala Ser Ala Thr Thr Asn Ser Trp Ala Ile Asn Phe
 1 5 10 15

Asp His Val Ser Val Thr Tyr Pro Asn Gly Thr Lys Ala Leu Asp Asp
 20 25 30

Val Ser Leu Thr Ile Asn Pro Gly Glu Met Val Ala Ile Val Gly Leu
 35 40 45

Ser Gly Ser Gly Lys Ser Thr Leu Ile Arg Thr Ile Asn Gly Leu Val
 50 55 60

Arg Ala Thr Glu Gly Thr Val Thr Val Gly Pro His Gln Ile Asn Thr
 65 70 75 80

Leu Lys Gly Lys Ala Leu Arg Asp Ala Arg Gly Gln Ile Gly Met Ile
 85 90 95

Phe Gln Gly Phe Asn Leu Ser Glu Arg Ser Ser Val Phe Gln Asn Val
 100 105 110

Leu Val Gly Arg Phe Ala His Thr Ala Trp Trp Arg Asn Leu Leu Gly
 115 120 125

Phe Pro Thr Glu His Asp Lys Gln Ile Ala Phe His Ala Leu Glu Ser
 130 135 140

Val Gly Ile Leu His Lys Val Trp Thr Arg Ala Gly Ala Leu Ser Gly
 145 150 155 160

Gly Gln Lys Gln Arg Val Ala Ile Ala Arg Ala Leu Ser Gln Asp Pro
 165 170 175

Ser Val Met Leu Ala Asp Glu Pro Val Ala Ser Leu Asp Pro Pro Thr
 180 185 190

Ala His Ser Val Met Arg Asp Leu Glu Asn Ile Asn Asn Val Glu Gly
 195 200 205

Leu Thr Val Leu Val Asn Leu His Leu Ile Asp Leu Ala Arg Gln Tyr
 210 215 220

Thr Thr Arg Leu Val Gly Leu Arg Ala Gly Lys Leu Val Tyr Asp Gly
 225 230 235 240

Pro Ile Ser Glu Ala Thr Asp Lys Asp Phe Glu Ala Ile Tyr Gly Arg

245 250 255

Pro Ile Gln Ala Lys Asp Leu Leu Gly Asp Arg Ala
260 265

<210> 293
<211> 440
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(417)
<223> FRXA01002

<400> 293

ccc acg gag cac gac aag cag att gct ttt cac gcg ttg gag tcc gtg 48
Pro Thr Glu His Asp Lys Gln Ile Ala Phe His Ala Leu Glu Ser Val
1 5 10 15

ggc att ttg gac aaa gtg tgg acc cga gct ggt gct ttg tcg ggt gga 96
Gly Ile Leu Asp Lys Val Trp Thr Arg Ala Gly Ala Leu Ser Gly Gly
20 25 30

cag aaa cag cgc gtt gct att gcg cgc gcc tta tcg caa gat ccg tct 144
Gln Lys Gln Arg Val Ala Ile Ala Arg Ala Leu Ser Gln Asp Pro Ser
35 40 45

gtc atg ctg gca gat gag cct gtg gca agc ctt gat ccg cca acc gcg 192
Val Met Leu Ala Asp Glu Pro Val Ala Ser Leu Asp Pro Pro Thr Ala
50 55 60

cat tcc gtg atg cgc gat cta gaa aac atc aac aac gtg gaa ggc ctc 240
His Ser Val Met Arg Asp Leu Glu Asn Ile Asn Asn Val Glu Gly Leu
65 70 75 80

acc gtg ttg gtg aac ttg cac ttg att gat ttg gct cgt caa tac acc 288
Thr Val Leu Val Asn Leu His Leu Ile Asp Leu Ala Arg Gln Tyr Thr
85 90 95

aca agg ctt gtg ggt ttg cgt gcc ggc aag ctg gtc tat gac ggt cct 336
Thr Arg Leu Val Gly Leu Arg Ala Gly Lys Leu Val Tyr Asp Gly Pro
100 105 110

atc tct gag gcc acc gat aaa gac ttt gaa gct atc tat ggt cgc ccc 384
Ile Ser Glu Ala Thr Asp Lys Asp Phe Glu Ala Ile Tyr Gly Arg Pro
115 120 125

atc cag gct aaa gac ctg cta ggt gat cgc gca tgaccacgcc ttctttctaca 437
Ile Gln Ala Lys Asp Leu Leu Gly Asp Arg Ala
130 135

ctt 440

<210> 294
<211> 139
<212> PRT
<213> Corynebacterium glutamicum

<400> 294

Pro Thr Glu His Asp Lys Gln Ile Ala Phe His Ala Leu Glu Ser Val
 1 5 10 15
 Gly Ile Leu Asp Lys Val Trp Thr Arg Ala Gly Ala Leu Ser Gly Gly
 20 25 30
 Gln Lys Gln Arg Val Ala Ile Ala Arg Ala Leu Ser Gln Asp Pro Ser
 35 40 45
 Val Met Leu Ala Asp Glu Pro Val Ala Ser Leu Asp Pro Pro Thr Ala
 50 55 60
 His Ser Val Met Arg Asp Leu Glu Asn Ile Asn Asn Val Glu Gly Leu
 65 70 75 80
 Thr Val Leu Val Asn Leu His Leu Ile Asp Leu Ala Arg Gln Tyr Thr
 85 90 95
 Thr Arg Leu Val Gly Leu Arg Ala Gly Lys Leu Val Tyr Asp Gly Pro
 100 105 110
 Ile Ser Glu Ala Thr Asp Lys Asp Phe Glu Ala Ile Tyr Gly Arg Pro
 115 120 125
 Ile Gln Ala Lys Asp Leu Leu Gly Asp Arg Ala
 130 135

<210> 295

<211> 969

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(946)

<223> RXN01000

<400> 295

ctttctatgc ctacgcggat gtttccgtga tcattctgga aatcctcacc gtggtgattg 60
 tcattgaagt aatctccaac gcacttcgaa agaggctggt atg agc acc tta acc 115
 Met Ser Thr Leu Thr
 1 5
 tct cac cgc aca gta ccg gcc ccc agc tct ccc ccg gcg cgc ccc aac 163
 Ser His Arg Thr Val Pro Ala Pro Ser Ser Pro Pro Ala Arg Pro Asn
 10 15 20
 aaa ctg gcg cgc aat atc gtt gca att gtc gct gcg ctg att gtc ctt 211
 Lys Leu Ala Arg Asn Ile Val Ala Ile Val Ala Ala Leu Ile Val Leu
 25 30 35
 ata gct acc gcc acg ctc aag atc gag tgg aat gag ctt ccg cag atg 259
 Ile Ala Thr Gly Thr Leu Lys Ile Glu Trp Asn Glu Leu Pro Gln Met
 40 45 50
 ccc gcg cag gtg tgg cat tac tta gag ctg atg ttt agc gat ccc gat 307
 Pro Ala Gln Val Trp His Tyr Leu Glu Leu Met Phe Ser Asp Pro Asp
 55 60 65

tgg tcg aag ttt ggc cgc gcc gtc cag gaa atg tgg cgt tcc atc gcc	355
Trp Ser Lys Phe Gly Arg Ala Val Gln Glu Met Trp Arg Ser Ile Ala	
70 75 80 85	
atg gcg tgg ttg ggt gcc att tta tgc gtg gtg gtc tct gtc cct ctg	403
Met Ala Trp Leu Gly Ala Ile Leu Cys Val Val Val Ser Val Pro Leu	
90 95 100	
gga atg ttg gct gcc cgc ggg gtg gga cct tat tgg ctg cgt acc gtt	451
Gly Met Leu Ala Ala Arg Gly Val Gly Pro Tyr Trp Leu Arg Thr Val	
105 110 115	
tta cgg ttc gtg ttc gcg gtg att cgt gcg ttc ccc gaa gtg gtt atc	499
Leu Arg Phe Val Phe Ala Val Ile Arg Ala Phe Pro Glu Val Val Ile	
120 125 130	
gca att att ttg cta act gtc acc ggc cta act cct ttt act ggt gcg	547
Ala Ile Ile Leu Leu Thr Val Thr Gly Leu Thr Pro Phe Thr Gly Ala	
135 140 145	
ctc gca ttg ggt atc tcc ggt att gga caa cag gca aag tgg acc tat	595
Leu Ala Leu Gly Ile Ser Gly Ile Gly Gln Gln Ala Lys Trp Thr Tyr	
150 155 160 165	
gaa gcc att gag tcc act ccc acc ggc ccg tca gag gca gtg cgt gca	643
Glu Ala Ile Glu Ser Thr Pro Thr Gly Pro Ser Glu Ala Val Arg Ala	
170 175 180	
gcg ggt gga act acg ccg gag gtt ctg ccg tgg gcg ttg tgg cca cag	691
Ala Gly Gly Thr Thr Pro Glu Val Leu Arg Trp Ala Leu Trp Pro Gln	
185 190 195	
gtt gcg cca tcc att gca tct ttt gcc ctg tac cgc ttt gag atc aac	739
Val Ala Pro Ser Ile Ala Ser Phe Ala Leu Tyr Arg Phe Glu Ile Asn	
200 205 210	
atc cgt acc tct gcg gta ttg ggc atc gtt ggt gca ggt ggt atc ggt	787
Ile Arg Thr Ser Ala Val Leu Gly Ile Val Gly Ala Gly Gly Ile Gly	
215 220 225	
agt atg ctt gcc aat tac acc aac tac agg cag tgg gac acc gtg ggc	835
Ser Met Leu Ala Asn Tyr Thr Asn Tyr Arg Gln Trp Asp Thr Val Gly	
230 235 240 245	
atg ctg ctc atc gtc gtg gtt gtc gca acg atg atc gtc gat ctc atc	883
Met Leu Leu Ile Val Val Val Val Ala Thr Met Ile Val Asp Leu Ile	
250 255 260	
tcc ggc acc atc cgc cgc cgc atc atg aag ggg gct agt gac cgt gtc	931
Ser Gly Thr Ile Arg Arg Arg Ile Met Lys Gly Ala Ser Asp Arg Val	
265 270 275	
gtg gca cca agc aac tgacgctcca ccaagcatcc gca	969
Val Ala Pro Ser Asn	
280	

<210> 296

<211> 282

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 296

Met Ser Thr Leu Thr Ser His Arg Thr Val Pro Ala Pro Ser Ser Pro
 1 5 10 15
 Pro Ala Arg Pro Asn Lys Leu Ala Arg Asn Ile Val Ala Ile Val Ala
 20 25 30
 Ala Leu Ile Val Leu Ile Ala Thr Gly Thr Leu Lys Ile Glu Trp Asn
 35 40 45
 Glu Leu Pro Gln Met Pro Ala Gln Val Trp His Tyr Leu Glu Leu Met
 50 55 60
 Phe Ser Asp Pro Asp Trp Ser Lys Phe Gly Arg Ala Val Gln Glu Met
 65 70 75 80
 Trp Arg Ser Ile Ala Met Ala Trp Leu Gly Ala Ile Leu Cys Val Val
 85 90 95
 Val Ser Val Pro Leu Gly Met Leu Ala Ala Arg Gly Val Gly Pro Tyr
 100 105 110
 Trp Leu Arg Thr Val Leu Arg Phe Val Phe Ala Val Ile Arg Ala Phe
 115 120 125
 Pro Glu Val Val Ile Ala Ile Ile Leu Leu Thr Val Thr Gly Leu Thr
 130 135 140
 Pro Phe Thr Gly Ala Leu Ala Leu Gly Ile Ser Gly Ile Gly Gln Gln
 145 150 155 160
 Ala Lys Trp Thr Tyr Glu Ala Ile Glu Ser Thr Pro Thr Gly Pro Ser
 165 170 175
 Glu Ala Val Arg Ala Ala Gly Gly Thr Thr Pro Glu Val Leu Arg Trp
 180 185 190
 Ala Leu Trp Pro Gln Val Ala Pro Ser Ile Ala Ser Phe Ala Leu Tyr
 195 200 205
 Arg Phe Glu Ile Asn Ile Arg Thr Ser Ala Val Leu Gly Ile Val Gly
 210 215 220
 Ala Gly Gly Ile Gly Ser Met Leu Ala Asn Tyr Thr Asn Tyr Arg Gln
 225 230 235 240
 Trp Asp Thr Val Gly Met Leu Leu Ile Val Val Val Val Ala Thr Met
 245 250 255
 Ile Val Asp Leu Ile Ser Gly Thr Ile Arg Arg Arg Ile Met Lys Gly
 260 265 270
 Ala Ser Asp Arg Val Val Ala Pro Ser Asn
 275 280

<210> 297

<211> 563

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(540)

<223> FRXA01000

<400> 297

atg ttg gct gcc cgc ggg gtg gga cct tat tgg ctg cgt acc gtt tta	48
Met Leu Ala Ala Arg Gly Val Gly Pro Tyr Trp Leu Arg Thr Val Leu	
1 5 10 15	
cgg ttc gtg ttc gcg gtg att cgt gcg ttc ccc gaa gtg gtt atc gca	96
Arg Phe Val Phe Ala Val Ile Arg Ala Phe Pro Glu Val Val Ile Ala	
20 25 30	
att att ttg cta act gtc acc ggc cta act cct ttt act ggt gcg ctc	144
Ile Ile Leu Leu Thr Val Thr Gly Leu Thr Pro Phe Thr Gly Ala Leu	
35 40 45	
gca ttg ggt atc tcc ggt att gga caa cag gca aag tgg acc tat gaa	192
Ala Leu Gly Ile Ser Gly Ile Gly Gln Gln Ala Lys Trp Thr Tyr Glu	
50 55 60	
gcc att gag tcc act ccc acc ggc ccg tca gag gca gtg cgt gca gcg	240
Ala Ile Glu Ser Thr Pro Thr Gly Pro Ser Glu Ala Val Arg Ala Ala	
65 70 75 80	
ggt gga act acg ccg gag gtt ctg cgg tgg gcg ttg tgg cca cag gtt	288
Gly Gly Thr Thr Pro Glu Val Leu Arg Trp Ala Leu Trp Pro Gln Val	
85 90 95	
gcg cca tcc att gca tct ttt gcc ctg tac cgc ttt gag atc aac atc	336
Ala Pro Ser Ile Ala Ser Phe Ala Leu Tyr Arg Phe Glu Ile Asn Ile	
100 105 110	
cgt acc tct gcg gta ttg ggc atc gtt ggt gca ggt ggt atc ggt agt	384
Arg Thr Ser Ala Val Leu Gly Ile Val Gly Ala Gly Gly Ile Gly Ser	
115 120 125	
atg ctt gcc aat tac acc aac tac agg cag tgg gac acc gtg ggc atg	432
Met Leu Ala Asn Tyr Thr Asn Tyr Arg Gln Trp Asp Thr Val Gly Met	
130 135 140	
ctg ctc atc gtc gtg gtt gtc gca acg atg atc gtc gat ctc atc tcc	480
Leu Leu Ile Val Val Val Val Ala Thr Met Ile Val Asp Leu Ile Ser	
145 150 155 160	
ggc acc atc cgc cgc cgc atc atg aag ggg gct agt gac cgt gtc gtg	528
Gly Thr Ile Arg Arg Arg Ile Met Lys Gly Ala Ser Asp Arg Val Val	
165 170 175	
gca cca agc aac tgacgctcca ccaagcatcc gca	563
Ala Pro Ser Asn	
180	

<210> 298

<211> 180

<212> PRT

<213> Corynebacterium glutamicum

<400> 298

Met Leu Ala Ala Arg Gly Val Gly Pro Tyr Trp Leu Arg Thr Val Leu
 1 5 10 15

Arg Phe Val Phe Ala Val Ile Arg Ala Phe Pro Glu Val Val Ile Ala
 20 25 30

Ile Ile Leu Leu Thr Val Thr Gly Leu Thr Pro Phe Thr Gly Ala Leu
 35 40 45

Ala Leu Gly Ile Ser Gly Ile Gly Gln Gln Ala Lys Trp Thr Tyr Glu
 50 55 60

Ala Ile Glu Ser Thr Pro Thr Gly Pro Ser Glu Ala Val Arg Ala Ala
 65 70 75 80

Gly Gly Thr Thr Pro Glu Val Leu Arg Trp Ala Leu Trp Pro Gln Val
 85 90 95

Ala Pro Ser Ile Ala Ser Phe Ala Leu Tyr Arg Phe Glu Ile Asn Ile
 100 105 110

Arg Thr Ser Ala Val Leu Gly Ile Val Gly Ala Gly Gly Ile Gly Ser
 115 120 125

Met Leu Ala Asn Tyr Thr Asn Tyr Arg Gln Trp Asp Thr Val Gly Met
 130 135 140

Leu Leu Ile Val Val Val Val Ala Thr Met Ile Val Asp Leu Ile Ser
 145 150 155 160

Gly Thr Ile Arg Arg Arg Ile Met Lys Gly Ala Ser Asp Arg Val Val
 165 170 175

Ala Pro Ser Asn
 180

<210> 299

<211> 927

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(904)

<223> RXA01003

<400> 299

agctggtcta tgacgggtcct atctctgagg ccaccgataa agactttgaa gctatctatg 60

gtcgccccat ccaggctaaa gacctgctag gtgatcgcg atg acc acg cct tct 115
 Met Thr Thr Pro Ser
 1 5

tct aca ctt atc cca caa aag cct cgg gct ggg gta aag acc tat ctc 163
 Ser Thr Leu Ile Pro Gln Lys Pro Arg Ala Gly Val Lys Thr Tyr Leu
 10 15 20

atc atc ggc gcc atc gtt gtc ttc acc gtg gca aca gca acc cca gcg 211

Ile Ile Gly Ala Ile Val Val Phe Thr Val Ala Thr Ala Thr Pro Ala	
25 30 35	
cta ggt ggc att gag ctt gat ttc gct tcc att gct gcg aat tgg cgc	259
Leu Gly Gly Ile Glu Leu Asp Phe Ala Ser Ile Ala Ala Asn Trp Arg	
40 45 50	
aat ggt gcc aac aaa ctc ctg caa atg ctg cag ccc aac ttt gcg ttc	307
Asn Gly Ala Asn Lys Leu Leu Gln Met Leu Gln Pro Asn Phe Ala Phe	
55 60 65	
ttg cct cgt acg tgg ctt ccc atg ttg gaa acc ctg cag atg gcg ctt	355
Leu Pro Arg Thr Trp Leu Pro Met Leu Glu Thr Leu Gln Met Ala Leu	
70 75 80 85	
gtt gga gct gtc ttg tct gct gcc gta tgc gtg cct ttg acg ttg tgg	403
Val Gly Ala Val Leu Ser Ala Ala Val Ser Val Pro Leu Thr Leu Trp	
90 95 100	
gca gcg cag gca acc aac acc agt gcg att ggt cgt ggc att gtc cgc	451
Ala Ala Gln Ala Thr Asn Thr Ser Ala Ile Gly Arg Gly Ile Val Arg	
105 110 115	
acc atc att aac gtg gtg cgc tct gtc ccc gac ttg gtg tat gcc acc	499
Thr Ile Ile Asn Val Val Arg Ser Val Pro Asp Leu Val Tyr Ala Thr	
120 125 130	
atc ttg gtc gcc atg gtt ggt gtc ggc gca tta cct ggc att ttg acg	547
Ile Leu Val Ala Met Val Gly Val Gly Ala Leu Pro Gly Ile Leu Thr	
135 140 145	
ctg ttt ctg ttc aac ctg ggc atc gtg gtc aag ctt gtc tct gag gcc	595
Leu Phe Leu Phe Asn Leu Gly Ile Val Val Lys Leu Val Ser Glu Ala	
150 155 160 165	
att gat tcc act gag cat ccc tat atg gaa gca gga cgc gca gca ggt	643
Ile Asp Ser Thr Glu His Pro Tyr Met Glu Ala Gly Arg Ala Ala Gly	
170 175 180	
gga tca cag ttc caa atc aac cga gtc tcc gcg ctt cct gaa gtc atg	691
Gly Ser Gln Phe Gln Ile Asn Arg Val Ser Ala Leu Pro Glu Val Met	
185 190 195	
ccg ctc ttt gcc aac caa tgg ctc tac acc cta gag ctg aat gta cgc	739
Pro Leu Phe Ala Asn Gln Trp Leu Tyr Thr Leu Glu Leu Asn Val Arg	
200 205 210	
atc tcc gcc atc ctt ggc atc gtg ggc gca ggt ggc atc ggc agg ctg	787
Ile Ser Ala Ile Leu Gly Ile Val Gly Ala Gly Gly Ile Gly Arg Leu	
215 220 225	
ctt gat gaa cgc cga gct ttc tat gcc tac gcg gat gtt tcc gtg atc	835
Leu Asp Glu Arg Arg Ala Phe Tyr Ala Tyr Ala Asp Val Ser Val Ile	
230 235 240 245	
att ctg gaa atc ctc atc gtg gtg att gtc att gaa gta atc tcc aac	883
Ile Leu Glu Ile Leu Ile Val Val Ile Val Ile Glu Val Ile Ser Asn	
250 255 260	
gca ctt cga aag agg ctg gta tgagcacctt aacctctcac cgc	927
Ala Leu Arg Lys Arg Leu Val	

265

<210> 300

<211> 268

<212> PRT

<213> Corynebacterium glutamicum

<400> 300

Met	Thr	Thr	Pro	Ser	Ser	Thr	Leu	Ile	Pro	Gln	Lys	Pro	Arg	Ala	Gly
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			20					25					30		

Thr	Ala	Thr	Pro	Ala	Leu	Gly	Gly	Ile	Glu	Leu	Asp	Phe	Ala	Ser	Ile
			35				40					45			

Ala	Ala	Asn	Trp	Arg	Asn	Gly	Ala	Asn	Lys	Leu	Leu	Gln	Met	Leu	Gln
	50					55					60				

Pro	Asn	Phe	Ala	Phe	Leu	Pro	Arg	Thr	Trp	Leu	Pro	Met	Leu	Glu	Thr
65					70					75				80	

Leu	Gln	Met	Ala	Leu	Val	Gly	Ala	Val	Leu	Ser	Ala	Ala	Val	Ser	Val
				85					90					95	

Pro	Leu	Thr	Leu	Trp	Ala	Ala	Gln	Ala	Thr	Asn	Thr	Ser	Ala	Ile	Gly
			100					105					110		

Arg	Gly	Ile	Val	Arg	Thr	Ile	Ile	Asn	Val	Val	Arg	Ser	Val	Pro	Asp
		115					120					125			

Leu	Val	Tyr	Ala	Thr	Ile	Leu	Val	Ala	Met	Val	Gly	Val	Gly	Ala	Leu
	130					135					140				

Pro	Gly	Ile	Leu	Thr	Leu	Phe	Leu	Phe	Asn	Leu	Gly	Ile	Val	Val	Lys
145					150					155					160

Leu	Val	Ser	Glu	Ala	Ile	Asp	Ser	Thr	Glu	His	Pro	Tyr	Met	Glu	Ala
				165					170					175	

Gly	Arg	Ala	Ala	Gly	Gly	Ser	Gln	Phe	Gln	Ile	Asn	Arg	Val	Ser	Ala
		180						185					190		

Leu	Pro	Glu	Val	Met	Pro	Leu	Phe	Ala	Asn	Gln	Trp	Leu	Tyr	Thr	Leu
		195					200					205			

Glu	Leu	Asn	Val	Arg	Ile	Ser	Ala	Ile	Leu	Gly	Ile	Val	Gly	Ala	Gly
	210					215					220				

Gly	Ile	Gly	Arg	Leu	Leu	Asp	Glu	Arg	Arg	Ala	Phe	Tyr	Ala	Tyr	Ala
225				230						235					240

Asp	Val	Ser	Val	Ile	Ile	Leu	Glu	Ile	Leu	Ile	Val	Val	Ile	Val	Ile
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Glu	Val	Ile	Ser	Asn	Ala	Leu	Arg	Lys	Arg	Leu	Val
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 <211> 594
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 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(594)
 <223> RXN00193

<220>
 <223> All occurrences of n = any nucleotide

<220>
 <223> All occurrences of Xaa = any amino acid

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 gtc ctc gtg gtc atc gtc tcc gtg atc aca gtc aac atc ttc gcc ttc 96
 Val Leu Val Val Ile Val Ser Val Ile Thr Val Asn Ile Phe Ala Phe
 20 25 30
 ctc ttg gcg tgg ttg ctg acc cgc aaa ctc cgc ggt acc aac ttt ttc 144
 Leu Leu Ala Trp Leu Leu Thr Arg Lys Leu Arg Gly Thr Asn Phe Phe
 35 40 45
 cgc aca gtc ttc ttt atg ccg aac ctt atc ggc ggc att gtg ctg ggt 192
 Arg Thr Val Phe Phe Met Pro Asn Leu Ile Gly Gly Ile Val Leu Gly
 50 55 60
 tat acc tgg cag acc atg atc aac gcc gtg ctt tcg cac tat gcc acg 240
 Tyr Thr Trp Gln Thr Met Ile Asn Ala Val Leu Ser His Tyr Ala Thr
 65 70 75 80
 act att agc gcg gac tgg aaa ttc ggc tac gcc ggc ctc atc atg cta 288
 Thr Ile Ser Ala Asp Trp Lys Phe Gly Tyr Ala Gly Leu Ile Met Leu
 85 90 95
 ctt aac tgg cag ctc atc ggc tac atg atg atc att tac atc gcc ggc 336
 Leu Asn Trp Gln Leu Ile Gly Tyr Met Met Ile Ile Tyr Ile Ala Gly
 100 105 110
 ctg caa aac gtc cca cca gag ctc att gag gct gcc gaa ctc gac ggc 384
 Leu Gln Asn Val Pro Pro Glu Leu Ile Glu Ala Ala Glu Leu Asp Gly
 115 120 125
 gtc aac aag tgg gag atg ctg cgg cac gtc act att ccg atg gtc atg 432
 Val Asn Lys Trp Glu Met Leu Arg His Val Thr Ile Pro Met Val Met
 130 135 140
 cca tcc atc acc atc tgc ctc ttt ttg act ttg tcg aac tcc ttt aag 480
 Pro Ser Ile Thr Ile Cys Leu Phe Leu Thr Leu Ser Asn Ser Phe Lys
 145 150 155 160
 ctc ttc gac cag aac ctg gcg ctg acc aac ggc gct cct ggc ggg caa 528
 Leu Phe Asp Gln Asn Leu Ala Leu Thr Asn Gly Ala Pro Gly Gly Gln
 165 170 175

act gag atg gtg gcg ctc aac atc atc aac acg ctg ttt aac cgt atg 576
 Thr Glu Met Val Ala Leu Asn Ile Ile Asn Thr Leu Phe Asn Arg Met
 180 185 190

aat gtc gag ggc gtc ggt 594
 Asn Val Glu Gly Val Gly
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<210> 302

<211> 198

<212> PRT

<213> Corynebacterium glutamicum

<220>

<223> All occurrences of Xaa = any amino acid

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Val Leu Val Val Ile Val Ser Val Ile Thr Val Asn Ile Phe Ala Phe
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Leu Leu Ala Trp Leu Leu Thr Arg Lys Leu Arg Gly Thr Asn Phe Phe
 35 40 45

Arg Thr Val Phe Phe Met Pro Asn Leu Ile Gly Gly Ile Val Leu Gly
 50 55 60

Tyr Thr Trp Gln Thr Met Ile Asn Ala Val Leu Ser His Tyr Ala Thr
 65 70 75 80

Thr Ile Ser Ala Asp Trp Lys Phe Gly Tyr Ala Gly Leu Ile Met Leu
 85 90 95

Leu Asn Trp Gln Leu Ile Gly Tyr Met Met Ile Ile Tyr Ile Ala Gly
 100 105 110

Leu Gln Asn Val Pro Pro Glu Leu Ile Glu Ala Ala Glu Leu Asp Gly
 115 120 125

Val Asn Lys Trp Glu Met Leu Arg His Val Thr Ile Pro Met Val Met
 130 135 140

Pro Ser Ile Thr Ile Cys Leu Phe Leu Thr Leu Ser Asn Ser Phe Lys
 145 150 155 160

Leu Phe Asp Gln Asn Leu Ala Leu Thr Asn Gly Ala Pro Gly Gly Gln
 165 170 175

Thr Glu Met Val Ala Leu Asn Ile Ile Asn Thr Leu Phe Asn Arg Met
 180 185 190

Asn Val Glu Gly Val Gly
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<210> 303

<211> 940

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (75)..(917)

<223> FRXA00193

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			Met	Gln	Ala	Thr	Leu	Lys	Lys	Tyr	Phe	Pro	Val	Phe	
			1				5					10			

gtc	ttg	ccc	acc	ctt	ctg	gca	ttc	atg	att	gcc	ttc	ttg	gtg	cgg	ttc	158
Val	Leu	Pro	Thr	Leu	Leu	Ala	Phe	Met	Ile	Ala	Phe	Leu	Val	Pro	Phe	
		15				20						25				

atc	gtg	ggt	ttc	ttc	ctc	tcc	ttt	acg	aag	ttc	acc	act	atc	acc	aac	206
Ile	Val	Gly	Phe	Phe	Leu	Ser	Phe	Thr	Lys	Phe	Thr	Thr	Ile	Thr	Asn	
	30					35					40					

gcc	aag	tgg	ggt	ggc	ata	gac	aac	tac	gtc	aaa	gct	ttc	tcc	caa	cgc	254
Ala	Lys	Trp	Val	Gly	Ile	Asp	Asn	Tyr	Val	Lys	Ala	Phe	Ser	Gln	Arg	
	45				50					55					60	

gaa	ggt	ttc	atc	tca	gcc	ttc	ggt	ttc	acc	gtc	ctc	gtg	gtc	atc	gtc	302
Glu	Gly	Phe	Ile	Ser	Ala	Phe	Gly	Phe	Thr	Val	Leu	Val	Val	Ile	Val	
				65					70					75		

tcc	gtg	atc	aca	gtc	aac	atc	ttc	gcc	ttc	ctc	ttg	gcg	tgg	ttg	ctg	350
Ser	Val	Ile	Thr	Val	Asn	Ile	Phe	Ala	Phe	Leu	Leu	Ala	Trp	Leu	Leu	
			80					85					90			

acc	cgc	aaa	ctc	cgc	ggt	acc	aac	ttt	ttc	cgc	aca	gtc	ttc	ttt	atg	398
Thr	Arg	Lys	Leu	Arg	Gly	Thr	Asn	Phe	Phe	Arg	Thr	Val	Phe	Phe	Met	
		95					100					105				

cgg	aac	ctt	atc	ggc	ggc	att	gtg	ctg	ggt	tat	acc	tgg	cag	acc	atg	446
Pro	Asn	Leu	Ile	Gly	Gly	Ile	Val	Leu	Gly	Tyr	Thr	Trp	Gln	Thr	Met	
	110					115					120					

atc	aac	gcc	gtg	ctt	tgg	cac	tat	gcc	acg	act	att	agc	gcg	gac	tgg	494
Ile	Asn	Ala	Val	Leu	Ser	His	Tyr	Ala	Thr	Thr	Ile	Ser	Ala	Asp	Trp	
	125				130					135					140	

aaa	ttc	ggc	tac	gcc	ggc	ctc	atc	atg	cta	ctt	aac	tgg	cag	ctc	atc	542
Lys	Phe	Gly	Tyr	Ala	Gly	Leu	Ile	Met	Leu	Leu	Asn	Trp	Gln	Leu	Ile	
				145					150					155		

ggc	tac	atg	atg	atc	att	tac	atc	gcc	ggc	ctg	caa	aac	gtc	cca	cca	590
Gly	Tyr	Met	Met	Ile	Ile	Tyr	Ile	Ala	Gly	Leu	Gln	Asn	Val	Pro	Pro	
			160					165					170			

gag	ctc	att	gag	gct	gcc	gaa	ctc	gac	ggc	gtc	aac	aag	tgg	gag	atg	638
Glu	Leu	Ile	Glu	Ala	Ala	Glu	Leu	Asp	Gly	Val	Asn	Lys	Trp	Glu	Met	
		175					180					185				

ctg	cgg	cac	gtc	act	att	cgg	atg	gtc	atg	cca	tcc	atc	acc	atc	tgc	686
Leu	Arg	His	Val	Thr	Ile	Pro	Met	Val	Met	Pro	Ser	Ile	Thr	Ile	Cys	
	190						195				200					

ctg ttt ttg act ttg tgc aac tcc ttt aag ctg ttc gac cag aac ctg 734
 Leu Phe Leu Thr Leu Ser Asn Ser Phe Lys Leu Phe Asp Gln Asn Leu
 205 210 215 220

 gcg ctg acc aac ggc gct cct ggc ggg caa act gag atg gtg gcg ctg 782
 Ala Leu Thr Asn Gly Ala Pro Gly Gly Gln Thr Glu Met Val Ala Leu
 225 230 235

 aac atc atc aac acg ctg ttt aac cgt atg aat gtc gag ggc gtc ggt 830
 Asn Ile Ile Asn Thr Leu Phe Asn Arg Met Asn Val Glu Gly Val Gly
 240 245 250

 cag gcc aag gcc gtt atc ttc gtc gtc gtt gtg gtc gtc atc gcg tac 878
 Gln Ala Lys Ala Val Ile Phe Val Val Val Val Val Val Ile Ala Tyr
 255 260 265

 ttc cag ctg cgc gcg acc cgc tcc aag gaa atc gag gct taagttatga 927
 Phe Gln Leu Arg Ala Thr Arg Ser Lys Glu Ile Glu Ala
 270 275 280

 ctaccagcac ttc 940

<210> 304

<211> 281

<212> PRT

<213> *Corynebacterium glutamicum*

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 Phe Leu Ser Phe Thr Lys Phe Thr Thr Ile Thr Asn Ala Lys Trp Val
 35 40 45

 Gly Ile Asp Asn Tyr Val Lys Ala Phe Ser Gln Arg Glu Gly Phe Ile
 50 55 60

 Ser Ala Phe Gly Phe Thr Val Leu Val Val Ile Val Ser Val Ile Thr
 65 70 75 80

 Val Asn Ile Phe Ala Phe Leu Leu Ala Trp Leu Leu Thr Arg Lys Leu
 85 90 95

 Arg Gly Thr Asn Phe Phe Arg Thr Val Phe Phe Met Pro Asn Leu Ile
 100 105 110

 Gly Gly Ile Val Leu Gly Tyr Thr Trp Gln Thr Met Ile Asn Ala Val
 115 120 125

 Leu Ser His Tyr Ala Thr Thr Ile Ser Ala Asp Trp Lys Phe Gly Tyr
 130 135 140

 Ala Gly Leu Ile Met Leu Leu Asn Trp Gln Leu Ile Gly Tyr Met Met
 145 150 155 160

 Ile Ile Tyr Ile Ala Gly Leu Gln Asn Val Pro Pro Glu Leu Ile Glu

165										170					175				
Ala	Ala	Glu	Leu	Asp	Gly	Val	Asn	Lys	Trp	Glu	Met	Leu	Arg	His	Val				
		180						185					190						
Thr	Ile	Pro	Met	Val	Met	Pro	Ser	Ile	Thr	Ile	Cys	Leu	Phe	Leu	Thr				
		195					200					205							
Leu	Ser	Asn	Ser	Phe	Lys	Leu	Phe	Asp	Gln	Asn	Leu	Ala	Leu	Thr	Asn				
	210					215					220								
Gly	Ala	Pro	Gly	Gly	Gln	Thr	Glu	Met	Val	Ala	Leu	Asn	Ile	Ile	Asn				
225					230					235					240				
Thr	Leu	Phe	Asn	Arg	Met	Asn	Val	Glu	Gly	Val	Gly	Gln	Ala	Lys	Ala				
			245						250					255					
Val	Ile	Phe	Val	Val	Val	Val	Val	Val	Ile	Ala	Tyr	Phe	Gln	Leu	Arg				
		260						265					270						
Ala	Thr	Arg	Ser	Lys	Glu	Ile	Glu	Ala											
	275						280												

<210> 305

<211> 1053

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1030)

<223> RXN01298

<400> 305

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				Val	Ser	Thr	Leu	Ile		
				1				5		

tct	gaa	ccc	gag	gtg	gat	aag	cta	cgt	aaa	cgt	gcc	aag	aga	tca	agg		163
Ser	Glu	Pro	Glu	Val	Asp	Lys	Leu	Arg	Lys	Arg	Ala	Lys	Arg	Ser	Arg		
			10					15					20				

cgg	aca	gaa	tgg	tgg	ctt	gcc	gcc	gca	ctt	ctt	gcc	cca	aac	ttg	ctt		211
Arg	Thr	Glu	Trp	Trp	Leu	Ala	Ala	Ala	Leu	Leu	Ala	Pro	Asn	Leu	Leu		
		25				30						35					

ctc	ttg	gcc	atc	ttt	acg	tat	cgg	cca	ctg	tta	gat	aac	ttc	cgg	ttg		259
Leu	Leu	Ala	Ile	Phe	Thr	Tyr	Arg	Pro	Leu	Leu	Asp	Asn	Phe	Arg	Leu		
		40				45					50						

tcc	ttt	ttc	aac	tgg	aac	att	tcc	tcg	ccc	aca	tca	acc	ttc	att	ggg		307
Ser	Phe	Phe	Asn	Trp	Asn	Ile	Ser	Ser	Pro	Thr	Ser	Thr	Phe	Ile	Gly		
	55				60					65							

ttt	gat	aac	tac	gtt	gag	ttc	ttc	act	cgt	agt	gac	act	ctc	caa	gtt		355
Phe	Asp	Asn	Tyr	Val	Glu	Phe	Phe	Thr	Arg	Ser	Asp	Thr	Leu	Gln	Val		
	70				75				80						85		

gtt tta aac acc gtc atc ttc acg gca tgt gct gtg atc gga tcg atg	403
Val Leu Asn Thr Val Ile Phe Thr Ala Cys Ala Val Ile Gly Ser Met	
90 95 100	
gtg ctc ggt ttg ctc ctg gcc atg ttg ttg gat cag aag ctt ttc ggc	451
Val Leu Gly Leu Leu Leu Ala Met Leu Leu Asp Gln Lys Leu Phe Gly	
105 110 115	
cgt aac ttt gtg cgt tcc atg gtg ttt gcc ccg ttt gtg att tcc ggt	499
Arg Asn Phe Val Arg Ser Met Val Phe Ala Pro Phe Val Ile Ser Gly	
120 125 130	
gct gcc att ggt gtt gct ttc cag ttc gtt ttt gac cct aat ttt ggt	547
Ala Ala Ile Gly Val Ala Phe Gln Phe Val Phe Asp Pro Asn Phe Gly	
135 140 145	
ttg gtt cag gac ttg ctg gga cgc atc ggc gtt gat tcg cca cag ttc	595
Leu Val Gln Asp Leu Leu Gly Arg Ile Gly Val Asp Ser Pro Gln Phe	
150 155 160 165	
tac caa aac cct aac tgg gca ttg ttc atg gtg acg ttc act ttc gtg	643
Tyr Gln Asn Pro Asn Trp Ala Leu Phe Met Val Thr Phe Thr Phe Val	
170 175 180	
tgg aag aac ttg ggc tac tcc ttt gtt atc tac ctg gct gca ttg cag	691
Trp Lys Asn Leu Gly Tyr Ser Phe Val Ile Tyr Leu Ala Ala Leu Gln	
185 190 195	
ggg cta aac aag gat ttg tct gag gcc gca ccg gtg gat ggc gcg agc	739
Gly Leu Asn Lys Asp Leu Ser Glu Ala Ala Pro Val Asp Gly Ala Ser	
200 205 210	
gcg tgg aca cgt ttt tgg aag gtt act ctt ccg cag ctt cgc cca acc	787
Ala Trp Thr Arg Phe Trp Lys Val Thr Leu Pro Gln Leu Arg Pro Thr	
215 220 225	
acg ttc ttc ctt tct att act gtc acg ctg aac tcg gtt cag gtc ttc	835
Thr Phe Phe Leu Ser Ile Thr Val Thr Leu Asn Ser Val Gln Val Phe	
230 235 240 245	
gac atc att cac acc atg act cgt ggt ggc ccc ttg ggt aac ggt acg	883
Asp Ile Ile His Thr Met Thr Arg Gly Gly Pro Leu Gly Asn Gly Thr	
250 255 260	
acc acc ttg gtt tac cag gtg tac acc gag act ttc acc aac tat cgc	931
Thr Thr Leu Val Tyr Gln Val Tyr Thr Glu Thr Phe Thr Asn Tyr Arg	
265 270 275	
gcg gga tat ggt gca aca atc gca acg att ttg ttc ctg ttg ctg ctg	979
Ala Gly Tyr Gly Ala Thr Ile Ala Thr Ile Leu Phe Leu Leu Leu Leu	
280 285 290	
att atc act gtt atc cag gtt cga tac atg gat aag gag aac aag cag	1027
Ile Ile Thr Val Ile Gln Val Arg Tyr Met Asp Lys Glu Asn Lys Gln	
295 300 305	
aaa tgatctcgac tgatagaaac gtt	1053
Lys	
310	

<210> 306

<211> 310

<212> PRT

<213> Corynebacterium glutamicum

<400> 306

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			20					25					30		
Ala	Pro	Asn	Leu	Leu	Leu	Leu	Ala	Ile	Phe	Thr	Tyr	Arg	Pro	Leu	Leu
		35					40					45			
Asp	Asn	Phe	Arg	Leu	Ser	Phe	Phe	Asn	Trp	Asn	Ile	Ser	Ser	Pro	Thr
	50					55					60				
Ser	Thr	Phe	Ile	Gly	Phe	Asp	Asn	Tyr	Val	Glu	Phe	Phe	Thr	Arg	Ser
65					70					75					80
Asp	Thr	Leu	Gln	Val	Val	Leu	Asn	Thr	Val	Ile	Phe	Thr	Ala	Cys	Ala
				85					90					95	
Val	Ile	Gly	Ser	Met	Val	Leu	Gly	Leu	Leu	Leu	Ala	Met	Leu	Leu	Asp
			100					105					110		
Gln	Lys	Leu	Phe	Gly	Arg	Asn	Phe	Val	Arg	Ser	Met	Val	Phe	Ala	Pro
		115					120					125			
Phe	Val	Ile	Ser	Gly	Ala	Ala	Ile	Gly	Val	Ala	Phe	Gln	Phe	Val	Phe
	130					135					140				
Asp	Pro	Asn	Phe	Gly	Leu	Val	Gln	Asp	Leu	Leu	Gly	Arg	Ile	Gly	Val
145					150					155					160
Asp	Ser	Pro	Gln	Phe	Tyr	Gln	Asn	Pro	Asn	Trp	Ala	Leu	Phe	Met	Val
				165					170					175	
Thr	Phe	Thr	Phe	Val	Trp	Lys	Asn	Leu	Gly	Tyr	Ser	Phe	Val	Ile	Tyr
			180					185					190		
Leu	Ala	Ala	Leu	Gln	Gly	Leu	Asn	Lys	Asp	Leu	Ser	Glu	Ala	Ala	Pro
		195					200					205			
Val	Asp	Gly	Ala	Ser	Ala	Trp	Thr	Arg	Phe	Trp	Lys	Val	Thr	Leu	Pro
	210					215					220				
Gln	Leu	Arg	Pro	Thr	Thr	Phe	Phe	Leu	Ser	Ile	Thr	Val	Thr	Leu	Asn
225					230					235					240
Ser	Val	Gln	Val	Phe	Asp	Ile	Ile	His	Thr	Met	Thr	Arg	Gly	Gly	Pro
				245					250					255	
Leu	Gly	Asn	Gly	Thr	Thr	Thr	Leu	Val	Tyr	Gln	Val	Tyr	Thr	Glu	Thr
			260					265					270		
Phe	Thr	Asn	Tyr	Arg	Ala	Gly	Tyr	Gly	Ala	Thr	Ile	Ala	Thr	Ile	Leu
		275					280					285			
Phe	Leu	Leu	Leu	Leu	Ile	Ile	Thr	Val	Ile	Gln	Val	Arg	Tyr	Met	Asp

290

295

300

Lys Glu Asn Lys Gln Lys
305 310

<210> 307

<211> 416

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(393)

<223> FRXA01298

<400> 307

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ttg cag ggg cta aac aag gat ttg tct gag gcc gca ccg gtg gat ggc 96
Leu Gln Gly Leu Asn Lys Asp Leu Ser Glu Ala Ala Pro Val Asp Gly
20 25 30

gcg agc gcg tgg aca cgt ttt tgg aag gtt act ctt ccg cag ctt cgc 144
Ala Ser Ala Trp Thr Arg Phe Trp Lys Val Thr Leu Pro Gln Leu Arg
35 40 45

cca acc acg ttc ttc ctt tct att act gtc acg ctg aac tcg gtt cag 192
Pro Thr Thr Phe Phe Leu Ser Ile Thr Val Thr Leu Asn Ser Val Gln
50 55 60

gtc ttc gac atc att cac acc atg act cgt ggt ggc ccc ttg ggt aac 240
Val Phe Asp Ile Ile His Thr Met Thr Arg Gly Gly Pro Leu Gly Asn
65 70 75 80

ggt acg acc acc ttg gtt tac cag gtg tac acc gag act ttc acc aac 288
Gly Thr Thr Thr Leu Val Tyr Gln Val Tyr Thr Glu Thr Phe Thr Asn
85 90 95

tat cgc gcg gga tat ggt gca aca atc gca acg att ttg ttc ctg ttg 336
Tyr Arg Ala Gly Tyr Gly Ala Thr Ile Ala Thr Ile Leu Phe Leu Leu
100 105 110

ctg ctg att atc act gtt atc cag gtt cga tac atg gat aag gag aac 384
Leu Leu Ile Ile Thr Val Ile Gln Val Arg Tyr Met Asp Lys Glu Asn
115 120 125

aag cag aaa tgatctcgac tgatagaaac gtt 416
Lys Gln Lys
130

<210> 308

<211> 131

<212> PRT

<213> Corynebacterium glutamicum

<400> 308

Phe Val Trp Lys Asn Leu Gly Tyr Ser Phe Val Ile Tyr Leu Ala Ala

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Leu Gln Gly	Leu Asn Lys Asp	Leu Ser Glu Ala Ala	Pro Val Asp Gly
	20	25	30
Ala Ser Ala	Trp Thr Arg Phe	Trp Lys Val Thr	Leu Pro Gln Leu Arg
	35	40	45
Pro Thr Thr	Phe Phe Leu Ser	Ile Thr Val Thr	Leu Asn Ser Val Gln
	50	55	60
Val Phe Asp	Ile Ile His Thr	Met Thr Arg Gly	Gly Pro Leu Gly Asn
	65	70	75
Gly Thr Thr	Thr Leu Val Tyr	Gln Val Tyr Thr	Glu Thr Phe Thr Asn
	85	90	95
Tyr Arg Ala	Gly Tyr Gly Ala	Thr Ile Ala Thr	Ile Leu Phe Leu Leu
	100	105	110
Leu Leu Ile	Ile Thr Val Ile	Gln Val Arg Tyr	Met Asp Lys Glu Asn
	115	120	125
Lys Gln Lys			
	130		

<210> 309

<211> 535

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(535)

<223> FRXA02422

<400> 309

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aacactaatc	ggacatttag	gtcacataac	atttcgctc	gtg tcc aca tta att	115
				Val Ser Thr Leu Ile	
				1 5	

tct gaa ccc	gag gtg gat aag	cta cgt aaa cgt	gcc aag aga tca agg	163
Ser Glu Pro	Glu Val Asp Lys	Leu Arg Lys Arg	Ala Lys Arg Ser Arg	
	10	15	20	

cgg aca gaa	tgg tgg ctt gcc	gcc gca ctt ctt	gcc cca aac ttg ctt	211
Arg Thr Glu	Trp Trp Leu Ala	Ala Ala Leu Leu	Ala Pro Asn Leu Leu	
	25	30	35	

ctc ttg gcc	atc ttt acg tat	cgg cca ctg tta	gat aac ttc cgg ttg	259
Leu Leu Ala	Ile Phe Thr Tyr	Arg Pro Leu Leu	Asp Asn Phe Arg Leu	
	40	45	50	

tcc ttt ttc	aac tgg aac att	tcc tcg ccc aca	tca acc ttc att ggg	307
Ser Phe Phe	Asn Trp Asn Ile	Ser Ser Pro Thr	Ser Thr Phe Ile Gly	
	55	60	65	

ttt gat aac	tac gtt gag ttc	ttc act cgt agt	gac act ctc caa gtt	355
-------------	-----------------	-----------------	---------------------	-----

Phe Asp Asn Tyr Val Glu Phe Phe Thr Arg Ser Asp Thr Leu Gln Val
 70 75 80 85
 gtt tta aac acc gtc atc ttc acg gca tgt gct gtg atc gga tcg atg 403
 Val Leu Asn Thr Val Ile Phe Thr Ala Cys Ala Val Ile Gly Ser Met
 90 95 100
 gtg ctc ggt ttg ctc ctg gcc atg ttg ttg gat cag aag ctt ttc ggc 451
 Val Leu Gly Leu Leu Leu Ala Met Leu Leu Asp Gln Lys Leu Phe Gly
 105 110 115
 cgt aac ttt gtg cgt tcc atg gtg ttt gcc ccg ttt gtg att tcc ggt 499
 Arg Asn Phe Val Arg Ser Met Val Phe Ala Pro Phe Val Ile Ser Gly
 120 125 130
 gct gcc att ggt ggt gct ttc cag ttc gtt ttt gac 535
 Ala Ala Ile Gly Gly Ala Phe Gln Phe Val Phe Asp
 135 140 145

<210> 310

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 310

Val Ser Thr Leu Ile Ser Glu Pro Glu Val Asp Lys Leu Arg Lys Arg
 1 5 10 15

Ala Lys Arg Ser Arg Arg Thr Glu Trp Trp Leu Ala Ala Ala Leu Leu
 20 25 30

Ala Pro Asn Leu Leu Leu Leu Ala Ile Phe Thr Tyr Arg Pro Leu Leu
 35 40 45

Asp Asn Phe Arg Leu Ser Phe Phe Asn Trp Asn Ile Ser Ser Pro Thr
 50 55 60

Ser Thr Phe Ile Gly Phe Asp Asn Tyr Val Glu Phe Phe Thr Arg Ser
 65 70 75 80

Asp Thr Leu Gln Val Val Leu Asn Thr Val Ile Phe Thr Ala Cys Ala
 85 90 95

Val Ile Gly Ser Met Val Leu Gly Leu Leu Leu Ala Met Leu Leu Asp
 100 105 110

Gln Lys Leu Phe Gly Arg Asn Phe Val Arg Ser Met Val Phe Ala Pro
 115 120 125

Phe Val Ile Ser Gly Ala Ala Ile Gly Gly Ala Phe Gln Phe Val Phe
 130 135 140

Asp
 145

<210> 311

<211> 879

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(856)

<223> RXN02515

<400> 311

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tcagttttaa attcgcttca accctgaaag attgtgacag atg agc act ctt gaa 115
                                     Met Ser Thr Leu Glu
                                     1 5

atc cgt aac ctg cac gca cag gtc ctg ccg tcc gat gag tcc gct gag 163
Ile Arg Asn Leu His Ala Gln Val Leu Pro Ser Asp Glu Ser Ala Glu
          10          15          20

cct aag gaa atc ctc aag ggc gtc aac ctc acc atc aac tct ggt gag 211
Pro Lys Glu Ile Leu Lys Gly Val Asn Leu Thr Ile Asn Ser Gly Glu
          25          30          35

atc cac gcc atc atg ggc cct aac ggt tcc ggc aag tcc act ctt gct 259
Ile His Ala Ile Met Gly Pro Asn Gly Ser Gly Lys Ser Thr Leu Ala
          40          45          50

tac acc ctt ggt gga cac cca cgc tac gag gta acc gca ggc gag gtc 307
Tyr Thr Leu Gly Gly His Pro Arg Tyr Glu Val Thr Ala Gly Glu Val
          55          60          65

ctc ctc gac ggc gag aac atc ctg gag atg gaa gtt gat gag cgt gca 355
Leu Leu Asp Gly Glu Asn Ile Leu Glu Met Glu Val Asp Glu Arg Ala
          70          75          80          85

cgc gct ggt ctc ttc ctg gcc atg cag tat cca act gaa atc cct ggc 403
Arg Ala Gly Leu Phe Leu Ala Met Gln Tyr Pro Thr Glu Ile Pro Gly
          90          95          100

gtt tcc gtt gct aac ttc ctg cgt tcc gca gcg acc gca atc cgc ggc 451
Val Ser Val Ala Asn Phe Leu Arg Ser Ala Ala Thr Ala Ile Arg Gly
          105          110          115

gag gct cct aag ctt cgc gag tgg gtt aag gaa gtc cgc acc gct cag 499
Glu Ala Pro Lys Leu Arg Glu Trp Val Lys Glu Val Arg Thr Ala Gln
          120          125          130

gaa gct ctg gca att gac cct gag ttc tcc aac cgc tca gtc aac gaa 547
Glu Ala Leu Ala Ile Asp Pro Glu Phe Ser Asn Arg Ser Val Asn Glu
          135          140          145

ggt ttc tcc ggt ggc gag aag aag cgc cac gag gtt ctg cag ctt gat 595
Gly Phe Ser Gly Gly Glu Lys Lys Arg His Glu Val Leu Gln Leu Asp
          150          155          160          165

ctg ctg aag cca aag ttc gcg atc atg gat gag acc gac tcc ggc ctt 643
Leu Leu Lys Pro Lys Phe Ala Ile Met Asp Glu Thr Asp Ser Gly Leu
          170          175          180

gac gtg gat gca ctg cgc att gtt tcc gag ggc atc aac tcc tac aag 691
Asp Val Asp Ala Leu Arg Ile Val Ser Glu Gly Ile Asn Ser Tyr Lys
          185          190          195

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cag gag acc gaa ggt ggc atc ttg atg atc acc cac tac aag cgc atc 739
 Gln Glu Thr Glu Gly Gly Ile Leu Met Ile Thr His Tyr Lys Arg Ile
 200 205 210

ctc aac tac gtt aag cct gac ttc att cac gtt ttc gcg aat ggc cag 787
 Leu Asn Tyr Val Lys Pro Asp Phe Ile His Val Phe Ala Asn Gly Gln
 215 220 225

att gtg acc acc ggt ggc gct gag ctt gct gac aag ctc gag gct gac 835
 Ile Val Thr Thr Gly Gly Ala Glu Leu Ala Asp Lys Leu Glu Ala Asp
 230 235 240 245

ggc tac gac cag ttc atc aag taacatgtcc gatttctca atg 879
 Gly Tyr Asp Gln Phe Ile Lys
 250

<210> 312

<211> 252

<212> PRT

<213> Corynebacterium glutamicum

<400> 312

Met Ser Thr Leu Glu Ile Arg Asn Leu His Ala Gln Val Leu Pro Ser
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Asp Glu Ser Ala Glu Pro Lys Glu Ile Leu Lys Gly Val Asn Leu Thr
 20 25 30

Ile Asn Ser Gly Glu Ile His Ala Ile Met Gly Pro Asn Gly Ser Gly
 35 40 45

Lys Ser Thr Leu Ala Tyr Thr Leu Gly Gly His Pro Arg Tyr Glu Val
 50 55 60

Thr Ala Gly Glu Val Leu Leu Asp Gly Glu Asn Ile Leu Glu Met Glu
 65 70 75 80

Val Asp Glu Arg Ala Arg Ala Gly Leu Phe Leu Ala Met Gln Tyr Pro
 85 90 95

Thr Glu Ile Pro Gly Val Ser Val Ala Asn Phe Leu Arg Ser Ala Ala
 100 105 110

Thr Ala Ile Arg Gly Glu Ala Pro Lys Leu Arg Glu Trp Val Lys Glu
 115 120 125

Val Arg Thr Ala Gln Glu Ala Leu Ala Ile Asp Pro Glu Phe Ser Asn
 130 135 140

Arg Ser Val Asn Glu Gly Phe Ser Gly Gly Glu Lys Lys Arg His Glu
 145 150 155 160

Val Leu Gln Leu Asp Leu Leu Lys Pro Lys Phe Ala Ile Met Asp Glu
 165 170 175

Thr Asp Ser Gly Leu Asp Val Asp Ala Leu Arg Ile Val Ser Glu Gly
 180 185 190

Ile Asn Ser Tyr Lys Gln Glu Thr Glu Gly Gly Ile Leu Met Ile Thr
 195 200 205

His Tyr Lys Arg Ile Leu Asn Tyr Val Lys Pro Asp Phe Ile His Val
210 215 220

Phe Ala Asn Gly Gln Ile Val Thr Thr Gly Gly Ala Glu Leu Ala Asp
225 230 235 240

Lys Leu Glu Ala Asp Gly Tyr Asp Gln Phe Ile Lys
245 250

<210> 313

<211> 879

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(856)

<223> FRXA02515

<400> 313

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tcagtttaaa attcgccttca accctgaaag attgtgacag atg agc act ctt gaa 115
Met Ser Thr Leu Glu
1 5

atc cgt aac ctg cac gca cag gtc ctg ccg tcc gat gag tcc gct gag 163
Ile Arg Asn Leu His Ala Gln Val Leu Pro Ser Asp Glu Ser Ala Glu
10 15 20

cct aag gaa atc ctc aag ggc gtc aac ctc acc atc aac tct ggt gag 211
Pro Lys Glu Ile Leu Lys Gly Val Asn Leu Thr Ile Asn Ser Gly Glu
25 30 35

atc cac gcc atc atg ggc cct aac ggt tcc ggc aag tcc act ctt gct 259
Ile His Ala Ile Met Gly Pro Asn Gly Ser Gly Lys Ser Thr Leu Ala
40 45 50

tac acc ctt ggt gga cac cca cgc tac gag gta acc gca ggc gag gtc 307
Tyr Thr Leu Gly Gly His Pro Arg Tyr Glu Val Thr Ala Gly Glu Val
55 60 65

ctc ctc gac ggc gag aac atc ctg gag atg gaa gtt gat gag cgt gca 355
Leu Leu Asp Gly Glu Asn Ile Leu Glu Met Glu Val Asp Glu Arg Ala
70 75 80 85

cgc gct ggt ctc ttc ctg gcc atg cag tat cca act gaa atc cct ggc 403
Arg Ala Gly Leu Phe Leu Ala Met Gln Tyr Pro Thr Glu Ile Pro Gly
90 95 100

gtt tcc gtt gct aac ttc ctg cgt tcc gca gcg acc gca atc cgc ggc 451
Val Ser Val Ala Asn Phe Leu Arg Ser Ala Ala Thr Ala Ile Arg Gly
105 110 115

gag gct cct aag ctt cgc gag tgg gtt aag gaa gtc cgc acc gct cag 499
Glu Ala Pro Lys Leu Arg Glu Trp Val Lys Glu Val Arg Thr Ala Gln
120 125 130

gaa gct ctg gca att gac cct gag ttc tcc aac cgc tca gtc aac gaa 547

Glu Ala Leu Ala Ile Asp Pro Glu Phe Ser Asn Arg Ser Val Asn Glu
 135 140 145
 ggt ttc tcc ggt ggc gag aag aag cgc cac gag gtt ctg cag ctt gat 595
 Gly Phe Ser Gly Gly Glu Lys Lys Arg His Glu Val Leu Gln Leu Asp
 150 155 160 165
 ctg ctg aag cca aag ttc gcg atc atg gat gag acc gac tcc ggc ctt 643
 Leu Leu Lys Pro Lys Phe Ala Ile Met Asp Glu Thr Asp Ser Gly Leu
 170 175 180
 gac gtg gat gca ctg cgc att gtt tcc gag ggc atc aac tcc tac aag 691
 Asp Val Asp Ala Leu Arg Ile Val Ser Glu Gly Ile Asn Ser Tyr Lys
 185 190 195
 cag gag acc gaa ggt ggc atc ttg atg atc acc cac tac aag cgc atc 739
 Gln Glu Thr Glu Gly Gly Ile Leu Met Ile Thr His Tyr Lys Arg Ile
 200 205 210
 ctc aac tac gtt aag cct gac ttc att cac gtt ttc gcg aat ggc cag 787
 Leu Asn Tyr Val Lys Pro Asp Phe Ile His Val Phe Ala Asn Gly Gln
 215 220 225
 att gtg acc acc ggt ggc gct gag ctt gct gac aag ctc gag gct gac 835
 Ile Val Thr Thr Gly Gly Ala Glu Leu Ala Asp Lys Leu Glu Ala Asp
 230 235 240 245
 ggc tac gac cag ttc atc aag taacatgtcc gatttcctca atg. 879
 Gly Tyr Asp Gln Phe Ile Lys
 250

<210> 314

<211> 252

<212> PRT

<213> Corynebacterium glutamicum

<400> 314

Met Ser Thr Leu Glu Ile Arg Asn Leu His Ala Gln Val Leu Pro Ser
 1 5 10 15
 Asp Glu Ser Ala Glu Pro Lys Glu Ile Leu Lys Gly Val Asn Leu Thr
 20 25 30
 Ile Asn Ser Gly Glu Ile His Ala Ile Met Gly Pro Asn Gly Ser Gly
 35 40 45
 Lys Ser Thr Leu Ala Tyr Thr Leu Gly Gly His Pro Arg Tyr Glu Val
 50 55 60
 Thr Ala Gly Glu Val Leu Leu Asp Gly Glu Asn Ile Leu Glu Met Glu
 65 70 75 80
 Val Asp Glu Arg Ala Arg Ala Gly Leu Phe Leu Ala Met Gln Tyr Pro
 85 90 95
 Thr Glu Ile Pro Gly Val Ser Val Ala Asn Phe Leu Arg Ser Ala Ala
 100 105 110
 Thr Ala Ile Arg Gly Glu Ala Pro Lys Leu Arg Glu Trp Val Lys Glu
 115 120 125

Val Arg Thr Ala Gln Glu Ala Leu Ala Ile Asp Pro Glu Phe Ser Asn
130 135 140

Arg Ser Val Asn Glu Gly Phe Ser Gly Gly Glu Lys Lys Arg His Glu
145 150 155 160

Val Leu Gln Leu Asp Leu Leu Lys Pro Lys Phe Ala Ile Met Asp Glu
165 170 175

Thr Asp Ser Gly Leu Asp Val Asp Ala Leu Arg Ile Val Ser Glu Gly
180 185 190

Ile Asn Ser Tyr Lys Gln Glu Thr Glu Gly Gly Ile Leu Met Ile Thr
195 200 205

His Tyr Lys Arg Ile Leu Asn Tyr Val Lys Pro Asp Phe Ile His Val
210 215 220

Phe Ala Asn Gly Gln Ile Val Thr Thr Gly Gly Ala Glu Leu Ala Asp
225 230 235 240

Lys Leu Glu Ala Asp Gly Tyr Asp Gln Phe Ile Lys
245 250

<210> 315

<211> 1461

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1438)

<223> RXN01995

<400> 315

ccgacgcacaaa ggcacgcgcc tgcgtgtctc gagtagtctc ctccccttcc tcgtccccaa 60

cctcgaccat tacggcgcgcc ctctcctaaa ggagcctggc atg gat atc cgc caa 115
Met Asp Ile Arg Gln
1 5

aca att aac gac aca gca atg tcg aga tat cag tgg ttc att gta ttt 163
Thr Ile Asn Asp Thr Ala Met Ser Arg Tyr Gln Trp Phe Ile Val Phe
10 15 20

atc gca gtg ctg ctc aac gca ctg gac ggc ttt gat gtc ctc gcc atg 211
Ile Ala Val Leu Leu Asn Ala Leu Asp Gly Phe Asp Val Leu Ala Met
25 30 35

tct ttt act gcg aat gca gtg acc gaa gaa ttt gga ctg agt ggc agc 259
Ser Phe Thr Ala Asn Ala Val Thr Glu Glu Phe Gly Leu Ser Gly Ser
40 45 50

cag ctt ggt gtg ctg ctg agt tcc gcg ctg ttc ggc atg acc gct gga 307
Gln Leu Gly Val Leu Leu Ser Ser Ala Leu Phe Gly Met Thr Ala Gly
55 60 65

tct ttg ctg ttc ggt ccg atc ggt gac cgt ttc ggc cgt aag aat gcc 355
Ser Leu Leu Phe Gly Pro Ile Gly Asp Arg Phe Gly Arg Lys Asn Ala

70	75	80	85	
ctg atg atc gcg ctg	ctg ttc aac gtg	gtg gga ttg gta ttg tcc gcc		403
Leu Met Ile Ala Leu	Leu Phe Asn Val Val	Gly Leu Val Leu Ser Ala		
	90	95	100	
acc gcg cag tcc gca	ggc cag ttg ggc	gtg tgg cgt ttg atc act ggt		451
Thr Ala Gln Ser Ala	Gly Gln Leu Gly	Val Trp Arg Leu Ile Thr Gly		
	105	110	115	
atc ggc atc ggc gga	atc ctc gcc tgc atc	aca gtg gtg atc agt gag		499
Ile Gly Ile Gly Gly	Ile Leu Ala Cys Ile	Thr Val Val Ile Ser Glu		
	120	125	130	
ttc tcc aac aac aaa	aac cgc ggc atg gcc	atg tcc atc tac gct gct		547
Phe Ser Asn Asn Lys	Asn Arg Gly Met Ala	Met Ser Ile Tyr Ala Ala		
	135	140	145	
ggg tac ggc atc ggc	gcg tcc ttg ggc	ggg ggt ttc ggc gca gcg cag ctc		595
Gly Tyr Gly Ile Gly	Ala Ser Leu Gly	Gly Gly Phe Gly Ala Ala Gln Leu		
	150	155	160	165
atc cca aca ttt gga	tgg cgc tcc gtg ttc	gca gcc ggt gcg atc gca		643
Ile Pro Thr Phe Gly	Trp Arg Ser Val Phe	Ala Ala Gly Ala Ile Ala		
	170	175	180	
act ggt atc gcc acc	atc gct act ttc ttc	ttc ctg cca gaa tcc gtt		691
Thr Gly Ile Ala Thr	Ile Ala Thr Phe Phe	Phe Leu Pro Glu Ser Val		
	185	190	195	
gat tgg ctg agc act	cgc cgc cct gcg ggc	gct cgc gac aag atc aat		739
Asp Trp Leu Ser Thr	Arg Arg Pro Ala Gly	Ala Arg Asp Lys Ile Asn		
	200	205	210	
tac att gcg cgc cgc	ctg ggc aaa gtc ggt	acc ttt gag ctt cca ggc		787
Tyr Ile Ala Arg Arg	Leu Gly Lys Val Gly	Thr Phe Glu Leu Pro Gly		
	215	220	225	
gaa caa agc ttg tcg	acg aaa aaa gcc ggt	ctc caa tcg tat gca gtg		835
Glu Gln Ser Leu Ser	Thr Lys Lys Ala Gly	Leu Gln Ser Tyr Ala Val		
	230	235	240	245
ctc gtt aac aaa gag	aac cgt gga acc agc	atc aag ctg tgg gtt gcg		883
Leu Val Asn Lys Glu	Asn Arg Gly Thr Ser	Ile Lys Leu Trp Val Ala		
	250	255	260	
ttc ggc atc gtg atg	ttc ggc ttc tac ttc	gcc aac act tgg acc ccg		931
Phe Gly Ile Val Met	Phe Gly Phe Tyr Phe	Ala Asn Thr Trp Thr Pro		
	265	270	275	
aag ctg ctc gtg gaa	acc gga atg tca gaa	cag cag ggc atc atc ggt		979
Lys Leu Leu Val Glu	Thr Gly Met Ser Glu	Gln Gln Gly Ile Ile Gly		
	280	285	290	
ggg ttg atg ttg tcc	atg ggt gga gca ttc	ggc tcc ctg ctc tac ggt		1027
Gly Leu Met Leu Ser	Met Gly Gly Ala Phe	Gly Ser Leu Leu Tyr Gly		
	295	300	305	
ttc ctc acc acc aag	ttc agc tcc cga aac	aca ctg atg acc ttc atg		1075
Phe Leu Thr Thr Lys	Phe Ser Ser Arg Asn	Thr Leu Met Thr Phe Met		
	310	315	320	325

gtg ctg tcc ggc ctg acg ctg atc ctg ttc att tcc tcc acc tct gtt 1123
 Val Leu Ser Gly Leu Thr Leu Ile Leu Phe Ile Ser Ser Thr Ser Val
 330 335 340

cca tcc atc gcg ttt gcc agc ggc gtt gtc gtg ggc atg ctg atc aat 1171
 Pro Ser Ile Ala Phe Ala Ser Gly Val Val Val Gly Met Leu Ile Asn
 345 350 355

ggt tgt gtg gct ggt ctg tac acc ctg tcc cca cag ctg tac tcc gct 1219
 Gly Cys Val Ala Gly Leu Tyr Thr Leu Ser Pro Gln Leu Tyr Ser Ala
 360 365 370

gaa gta cgc acc act ggt gtg ggc gct gcg att ggt atg ggt cgt gtc 1267
 Glu Val Arg Thr Thr Gly Val Gly Ala Ala Ile Gly Met Gly Arg Val
 375 380 385

ggt gcg att tcc gcg cca ctg ctg gtg ggt ggc ctg ctg gat tct ggc 1315
 Gly Ala Ile Ser Ala Pro Leu Leu Val Gly Gly Leu Leu Asp Ser Gly
 390 395 400 405

tgg tcc cca acg cag ctg tat gtt ggt gtg gca gtg att gtt att gcc 1363
 Trp Ser Pro Thr Gln Leu Tyr Val Gly Val Ala Val Ile Val Ile Ala
 410 415 420

ggt gca acc gca ttg att ggg atg cgc act cag gcg gta gcc gtc gaa 1411
 Gly Ala Thr Ala Leu Ile Gly Met Arg Thr Gln Ala Val Ala Val Glu
 425 430 435

aag cag cct gaa gcc cta gcg acc aaa tagggccgcg attcctagca tgc 1461
 Lys Gln Pro Glu Ala Leu Ala Thr Lys
 440 445

<210> 316

<211> 446

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 316

Met Asp Ile Arg Gln Thr Ile Asn Asp Thr Ala Met Ser Arg Tyr Gln
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Trp Phe Ile Val Phe Ile Ala Val Leu Leu Asn Ala Leu Asp Gly Phe
 20 25 30

Asp Val Leu Ala Met Ser Phe Thr Ala Asn Ala Val Thr Glu Glu Phe
 35 40 45

Gly Leu Ser Gly Ser Gln Leu Gly Val Leu Leu Ser Ser Ala Leu Phe
 50 55 60

Gly Met Thr Ala Gly Ser Leu Leu Phe Gly Pro Ile Gly Asp Arg Phe
 65 70 75 80

Gly Arg Lys Asn Ala Leu Met Ile Ala Leu Leu Phe Asn Val Val Gly
 85 90 95

Leu Val Leu Ser Ala Thr Ala Gln Ser Ala Gly Gln Leu Gly Val Trp
 100 105 110

Arg Leu Ile Thr Gly Ile Gly Ile Gly Gly Ile Leu Ala Cys Ile Thr
 115 120 125
 Val Val Ile Ser Glu Phe Ser Asn Asn Lys Asn Arg Gly Met Ala Met
 130 135 140
 Ser Ile Tyr Ala Ala Gly Tyr Gly Ile Gly Ala Ser Leu Gly Gly Phe
 145 150 155 160
 Gly Ala Ala Gln Leu Ile Pro Thr Phe Gly Trp Arg Ser Val Phe Ala
 165 170 175
 Ala Gly Ala Ile Ala Thr Gly Ile Ala Thr Ile Ala Thr Phe Phe Phe
 180 185 190
 Leu Pro Glu Ser Val Asp Trp Leu Ser Thr Arg Arg Pro Ala Gly Ala
 195 200 205
 Arg Asp Lys Ile Asn Tyr Ile Ala Arg Arg Leu Gly Lys Val Gly Thr
 210 215 220
 Phe Glu Leu Pro Gly Glu Gln Ser Leu Ser Thr Lys Lys Ala Gly Leu
 225 230 235 240
 Gln Ser Tyr Ala Val Leu Val Asn Lys Glu Asn Arg Gly Thr Ser Ile
 245 250 255
 Lys Leu Trp Val Ala Phe Gly Ile Val Met Phe Gly Phe Tyr Phe Ala
 260 265 270
 Asn Thr Trp Thr Pro Lys Leu Leu Val Glu Thr Gly Met Ser Glu Gln
 275 280 285
 Gln Gly Ile Ile Gly Gly Leu Met Leu Ser Met Gly Gly Ala Phe Gly
 290 295 300
 Ser Leu Leu Tyr Gly Phe Leu Thr Thr Lys Phe Ser Ser Arg Asn Thr
 305 310 315 320
 Leu Met Thr Phe Met Val Leu Ser Gly Leu Thr Leu Ile Leu Phe Ile
 325 330 335
 Ser Ser Thr Ser Val Pro Ser Ile Ala Phe Ala Ser Gly Val Val Val
 340 345 350
 Gly Met Leu Ile Asn Gly Cys Val Ala Gly Leu Tyr Thr Leu Ser Pro
 355 360 365
 Gln Leu Tyr Ser Ala Glu Val Arg Thr Thr Gly Val Gly Ala Ala Ile
 370 375 380
 Gly Met Gly Arg Val Gly Ala Ile Ser Ala Pro Leu Leu Val Gly Gly
 385 390 395 400
 Leu Leu Asp Ser Gly Trp Ser Pro Thr Gln Leu Tyr Val Gly Val Ala
 405 410 415
 Val Ile Val Ile Ala Gly Ala Thr Ala Leu Ile Gly Met Arg Thr Gln
 420 425 430
 Ala Val Ala Val Glu Lys Gln Pro Glu Ala Leu Ala Thr Lys

435

440

445

<210> 317
 <211> 754
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(754)
 <223> FRXA01995

<400> 317
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 Met Asp Ile Arg Gln
 1 5
 aca att aac gac aca gca atg tcg aga tat cag tgg ttc att gta ttt 163
 Thr Ile Asn Asp Thr Ala Met Ser Arg Tyr Gln Trp Phe Ile Val Phe
 10 15 20
 atc gca gtg ctg ctc aac gca ctg gac ggc ttt gat gtc ctc gcc atg 211
 Ile Ala Val Leu Leu Asn Ala Leu Asp Gly Phe Asp Val Leu Ala Met
 25 30 35
 tct ttt act gcg aat gca gtg acc gaa gaa ttt gga ctg agt ggc agc 259
 Ser Phe Thr Ala Asn Ala Val Thr Glu Glu Phe Gly Leu Ser Gly Ser
 40 45 50
 cag ctt ggt gtg ctg ctg agt tcc gcg ctg ttc ggc atg acc gct gga 307
 Gln Leu Gly Val Leu Leu Ser Ser Ala Leu Phe Gly Met Thr Ala Gly
 55 60 65
 tct ttg ctg ttc ggt ccg atc ggt gac cgt ttc ggc cgt aag aat gcc 355
 Ser Leu Leu Phe Gly Pro Ile Gly Asp Arg Phe Gly Arg Lys Asn Ala
 70 75 80 85
 ctg atg atc gcg ctg ctg ttc aac gtg gtg gga ttg gta ttg tcc gcc 403
 Leu Met Ile Ala Leu Leu Phe Asn Val Val Gly Leu Val Leu Ser Ala
 90 95 100
 acc gcg cag tcc gca ggc cag ttg ggc gtg tgg cgt ttg atc act ggt 451
 Thr Ala Gln Ser Ala Gly Gln Leu Gly Val Trp Arg Leu Ile Thr Gly
 105 110 115
 atc ggc atc ggc gga atc ctc gcc tgc atc aca gtg gtg atc agt gag 499
 Ile Gly Ile Gly Gly Ile Leu Ala Cys Ile Thr Val Val Ile Ser Glu
 120 125 130
 ttc tcc aac aac aaa aac cgc ggc atg gcc atg tcc atc tac gct gct 547
 Phe Ser Asn Asn Lys Asn Arg Gly Met Ala Met Ser Ile Tyr Ala Ala
 135 140 145
 ggt tac ggc atc ggc gcg tcc ttg ggc ggt ttc ggc gca gcg cag ctc 595
 Gly Tyr Gly Ile Gly Ala Ser Leu Gly Gly Phe Gly Ala Ala Gln Leu
 150 155 160 165
 atc cca aca ttt gga tgg cgc tcc gtg ttc gca gcc ggt gcg atc gca 643

Ile Pro Thr Phe Gly Trp Arg Ser Val Phe Ala Ala Gly Ala Ile Ala
 170 175 180

act ggt atc gcc acc atc gct act ttc ttc ttc ctg cca gaa tcc gtt 691
 Thr Gly Ile Ala Thr Ile Ala Thr Phe Phe Phe Leu Pro Glu Ser Val
 185 190 195

gat tgg ctg agc act cgc cgc cct gcg ggc gct cgc gac aag atc aat 739
 Asp Trp Leu Ser Thr Arg Arg Pro Ala Gly Ala Arg Asp Lys Ile Asn
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 <213> Corynebacterium glutamicum

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Asp Val Leu Ala Met Ser Phe Thr Ala Asn Ala Val Thr Glu Glu Phe
 35 40 45

Gly Leu Ser Gly Ser Gln Leu Gly Val Leu Leu Ser Ser Ala Leu Phe
 50 55 60

Gly Met Thr Ala Gly Ser Leu Leu Phe Gly Pro Ile Gly Asp Arg Phe
 65 70 75 80

Gly Arg Lys Asn Ala Leu Met Ile Ala Leu Leu Phe Asn Val Val Gly
 85 90 95

Leu Val Leu Ser Ala Thr Ala Gln Ser Ala Gly Gln Leu Gly Val Trp
 100 105 110

Arg Leu Ile Thr Gly Ile Gly Ile Gly Gly Ile Leu Ala Cys Ile Thr
 115 120 125

Val Val Ile Ser Glu Phe Ser Asn Asn Lys Asn Arg Gly Met Ala Met
 130 135 140

Ser Ile Tyr Ala Ala Gly Tyr Gly Ile Gly Ala Ser Leu Gly Gly Phe
 145 150 155 160

Gly Ala Ala Gln Leu Ile Pro Thr Phe Gly Trp Arg Ser Val Phe Ala
 165 170 175

Ala Gly Ala Ile Ala Thr Gly Ile Ala Thr Ile Ala Thr Phe Phe Phe
 180 185 190

Leu Pro Glu Ser Val Asp Trp Leu Ser Thr Arg Arg Pro Ala Gly Ala
 195 200 205

Arg Asp Lys Ile Asn Tyr Ile Ala Arg Arg
210 215

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<223> RXA01188

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Met Met Asn Gly Val
1 5
gta cag cct cag gaa cat ctg gat gca acg ttg att gct gca gac ttc 163
Val Gln Pro Gln Glu His Leu Asp Ala Thr Leu Ile Ala Ala Asp Phe
10 15 20
cac ggc aac ccc gaa aac tct ggt gac cgc aaa gag cgc ctg aat ttt 211
His Gly Asn Pro Glu Asn Ser Gly Asp Arg Lys Glu Arg Leu Asn Phe
25 30 35
caa ggt tgg aag tat gcc ctt aat cgc acg gtc agg gat gtt ttt cca 259
Gln Gly Trp Lys Tyr Ala Leu Asn Arg Thr Val Arg Asp Val Phe Pro
40 45 50
gat ggc ctg ctg gat ttg gcg gcc ttg ttg acg ttc ttt tcc att ctg 307
Asp Gly Leu Leu Asp Leu Ala Ala Leu Leu Thr Phe Phe Ser Ile Leu
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tcg atc gcc cct gca gtg ctg ctg ggc tat tcg gtg atc acg att ttt 355
Ser Ile Ala Pro Ala Val Leu Leu Gly Tyr Ser Val Ile Thr Ile Phe
70 75 80 85
ctg gcc agt gac tcc acc gaa atc ctg aac ctt gtc cgc gat gag gta 403
Leu Ala Ser Asp Ser Thr Glu Ile Leu Asn Leu Val Arg Asp Glu Val
90 95 100
aat cag tac gtt ccg gaa gat caa tcc cat gtt gtc aac ggc gtg att 451
Asn Gln Tyr Val Pro Glu Asp Gln Ser His Val Val Asn Gly Val Ile
105 110 115
gat tcg atc gca ggc tcg gca gct gca ggt cag gtc ggt gtc gcg gtc 499
Asp Ser Ile Ala Gly Ser Ala Ala Ala Gly Gln Val Gly Val Ala Val
120 125 130
ggt gtg atc acg gca ttg tgg aca tct tcg gca tat gtg cgc gct ttt 547
Gly Val Ile Thr Ala Leu Trp Thr Ser Ser Ala Tyr Val Arg Ala Phe
135 140 145
tcc aga tgt gcc aac gct gtt tat ggc cga agc gaa ggc cgc aca ttg 595
Ser Arg Cys Ala Asn Ala Val Tyr Gly Arg Ser Glu Gly Arg Thr Leu
150 155 160 165

atc aaa cgc tgg gca atg ctg ctt ttc ctc aac ctt gct ttg ctg ctt 643
 Ile Lys Arg Trp Ala Met Leu Leu Phe Leu Asn Leu Ala Leu Leu Leu
 170 175 180

gga atc atc atc att ttg gtc tcc tgg gtg ctc aac gag acc ttg gtg 691
 Gly Ile Ile Ile Ile Leu Val Ser Trp Val Leu Asn Glu Thr Leu Val
 185 190 195

atg gga att ttc gcc ccc atc gcg gaa cca ctt cat ctc acg aat gtg 739
 Met Gly Ile Phe Ala Pro Ile Ala Glu Pro Leu His Leu Thr Asn Val
 200 205 210

ctc agc ttc ctc acg gac cgg ttc atg ccg atc tgg atc tgg gtg cgg 787
 Leu Ser Phe Leu Thr Asp Arg Phe Met Pro Ile Trp Ile Trp Val Arg
 215 220 225

ttc cca gtg att gtg ggg gtg ctc atc atg ttc gtg gcc acg ctg tat 835
 Phe Pro Val Ile Val Gly Val Leu Ile Met Phe Val Ala Thr Leu Tyr
 230 235 240 245

tac tgg gcc ccg aac gcc cgc ccg tgg aag ttt cgc tgg ctc agc ctc 883
 Tyr Trp Ala Pro Asn Ala Arg Pro Trp Lys Phe Arg Trp Leu Ser Leu
 250 255 260

gga tca ttc ttg gcg atc gtt ggc atc ctg ctc gca ggc gtg ggc ttg 931
 Gly Ser Phe Leu Ala Ile Val Gly Ile Leu Leu Ala Gly Val Gly Leu
 265 270 275

aat ttc tac ttc acg ctg ttc gcc gct ttt agt tcc tac ggc gcg gtg 979
 Asn Phe Tyr Phe Thr Leu Phe Ala Ala Phe Ser Ser Tyr Gly Ala Val
 280 285 290

ggt tcg ctg ctc gcg gtt ttt att gcg ctg tgg gtg ttc aac att tgc 1027
 Gly Ser Leu Leu Ala Val Phe Ile Ala Leu Trp Val Phe Asn Ile Cys
 295 300 305

tta atc atc ggc ctg aaa atc gac gtg gag atc agc cgc gcc aag caa 1075
 Leu Ile Ile Gly Leu Lys Ile Asp Val Glu Ile Ser Arg Ala Lys Gln
 310 315 320 325

ctg cag gca gga atg ccg gcg gag gat tac agt tta gtg cca cca cgc 1123
 Leu Gln Ala Gly Met Pro Ala Glu Asp Tyr Ser Leu Val Pro Pro Arg
 330 335 340

tct atc gag aag gtg gcg aaa atg aag cag cgc cag cag cgc ttg atg 1171
 Ser Ile Glu Lys Val Ala Lys Met Lys Gln Arg Gln Gln Arg Leu Met
 345 350 355

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<210> 320

<211> 368

<212> PRT

<213> Corynebacterium glutamicum

<400> 320

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 Ile Ala Ala Asp Phe His Gly Asn Pro Glu Asn Ser Gly Asp Arg Lys
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 Glu Arg Leu Asn Phe Gln Gly Trp Lys Tyr Ala Leu Asn Arg Thr Val
 35 40 45
 Arg Asp Val Phe Pro Asp Gly Leu Leu Asp Leu Ala Ala Leu Leu Thr
 50 55 60
 Phe Phe Ser Ile Leu Ser Ile Ala Pro Ala Val Leu Leu Gly Tyr Ser
 65 70 75 80
 Val Ile Thr Ile Phe Leu Ala Ser Asp Ser Thr Glu Ile Leu Asn Leu
 85 90 95
 Val Arg Asp Glu Val Asn Gln Tyr Val Pro Glu Asp Gln Ser His Val
 100 105 110
 Val Asn Gly Val Ile Asp Ser Ile Ala Gly Ser Ala Ala Ala Gly Gln
 115 120 125
 Val Gly Val Ala Val Gly Val Ile Thr Ala Leu Trp Thr Ser Ser Ala
 130 135 140
 Tyr Val Arg Ala Phe Ser Arg Cys Ala Asn Ala Val Tyr Gly Arg Ser
 145 150 155 160
 Glu Gly Arg Thr Leu Ile Lys Arg Trp Ala Met Leu Leu Phe Leu Asn
 165 170 175
 Leu Ala Leu Leu Leu Gly Ile Ile Ile Ile Leu Val Ser Trp Val Leu
 180 185 190
 Asn Glu Thr Leu Val Met Gly Ile Phe Ala Pro Ile Ala Glu Pro Leu
 195 200 205
 His Leu Thr Asn Val Leu Ser Phe Leu Thr Asp Arg Phe Met Pro Ile
 210 215 220
 Trp Ile Trp Val Arg Phe Pro Val Ile Val Gly Val Leu Ile Met Phe
 225 230 235 240
 Val Ala Thr Leu Tyr Tyr Trp Ala Pro Asn Ala Arg Pro Trp Lys Phe
 245 250 255
 Arg Trp Leu Ser Leu Gly Ser Phe Leu Ala Ile Val Gly Ile Leu Leu
 260 265 270
 Ala Gly Val Gly Leu Asn Phe Tyr Phe Thr Leu Phe Ala Ala Phe Ser
 275 280 285
 Ser Tyr Gly Ala Val Gly Ser Leu Leu Ala Val Phe Ile Ala Leu Trp
 290 295 300
 Val Phe Asn Ile Cys Leu Ile Ile Gly Leu Lys Ile Asp Val Glu Ile
 305 310 315 320
 Ser Arg Ala Lys Gln Leu Gln Ala Gly Met Pro Ala Glu Asp Tyr Ser

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Leu	Val	Pro	Pro	Arg	Ser	Ile	Glu	Lys	Val	Ala	Lys	Met	Lys	Gln	Arg		
			340					345						350			
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				Val Ala Thr Gly Leu													
				1 5													
ctg tcg gcg att ggt ctg ttt atc gcc acc aat atc gac gac atc atc	163																
Leu Ser Ala Ile Gly Leu Phe Ile Ala Thr Asn Ile Asp Asp Ile Ile																	
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gtg ctc tcg ctg ttt ttt gcc cgc ggg gcg ggg caa aaa ggg acc acg	211																
Val Leu Ser Leu Phe Phe Ala Arg Gly Ala Gly Gln Lys Gly Thr Thr								30					35				
			25														
ctt cgg att ctg gct ggt cag tac ctc ggc ttc atg ggc atc ctc gcg	259																
Leu Arg Ile Leu Ala Gly Gln Tyr Leu Gly Phe Met Gly Ile Leu Ala																	
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gcc gca gtc ctg gtc acg ctg ggg gca gga gca ttc cta cct gct gag	307																
Ala Ala Val Leu Val Thr Leu Gly Ala Gly Ala Phe Leu Pro Ala Glu							60					65					
		55															
gcg atc ccg tac ttc gga cta att ccc ctg gcc ctg gga cta tgg gcg	355																
Ala Ile Pro Tyr Phe Gly Leu Ile Pro Leu Ala Leu Gly Leu Trp Ala							75			80					85		
	70																
gcc tgg cag gcc tgg cga agc gat gat gac gac gat gat gat gcg gag	403																
Ala Trp Gln Ala Trp Arg Ser Asp Asp Asp Asp Asp Asp Ala Glu															100		
				90						95							
atc gcc ggg aaa aag gtg ggt gtg ctg acc gtc gcc ggt gtg acg ttt	451																
Ile Ala Gly Lys Lys Val Gly Val Leu Thr Val Ala Gly Val Thr Phe																	
			105						110					115			
gcc aac ggt ggc gac aat atc ggc gtc tac gtc ccg gtc ttc ctc aac	499																
Ala Asn Gly Gly Asp Asn Ile Gly Val Tyr Val Pro Val Phe Leu Asn																	
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gtg gac act gcc gcc gtc atc atc tac tgc atc gtt ttc ctc gtc ctg	547																
Val Asp Thr Ala Ala Val Ile Ile Tyr Cys Ile Val Phe Leu Val Leu																	
		135				140					145						

gtg gca ggc ctg gtc ctg ctg gca aag ttc gtg gcc acc cgc ccg ccc 595
 Val Ala Gly Leu Val Leu Leu Ala Lys Phe Val Ala Thr Arg Pro Pro
 150 155 160 165

atc gca gaa gtc ctt gag cgc tgg gag cac gtg ctg ttc ccg atc gtc 643
 Ile Ala Glu Val Leu Glu Arg Trp Glu His Val Leu Phe Pro Ile Val
 170 175 180

ctg atc ggc ctg ggc atc ttc atc ctc gtc agc ggc ggc gcc ttc ggc 691
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 185 190 195

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<210> 322

<211> 198

<212> PRT

<213> Corynebacterium glutamicum

<400> 322

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Ile Asp Asp Ile Ile Val Leu Ser Leu Phe Phe Ala Arg Gly Ala Gly
 20 25 30

Gln Lys Gly Thr Thr Leu Arg Ile Leu Ala Gly Gln Tyr Leu Gly Phe
 35 40 45

Met Gly Ile Leu Ala Ala Ala Val Leu Val Thr Leu Gly Ala Gly Ala
 50 55 60

Phe Leu Pro Ala Glu Ala Ile Pro Tyr Phe Gly Leu Ile Pro Leu Ala
 65 70 75 80

Leu Gly Leu Trp Ala Ala Trp Gln Ala Trp Arg Ser Asp Asp Asp Asp
 85 90 95

Asp Asp Asp Ala Glu Ile Ala Gly Lys Lys Val Gly Val Leu Thr Val
 100 105 110

Ala Gly Val Thr Phe Ala Asn Gly Gly Asp Asn Ile Gly Val Tyr Val
 115 120 125

Pro Val Phe Leu Asn Val Asp Thr Ala Ala Val Ile Ile Tyr Cys Ile
 130 135 140

Val Phe Leu Val Leu Val Ala Gly Leu Val Leu Leu Ala Lys Phe Val
 145 150 155 160

Ala Thr Arg Pro Pro Ile Ala Glu Val Leu Glu Arg Trp Glu His Val
 165 170 175

Leu Phe Pro Ile Val Leu Ile Gly Leu Gly Ile Phe Ile Leu Val Ser
 180 185 190

Gly Gly Ala Phe Gly Leu

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<222> (101)..(955)
<223> RXA00311
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Met Glu His Ser Pro																	115
1 5																	
gaa ggc aag cgt gga ttc ttc acc tca tcg gtg atg gcg ggt tgc tca																	163
Glu Gly Lys Arg Gly Phe Phe Thr Ser Ser Val Met Ala Gly Cys Ser																	
10 15 20																	
gtt gga aac gtc ctg gct ggc ttg gta ttt atc ccg ttc ttg atg ctg																	211
Val Gly Asn Val Leu Ala Gly Leu Val Phe Ile Pro Phe Leu Met Leu																	
25 30 35																	
ccg gaa gaa cac ctc atg tca tgg ggc tgg cgc gta cct ttc ctg ctt																	259
Pro Glu Glu His Leu Met Ser Trp Gly Trp Arg Val Pro Phe Leu Leu																	
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Ser Ala Leu Val Leu Val Val Ala Tyr Phe Val Arg Thr Arg Leu Glu																	
55 60 65																	
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Glu Ala Ser Thr Glu Lys Ala Glu Glu Asp Ala Gly Ala Pro Ala Leu																	
70 75 80 85																	
gct gtg ctg cgc acc cag ggc att gat gtc gca cga gtt ttc ctg atc																	403
Ala Val Leu Arg Thr Gln Gly Ile Asp Val Ala Arg Val Phe Leu Ile																	
90 95 100																	
acc ttc ttc gcc gtt gtt cag acc act ttc aac gtt tac gca ctg gca																	451
Thr Phe Phe Ala Val Val Gln Thr Thr Phe Asn Val Tyr Ala Leu Ala																	
105 110 115																	
tac gcc gcc aac gaa atc ggc atc gat cgt tcc ttc atg gtg atg gtg																	499
Tyr Ala Ala Asn Glu Ile Gly Ile Asp Arg Ser Phe Met Val Met Val																	
120 125 130																	
aac acc atc gcg ctg ggg ctt tcc atc gga acg att cct ttg gcc gcg																	547
Asn Thr Ile Ala Leu Gly Leu Ser Ile Gly Thr Ile Pro Leu Ala Ala																	
135 140 145																	
tgg gtc tct gac cgc att ggc cgc aag cca gtc ttg ctg ttc ggg gcc																	595
Trp Val Ser Asp Arg Ile Gly Arg Lys Pro Val Leu Leu Phe Gly Ala																	
150 155 160 165																	
atc acc tgt gca atc acc acc tac ttc tac ttc cag gca atc tct gaa																	643

Ile Thr Cys Ala Ile Thr Thr Tyr Phe Tyr Phe Gln Ala Ile Ser Glu
 170 175 180

gct gac ctt gtg ctg atc ttc gca ctg tgc ttg gtc aac caa ggt ttg 691
 Ala Asp Leu Val Leu Ile Phe Ala Leu Cys Leu Val Asn Gln Gly Leu
 185 190 195

ttc tac tcc tgc tgg aac ggc gtg tgg acc att ttc ttc cca gaa atg 739
 Phe Tyr Ser Cys Trp Asn Gly Val Trp Thr Ile Phe Phe Pro Glu Met
 200 205 210

ttc gca tct tcc gtg cgc tac acc ggc atg gct atg ggc aac cag ctg 787
 Phe Ala Ser Ser Val Arg Tyr Thr Gly Met Ala Met Gly Asn Gln Leu
 215 220 225

ggt ctg atc atc gtt ggt ttc gca cca acc atc gcc acc gcc ctg tac 835
 Gly Leu Ile Ile Val Gly Phe Ala Pro Thr Ile Ala Thr Ala Leu Tyr
 230 235 240 245

gca tgg aac ggt tgg gaa gct gtt gcg gga ttc atc atc ggc gca atc 883
 Ala Trp Asn Gly Trp Glu Ala Val Ala Gly Phe Ile Ile Gly Ala Ile
 250 255 260

gca ctg tct gcc gca gtt att ttg acc acc aag gaa acc gcc ttc acc 931
 Ala Leu Ser Ala Ala Val Ile Leu Thr Thr Lys Glu Thr Ala Phe Thr
 265 270 275

aag ctt gaa gat cta ggg aag aaa taatgtctga caagatctgg aaa 978
 Lys Leu Glu Asp Leu Gly Lys Lys
 280 285

<210> 324

<211> 285

<212> PRT

<213> Corynebacterium glutamicum

<400> 324

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 20 25 30

Pro Phe Leu Met Leu Pro Glu Glu His Leu Met Ser Trp Gly Trp Arg
 35 40 45

Val Pro Phe Leu Leu Ser Ala Leu Val Leu Val Val Ala Tyr Phe Val
 50 55 60

Arg Thr Arg Leu Glu Glu Ala Ser Thr Glu Lys Ala Glu Glu Asp Ala
 65 70 75 80

Gly Ala Pro Ala Leu Ala Val Leu Arg Thr Gln Gly Ile Asp Val Ala
 85 90 95

Arg Val Phe Leu Ile Thr Phe Phe Ala Val Val Gln Thr Thr Phe Asn
 100 105 110

Val Tyr Ala Leu Ala Tyr Ala Ala Asn Glu Ile Gly Ile Asp Arg Ser
 115 120 125

Phe Met Val Met Val Asn Thr Ile Ala Leu Gly Leu Ser Ile Gly Thr
 130 135 140
 Ile Pro Leu Ala Ala Trp Val Ser Asp Arg Ile Gly Arg Lys Pro Val
 145 150 155 160
 Leu Leu Phe Gly Ala Ile Thr Cys Ala Ile Thr Thr Tyr Phe Tyr Phe
 165 170 175
 Gln Ala Ile Ser Glu Ala Asp Leu Val Leu Ile Phe Ala Leu Cys Leu
 180 185 190
 Val Asn Gln Gly Leu Phe Tyr Ser Cys Trp Asn Gly Val Trp Thr Ile
 195 200 205
 Phe Phe Pro Glu Met Phe Ala Ser Ser Val Arg Tyr Thr Gly Met Ala
 210 215 220
 Met Gly Asn Gln Leu Gly Leu Ile Ile Val Gly Phe Ala Pro Thr Ile
 225 230 235 240
 Ala Thr Ala Leu Tyr Ala Trp Asn Gly Trp Glu Ala Val Ala Gly Phe
 245 250 255
 Ile Ile Gly Ala Ile Ala Leu Ser Ala Ala Val Ile Leu Thr Thr Lys
 260 265 270
 Glu Thr Ala Phe Thr Lys Leu Glu Asp Leu Gly Lys Lys
 275 280 285

<210> 325

<211> 549

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(526)

<223> RXA00312

<400> 325

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 Met Glu Thr Val Arg
 1 5

acc gca acc gcc gct cct gaa act gca tct ttg aag ctg cgt gag gca 163
 Thr Ala Thr Ala Ala Pro Glu Thr Ala Ser Leu Lys Leu Arg Glu Ala
 10 15 20

gaa agc cca gca aag tcc cca aag aaa gcc gcc ttg gcg tca ctt ttg 211
 Glu Ser Pro Ala Lys Ser Pro Lys Lys Ala Ala Leu Ala Ser Leu Leu
 25 30 35

ggt tcg act ctg gag tac tac gac ttt gtc att tac ggc acc gcc tcc 259
 Gly Ser Thr Leu Glu Tyr Tyr Asp Phe Val Ile Tyr Gly Thr Ala Ser
 40 45 50

gcg ctg ctg ttc aat cac ctc ttc ttc cca cag ggc gac cca gtc gtc 307
 Ala Leu Leu Phe Asn His Leu Phe Phe Pro Gln Gly Asp Pro Val Val
 55 60 65

gcg acg atc ggc tct ctc gcc tca ttc ggt gtt gcg tac att gcg cgc 355
 Ala Thr Ile Gly Ser Leu Ala Ser Phe Gly Val Ala Tyr Ile Ala Arg
 70 75 80 85

ccc atc ggt ggt ctg gtg atg gga cat gtt ggc gat aag atc agt cgc 403
 Pro Ile Gly Gly Leu Val Met Gly His Val Gly Asp Lys Ile Ser Arg
 90 95 100

aaa acc gcc ctc atg gtg acg ttg atg atc atg ggt atc gcc tcc att 451
 Lys Thr Ala Leu Met Val Thr Leu Met Ile Met Gly Ile Ala Ser Ile
 105 110 115

tcc atc gga ctt ctg ccc acc tac gga cag atc ggc att tgg gcg acc 499
 Ser Ile Gly Leu Leu Pro Thr Tyr Gly Gln Ile Gly Ile Trp Ala Thr
 120 125 130

gtg ctg ttg atg atc gcc cgc atc gca tagggattct ctgcagtcgc aga 549
 Val Leu Leu Met Ile Ala Arg Ile Ala
 135 140

<210> 326

<211> 142

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 326

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Lys Leu Arg Glu Ala Glu Ser Pro Ala Lys Ser Pro Lys Lys Ala Ala
 20 25 30

Leu Ala Ser Leu Leu Gly Ser Thr Leu Glu Tyr Tyr Asp Phe Val Ile
 35 40 45

Tyr Gly Thr Ala Ser Ala Leu Leu Phe Asn His Leu Phe Phe Pro Gln
 50 55 60

Gly Asp Pro Val Val Ala Thr Ile Gly Ser Leu Ala Ser Phe Gly Val
 65 70 75 80

Ala Tyr Ile Ala Arg Pro Ile Gly Gly Leu Val Met Gly His Val Gly
 85 90 95

Asp Lys Ile Ser Arg Lys Thr Ala Leu Met Val Thr Leu Met Ile Met
 100 105 110

Gly Ile Ala Ser Ile Ser Ile Gly Leu Leu Pro Thr Tyr Gly Gln Ile
 115 120 125

Gly Ile Trp Ala Thr Val Leu Leu Met Ile Ala Arg Ile Ala
 130 135 140

<210> 327

<211> 888

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(865)

<223> RXN01411

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                                         Met Leu Gly Val Gly
                                         1                               5

tgg cgc att cca ttc ctg atg gcc gtg cca cta ggg ctt atc ggc tgg 163
Trp Arg Ile Pro Phe Leu Met Ala Val Pro Leu Gly Leu Ile Gly Trp
                        10                        15                        20

tgg atc cgc acc ggt gcc cag gaa aat gta cgc ccc gca tcc gaa cgc 211
Trp Ile Arg Thr Gly Ala Gln Glu Asn Val Arg Pro Ala Ser Glu Arg
                        25                        30                        35

ccc gaa gct cct att aag cag gca ttg cgt act gag tgg aag atg atg 259
Pro Glu Ala Pro Ile Lys Gln Ala Leu Arg Thr Glu Trp Lys Met Met
                        40                        45                        50

ttg cgg gta ggt ggc ttt atc tct tgc acc ggt ctg agc ttc tac att 307
Leu Arg Val Gly Gly Phe Ile Ser Cys Thr Gly Leu Ser Phe Tyr Ile
                        55                        60                        65

ttc acc acg tac atg acc act ttc ctg cgc agc acc gtc gga ctg gag 355
Phe Thr Thr Tyr Met Thr Thr Phe Leu Arg Ser Thr Val Gly Leu Glu
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ggc acg tta gtg ctg gct gga aac atc atc gct ctc agc atg gca gca 403
Gly Thr Leu Val Leu Ala Gly Asn Ile Ile Ala Leu Ser Met Ala Ala
                        90                        95                        100

att gtg gcc cca ttt gtt ggc cgc gca att gat aaa ttc ccc cgc cgg 451
Ile Val Ala Pro Phe Val Gly Arg Ala Ile Asp Lys Phe Pro Arg Arg
                        105                        110                        115

aac atc atg gct ttc gct acc tta agc aca gta att atg gcg atc ccg 499
Asn Ile Met Ala Phe Ala Thr Leu Ser Thr Val Ile Met Ala Ile Pro
                        120                        125                        130

gcc tac atc att gca ggt caa ggt act ttg act gct tct ttg att gcg 547
Ala Tyr Ile Ile Ala Gly Gln Gly Thr Leu Thr Ala Ser Leu Ile Ala
                        135                        140                        145

cag gta atg ctt gga atc ggc gcg gtt acc gct aac tgc gtt acc tca 595
Gln Val Met Leu Gly Ile Gly Ala Val Thr Ala Asn Cys Val Thr Ser
                        150                        155                        160                        165

gta atg atg gcc gag gtc ttc caa gag gtc acc cgc ggt act tcc gcc 643
Val Met Met Ala Glu Val Phe Gln Glu Val Thr Arg Gly Thr Ser Ala
                        170                        175                        180

ggc att acc tac aac gtc act tac gca atc ttc ggc ggc tcg gct cca 691
Gly Ile Thr Tyr Asn Val Thr Tyr Ala Ile Phe Gly Gly Ser Ala Pro

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185	190	195	
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Phe Ile Ser Thr Ala Leu Val Ser Trp Thr Gly Ser Pro Leu Ala Pro			
200	205	210	
gcg gta tac atg atc atc att gcg ctc ttc gcc ttc acc gcg tcc cgc			787
Ala Val Tyr Met Ile Ile Ile Ala Leu Phe Ala Phe Thr Ala Ser Arg			
215	220	225	
ttc att cct gaa acc tcc cca gtt ttt gtc acc gca acc ccg gcc att			835
Phe Ile Pro Glu Thr Ser Pro Val Phe Val Thr Ala Thr Pro Ala Ile			
230	235	240	245
aag gca cca aag gtg ctg gtc aac ccg ggt taaaccacgc ttttcgacga			885
Lys Ala Pro Lys Val Leu Val Asn Pro Gly			
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<212> PRT

<213> Corynebacterium glutamicum

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Pro Ala Ser Glu Arg Pro Glu Ala Pro Ile Lys Gln Ala Leu Arg Thr			
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Glu Trp Lys Met Met Leu Arg Val Gly Gly Phe Ile Ser Cys Thr Gly			
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Leu Ser Phe Tyr Ile Phe Thr Thr Tyr Met Thr Thr Phe Leu Arg Ser			
65	70	75	80
Thr Val Gly Leu Glu Gly Thr Leu Val Leu Ala Gly Asn Ile Ile Ala			
85	90	95	
Leu Ser Met Ala Ala Ile Val Ala Pro Phe Val Gly Arg Ala Ile Asp			
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Lys Phe Pro Arg Arg Asn Ile Met Ala Phe Ala Thr Leu Ser Thr Val			
115	120	125	
Ile Met Ala Ile Pro Ala Tyr Ile Ile Ala Gly Gln Gly Thr Leu Thr			
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Ala Ser Leu Ile Ala Gln Val Met Leu Gly Ile Gly Ala Val Thr Ala			
145	150	155	160
Asn Cys Val Thr Ser Val Met Met Ala Glu Val Phe Gln Glu Val Thr			
165	170	175	
Arg Gly Thr Ser Ala Gly Ile Thr Tyr Asn Val Thr Tyr Ala Ile Phe			

180	185	190
Gly Gly Ser Ala Pro Phe Ile Ser Thr Ala Leu Val Ser Trp Thr Gly		
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Ser Pro Leu Ala Pro Ala Val Tyr Met Ile Ile Ile Ala Leu Phe Ala		
210	215	220
Phe Thr Ala Ser Arg Phe Ile Pro Glu Thr Ser Pro Val Phe Val Thr		
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<223> FRXA01411

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ggt acc tca gta atg atg gcc gag gtc ttc caa gag gtc acc cgc ggt	96
Val Thr Ser Val Met Met Ala Glu Val Phe Gln Glu Val Thr Arg Gly	
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act tcc gcc ggc att acc tac aac gtc act tac gca atc ttc ggc ggc	144
Thr Ser Ala Gly Ile Thr Tyr Asn Val Thr Tyr Ala Ile Phe Gly Gly	
35 40 45	
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Ser Ala Pro Phe Ile Ser Thr Ala Leu Val Ser Trp Thr Gly Ser Pro	
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Leu Ala Pro Ala Val Tyr Met Ile Ile Ile Ala Leu Phe Ala Phe Thr	
65 70 75 80	
gcg tcc cgc ttc att cct gaa acc tcc cca gtt ttt gtc acc gca acc	288
Ala Ser Arg Phe Ile Pro Glu Thr Ser Pro Val Phe Val Thr Ala Thr	
85 90 95	
ccg gcc att aag gca cca aag gtg ctg gtc aac ccg ggt taaaccacgc	337
Pro Ala Ile Lys Ala Pro Lys Val Leu Val Asn Pro Gly	
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<213> Corynebacterium glutamicum

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 Thr Ser Ala Gly Ile Thr Tyr Asn Val Thr Tyr Ala Ile Phe Gly Gly
 35 40 45
 Ser Ala Pro Phe Ile Ser Thr Ala Leu Val Ser Trp Thr Gly Ser Pro
 50 55 60
 Leu Ala Pro Ala Val Tyr Met Ile Ile Ile Ala Leu Phe Ala Phe Thr
 65 70 75 80
 Ala Ser Arg Phe Ile Pro Glu Thr Ser Pro Val Phe Val Thr Ala Thr
 85 90 95
 Pro Ala Ile Lys Ala Pro Lys Val Leu Val Asn Pro Gly
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<222> (101)..(1399)

<223> RXA01900

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 Met Thr Thr Ala Val
 1 5
 gat caa aac tca ccg ccc aag cag caa ctc aac aag cgc gtc ctg ctg 163
 Asp Gln Asn Ser Pro Pro Lys Gln Gln Leu Asn Lys Arg Val Leu Leu
 10 15 20
 ggc agc ttg agt ggc agc gtt atc gaa tgg ttc gac ttc ctg gtt tac 211
 Gly Ser Leu Ser Gly Ser Val Ile Glu Trp Phe Asp Phe Leu Val Tyr
 25 30 35
 gga acc gtc gcc gcg ctg gtc ttc aac aag atg tac ttc ccc agc ggc 259
 Gly Thr Val Ala Ala Leu Val Phe Asn Lys Met Tyr Phe Pro Ser Gly
 40 45 50
 aac gag ttc ctc tcc aca atc ctg gcg tac gca tcc ttc tcc ctg acc 307
 Asn Glu Phe Leu Ser Thr Ile Leu Ala Tyr Ala Ser Phe Ser Leu Thr
 55 60 65
 ttc ttc ttc cgc ccc att ggt ggc gtc atc ttc gcc cac atc ggc gac 355
 Phe Phe Phe Arg Pro Ile Gly Gly Val Ile Phe Ala His Ile Gly Asp
 70 75 80 85

cgc att ggg cgt aag aag acc ctg ttc atc acc ttg atg ctc atg ggt	403
Arg Ile Gly Arg Lys Lys Thr Leu Phe Ile Thr Leu Met Leu Met Gly	
90 95 100	
ggc ggc acc gtc gcc att ggt ttg ctg ccc gac tac aac gcc atc ggc	451
Gly Gly Thr Val Ala Ile Gly Leu Leu Pro Asp Tyr Asn Ala Ile Gly	
105 110 115	
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Ile Trp Ala Pro Ile Leu Leu Met Phe Leu Arg Ile Leu Gln Gly Ile	
120 125 130	
gga att ggc ggc gaa tgg ggt ggc gca ctg ctc ctg gca tac gaa tac	547
Gly Ile Gly Gly Glu Trp Gly Gly Ala Leu Leu Ala Tyr Glu Tyr	
135 140 145	
gct cca aag aag cag cgt ggg ctc tac ggc gca gtt cct caa atg ggc	595
Ala Pro Lys Lys Gln Arg Gly Leu Tyr Gly Ala Val Pro Gln Met Gly	
150 155 160 165	
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Ile Ser Leu Gly Met Leu Leu Ala Ala Gly Val Ile Ser Leu Leu Thr	
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ctc atg ccg gaa gat cag ttc ctc acc tgg ggc tgg cgc atc cca ttc	691
Leu Met Pro Glu Asp Gln Phe Leu Thr Trp Gly Trp Arg Ile Pro Phe	
185 190 195	
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Val Gly Ser Ile Leu Leu Val Phe Ile Gly Leu Phe Ile Arg Asn Gly	
200 205 210	
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Leu Asp Glu Thr Pro Glu Phe Lys Arg Ile Arg Asp Ser Gly Gln Gln	
215 220 225	
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Val Lys Met Pro Leu Lys Glu Val Leu Thr Lys Tyr Trp Pro Ala Val	
230 235 240 245	
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Leu Val Ser Ile Gly Ala Lys Ala Ala Glu Thr Gly Pro Phe Tyr Ile	
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Phe Gly Thr Tyr Ile Val Ala Tyr Ala Thr Asn Phe Leu Asn Ile Arg	
265 270 275	
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Asp Asn Ile Val Leu Leu Ala Val Ala Cys Ala Ala Leu Val Ala Thr	
280 285 290	
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Ile Trp Met Pro Leu Phe Gly Ser Phe Ser Asp Arg Val Asn Arg Ala	
295 300 305	
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Val Leu Tyr Arg Ile Cys Ala Ser Ala Thr Ile Val Leu Ile Val Pro	
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tac tac ttg gtc ctc aac acc ggc gaa att tgg gca ctg ttt atc act	1123

Tyr Tyr Leu Val Leu Asn Thr Gly Glu Ile Trp Ala Leu Phe Ile Thr
 330 335 340
 acc gtg att ggc ttc ggc atc ctc tgg ggt agc gtc aac gca atc ctc 1171
 Thr Val Ile Gly Phe Gly Ile Leu Trp Gly Ser Val Asn Ala Ile Leu
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 Gly Thr Val Ile Ala Glu Asn Phe Ala Pro Glu Val Arg Tyr Thr Gly
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 Ala Thr Leu Gly Tyr Gln Val Gly Ala Ala Leu Phe Gly Gly Thr Ala
 375 380 385
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 Pro Ile Ile Ala Ala Trp Leu Phe Glu Ile Ser Gly Gly Gln Trp Trp
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 cca atc gcc gtc tac gtc gct gca tgt tgc ctt ctc tct gtg atc gcc 1363
 Pro Ile Ala Val Tyr Val Ala Ala Cys Cys Leu Leu Ser Val Ile Ala
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 35 40 45
 Tyr Phe Pro Ser Gly Asn Glu Phe Leu Ser Thr Ile Leu Ala Tyr Ala
 50 55 60
 Ser Phe Ser Leu Thr Phe Phe Phe Arg Pro Ile Gly Gly Val Ile Phe
 65 70 75 80
 Ala His Ile Gly Asp Arg Ile Gly Arg Lys Lys Thr Leu Phe Ile Thr
 85 90 95
 Leu Met Leu Met Gly Gly Gly Thr Val Ala Ile Gly Leu Leu Pro Asp
 100 105 110
 Tyr Asn Ala Ile Gly Ile Trp Ala Pro Ile Leu Leu Met Phe Leu Arg
 115 120 125
 Ile Leu Gln Gly Ile Gly Ile Gly Gly Glu Trp Gly Gly Ala Leu Leu

130	135	140
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Val Pro Gln Met Gly Ile Ser Leu Gly Met Leu Leu Ala Ala Gly Val 165 170 175		
Ile Ser Leu Leu Thr Leu Met Pro Glu Asp Gln Phe Leu Thr Trp Gly 180 185 190		
Trp Arg Ile Pro Phe Val Gly Ser Ile Leu Leu Val Phe Ile Gly Leu 195 200 205		
Phe Ile Arg Asn Gly Leu Asp Glu Thr Pro Glu Phe Lys Arg Ile Arg 210 215 220		
Asp Ser Gly Gln Gln Val Lys Met Pro Leu Lys Glu Val Leu Thr Lys 225 230 235 240		
Tyr Trp Pro Ala Val Leu Val Ser Ile Gly Ala Lys Ala Ala Glu Thr 245 250 255		
Gly Pro Phe Tyr Ile Phe Gly Thr Tyr Ile Val Ala Tyr Ala Thr Asn 260 265 270		
Phe Leu Asn Ile Arg Asp Asn Ile Val Leu Leu Ala Val Ala Cys Ala 275 280 285		
Ala Leu Val Ala Thr Ile Trp Met Pro Leu Phe Gly Ser Phe Ser Asp 290 295 300		
Arg Val Asn Arg Ala Val Leu Tyr Arg Ile Cys Ala Ser Ala Thr Ile 305 310 315 320		
Val Leu Ile Val Pro Tyr Tyr Leu Val Leu Asn Thr Gly Glu Ile Trp 325 330 335		
Ala Leu Phe Ile Thr Thr Val Ile Gly Phe Gly Ile Leu Trp Gly Ser 340 345 350		
Val Asn Ala Ile Leu Gly Thr Val Ile Ala Glu Asn Phe Ala Pro Glu 355 360 365		
Val Arg Tyr Thr Gly Ala Thr Leu Gly Tyr Gln Val Gly Ala Ala Leu 370 375 380		
Phe Gly Gly Thr Ala Pro Ile Ile Ala Ala Trp Leu Phe Glu Ile Ser 385 390 395 400		
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Leu Ser Val Ile Ala Ser Phe Phe Ile Gln Arg Val Ala His Gln Glu 420 425 430		

Asn

<210> 333

<211> 1524
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1501)
 <223> RXA02507

<400> 333

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                                         Met Ser Glu Gln Leu
                                         1           5

cag ggt gta act cac tcc gaa tca act ccg ggc aag acg ccc aag cga 163
Gln Gly Val Thr His Ser Glu Ser Thr Pro Gly Lys Thr Pro Lys Arg
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gca gca cta tcc agc tgg atc ggc tca gct ctc gaa tac tac gac ttc 211
Ala Ala Leu Ser Ser Trp Ile Gly Ser Ala Leu Glu Tyr Tyr Asp Phe
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gct gtt tac gga acc gct gca gcg ctg gtt ctt aac cac ctc ttc ttc 259
Ala Val Tyr Gly Thr Ala Ala Ala Leu Val Leu Asn His Leu Phe Phe
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cca gct gat act tca cca ggc atc gca att ttg gct gcg atg ggt acc 307
Pro Ala Asp Thr Ser Pro Gly Ile Ala Ile Leu Ala Ala Met Gly Thr
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Val Gly Val Ala Tyr Val Val Arg Pro Leu Gly Ala Leu Ile Met Gly
                        70                        75                        80                        85

cca tta ggt gac cgt tac gga cgt aaa ttt gtc ctc atg ctg tgc ctc 403
Pro Leu Gly Asp Arg Tyr Gly Arg Lys Phe Val Leu Met Leu Cys Leu
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ttc ctg att gga gca tcc act ttc gca gtt ggc tgc ttg cca aca ttt 451
Phe Leu Ile Gly Ala Ser Thr Phe Ala Val Gly Cys Leu Pro Thr Phe
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gat cag gtc ggt tac ttg gct ccg gca ctg ttg gtg ctg tgc cgt gtg 499
Asp Gln Val Gly Tyr Leu Ala Pro Ala Leu Leu Val Leu Cys Arg Val
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                        135                        140                        145

tct ttg gag cac gcc gat gag cgt cac cgc gca ttt act gct agc tgg 595
Ser Leu Glu His Ala Asp Glu Arg His Arg Ala Phe Thr Ala Ser Trp
                        150                        155                        160                        165

act ctt cac gga acc cag ttc ggt acc ttg ctg gca acc gga gta ttt 643
Thr Leu His Gly Thr Gln Phe Gly Thr Leu Leu Ala Thr Gly Val Phe
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atc cca ttc acc ttg ttc ctg agt gaa gat gct cta atg tca tgg ggt 691

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Trp	Arg	Val	Pro	Phe	Trp	Leu	Ser	Ala	Ala	Val	Val	Leu	Val	Ala	Phe	
		200					205					210				
ctc	atc	cgt	cgt	gga	ctg	gaa	gag	cca	cca	gca	ttc	cgt	gaa	aac	aag	787
Leu	Ile	Arg	Arg	Gly	Leu	Glu	Glu	Pro	Pro	Ala	Phe	Arg	Glu	Asn	Lys	
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gaa	gca	gtt	gca	ggc	gca	gca	tct	cca	ctg	gcg	atg	acc	ttg	cgt	tac	835
Glu	Ala	Val	Ala	Gly	Ala	Ala	Ser	Pro	Leu	Ala	Met	Thr	Leu	Arg	Tyr	
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His	Lys	Ala	Ala	Val	Ala	Arg	Val	Ala	Ile	Ala	Ala	Met	Ile	Asn	Ser	
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Val	Asn	Ile	Val	Phe	Thr	Val	Trp	Ala	Leu	Ser	Phe	Ala	Thr	Asn	Ile	
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Val	Gly	Leu	Asp	Arg	Ser	Thr	Val	Leu	Leu	Val	Pro	Val	Val	Ala	Asn	
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Leu	Val	Ala	Leu	Ile	Ala	Ile	Pro	Leu	Ser	Gly	Met	Leu	Ala	Asp	Arg	
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Ile	Gly	Arg	Arg	Pro	Val	Phe	Ile	Met	Gly	Ala	Ile	Gly	Gly	Gly	Leu	
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Ile	Phe	Phe	Met	Gly	Val	Leu	Met	Ser	Gly	Leu	Leu	Tyr	Ser	Met	Gly	
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aac	gcc	gtg	tgg	cca	gcg	ttc	tac	gca	gaa	atg	ttc	cca	acc	tct	gtg	1219
Asn	Ala	Val	Trp	Pro	Ala	Phe	Tyr	Ala	Glu	Met	Phe	Pro	Thr	Ser	Val	
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cgt	gtc	acc	ggc	ttg	gct	ctt	gga	act	cag	att	ggc	ttc	gca	gtc	tct	1267
Arg	Val	Thr	Gly	Leu	Ala	Leu	Gly	Thr	Gln	Ile	Gly	Phe	Ala	Val	Ser	
	375					380					385					
ggc	ggc	ttc	gtc	cca	gtt	atc	gca	tcc	gcg	ctt	gct	ggc	gat	cag	ggc	1315
Gly	Gly	Phe	Val	Pro	Val	Ile	Ala	Ser	Ala	Leu	Ala	Gly	Asp	Gln	Gly	
390					395				400					405		
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Asp	Gln	Trp	Met	Lys	Val	Ser	Ile	Phe	Val	Gly	Val	Val	Cys	Val	Ile	
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tct	gca	ctg	gtt	gcc	atg	acc	gct	aag	gaa	acc	aag	gct	ctg	act	ctg	1411
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Glu	Tyr	Tyr	Asp	Phe	Ala	Val	Tyr	Gly	Thr	Ala	Ala	Ala	Leu	Val	Leu	
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Ala	Ala	Met	Gly	Thr	Val	Gly	Val	Ala	Tyr	Val	Val	Arg	Pro	Leu	Gly	
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Ala	Leu	Ile	Met	Gly	Pro	Leu	Gly	Asp	Arg	Tyr	Gly	Arg	Lys	Phe	Val	
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Leu	Met	Leu	Cys	Leu	Phe	Leu	Ile	Gly	Ala	Ser	Thr	Phe	Ala	Val	Gly	
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Cys	Leu	Pro	Thr	Phe	Asp	Gln	Val	Gly	Tyr	Leu	Ala	Pro	Ala	Leu	Leu	
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Val	Leu	Cys	Arg	Val	Ile	Gln	Gly	Leu	Ser	Ala	Ser	Gly	Glu	Gln	Ser	
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Ala	Thr	Gly	Val	Phe	Ile	Pro	Phe	Thr	Leu	Phe	Leu	Ser	Glu	Asp	Ala	
			180					185					190			
Leu	Met	Ser	Trp	Gly	Trp	Arg	Val	Pro	Phe	Trp	Leu	Ser	Ala	Ala	Val	
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Val	Leu	Val	Ala	Phe	Leu	Ile	Arg	Arg	Gly	Leu	Glu	Glu	Pro	Pro	Ala	
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Phe Arg Glu Asn Lys Glu Ala Val Ala Gly Ala Ala Ser Pro Leu Ala
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 Met Thr Leu Arg Tyr His Lys Ala Ala Val Ala Arg Val Ala Ile Ala
 245 250 255
 Ala Met Ile Asn Ser Val Asn Ile Val Phe Thr Val Trp Ala Leu Ser
 260 265 270
 Phe Ala Thr Asn Ile Val Gly Leu Asp Arg Ser Thr Val Leu Leu Val
 275 280 285
 Pro Val Val Ala Asn Leu Val Ala Leu Ile Ala Ile Pro Leu Ser Gly
 290 295 300
 Met Leu Ala Asp Arg Ile Gly Arg Arg Pro Val Phe Ile Met Gly Ala
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 Ile Gly Gly Gly Leu Ala Met Asn Gly Tyr Leu Gly Ala Ile Tyr Ser
 325 330 335
 Gly Asn Trp Thr Met Ile Phe Phe Met Gly Val Leu Met Ser Gly Leu
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 Leu Tyr Ser Met Gly Asn Ala Val Trp Pro Ala Phe Tyr Ala Glu Met
 355 360 365
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 370 375 380
 Gly Phe Ala Val Ser Gly Gly Phe Val Pro Val Ile Ala Ser Ala Leu
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 Ala Gly Asp Gln Gly Asp Gln Trp Met Lys Val Ser Ile Phe Val Gly
 405 410 415
 Val Val Cys Val Ile Ser Ala Leu Val Ala Met Thr Ala Lys Glu Thr
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<212> DNA

<213> *Corynebacterium glutamicum*

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<222> (21)..(932)

<223> RXA00445

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Phe	Phe	Gly	Asp	Ala	Ile	Ala	Leu	Asn	Asp	Val	Ser	Leu	Thr	Val	Pro		
				15				20				25					
tca	ggc	tcc	atc	acc	gcc	atc	atc	ggg	cgc	tcc	ggg	agc	ggt	aaa	acc	149	
Ser	Gly	Ser	Ile	Thr	Ala	Ile	Ile	Gly	Pro	Ser	Gly	Ser	Gly	Lys	Thr		
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acg	tta	ctg	cgt	ttg	ctg	gca	ggc	ctt	gat	tca	ccc	gat	gaa	ggc	acc	197	
Thr	Leu	Leu	Arg	Leu	Leu	Ala	Gly	Leu	Asp	Ser	Pro	Asp	Glu	Gly	Thr		
				45				50				55					
gtg	agc	att	ggg	aat	aag	atc	gcc	aag	ctg	ggt	gac	act	gcg	ctg	tgt	245	
Val	Ser	Ile	Gly	Asn	Lys	Ile	Ala	Lys	Leu	Gly	Asp	Thr	Ala	Leu	Cys		
				60				65				70				75	
ttc	cag	gat	tcg	cct	ttg	tat	ccg	cac	ctt	aat	gtg	tggt	gaa	aac	gtg	293	
Phe	Gln	Asp	Ser	Pro	Leu	Tyr	Pro	His	Leu	Asn	Val	Trp	Glu	Asn	Val		
				80				85				90					
gca	ttt	ccg	ctc	aag	ctc	aaa	gcc	acc	aat	act	gca	gat	gag	gtg	gtg	341	
Ala	Phe	Pro	Leu	Lys	Leu	Lys	Ala	Thr	Asn	Thr	Ala	Asp	Glu	Val	Val		
				95				100				105					
aaa	aag	cgg	gtg	agt	gat	gtt	ttg	gaa	atg	ctc	gaa	att	gct	ccc	ctc	389	
Lys	Lys	Arg	Val	Ser	Asp	Val	Leu	Glu	Met	Leu	Glu	Ile	Ala	Pro	Leu		
				110				115				120					
gcc	cgc	cgg	aaa	att	acc	gaa	ctc	tcc	ggc	ggg	caa	aaa	cag	cgc	gtc	437	
Ala	Arg	Arg	Lys	Ile	Thr	Glu	Leu	Ser	Gly	Gly	Gln	Lys	Gln	Arg	Val		
				125				130				135					
ggc	att	gct	cga	gca	ctg	gtc	aga	gac	gta	gag	gtt	tac	ctt	ttc	gac	485	
Gly	Ile	Ala	Arg	Ala	Leu	Val	Arg	Asp	Val	Glu	Val	Tyr	Leu	Phe	Asp		
				140				145				150				155	
gaa	ccg	atg	gcc	cac	ctc	gac	caa	gcc	tta	gcc	cgc	gat	att	gtg	gcc	533	
Glu	Pro	Met	Ala	His	Leu	Asp	Gln	Ala	Leu	Ala	Arg	Asp	Ile	Val	Ala		
				160				165				170					
gat	ctg	cgc	aaa	att	caa	caa	tcg	ttg	gga	ctg	acg	ttt	gta	tac	gtc	581	
Asp	Leu	Arg	Lys	Ile	Gln	Gln	Ser	Leu	Gly	Leu	Thr	Phe	Val	Tyr	Val		
				175				180				185					
acc	cac	agc	aaa	tcc	gag	gca	ttc	gcg	ctc	gcc	gac	caa	att	gtc	gtg	629	
Thr	His	Ser	Lys	Ser	Glu	Ala	Phe	Ala	Leu	Ala	Asp	Gln	Ile	Val	Val		
				190				195				200					
ctg	gta	gat	ggc	caa	gtc	gcg	cag	gtt	ggt	gag	gcg	gag	gag	ctc	gtc	677	
Leu	Val	Asp	Gly	Gln	Val	Ala	Gln	Val	Gly	Glu	Ala	Glu	Glu	Leu	Val		
				205				210				215					
gaa	aag	cca	aaa	acc	cta	gaa	ata	gcc	gag	ttc	ctc	tcc	ccc	acc	gag	725	
Glu	Lys	Pro	Lys	Thr	Leu	Glu	Ile	Ala	Glu	Phe	Leu	Ser	Pro	Thr	Glu		
				220				225				230				235	
ctc	aat	gtg	cgc	cgg	cgt	ggg	gac	gcc	gtg	gag	gca	tggt	cga	ccc	gaa	773	
Leu	Asn	Val	Arg	Arg	Arg	Gly	Asp	Ala	Val	Glu	Ala	Trp	Arg	Pro	Glu		

	240	245	250	
gac acc cag ctc gcc cgc ggt ggc act gcg acc gtg gaa gcc gtg acg				821
Asp Thr Gln Leu Ala Arg Gly Gly Thr Ala Thr Val Glu Ala Val Thr				
	255	260	265	
tat ttg ggc cgc gag tgg ctt gta caa acc acc gag ggg cac gcc gtg				869
Tyr Leu Gly Arg Glu Trp Leu Val Gln Thr Thr Glu Gly His Ala Val				
	270	275	280	
tcg gag gaa aaa ttc gac gtc ggc gaa agc gtc acg cta acc cag aag				917
Ser Glu Glu Lys Phe Asp Val Gly Glu Ser Val Thr Leu Thr Gln Lys				
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aag gtg ttt agt ttc tagccgcctg caaaaggagg gag				955
Lys Val Phe Ser Phe				
300				

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<211> 304

<212> PRT

<213> Corynebacterium glutamicum

<400> 336

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Ala Ile Ile Gly Pro Ser Gly Ser Gly Lys Thr Thr Leu Leu Arg Leu				
	35	40	45	
Leu Ala Gly Leu Asp Ser Pro Asp Glu Gly Thr Val Ser Ile Gly Asn				
	50	55	60	
Lys Ile Ala Lys Leu Gly Asp Thr Ala Leu Cys Phe Gln Asp Ser Pro				
	65	70	75	80
Leu Tyr Pro His Leu Asn Val Trp Glu Asn Val Ala Phe Pro Leu Lys				
	85	90	95	
Leu Lys Ala Thr Asn Thr Ala Asp Glu Val Val Lys Lys Arg Val Ser				
	100	105	110	
Asp Val Leu Glu Met Leu Glu Ile Ala Pro Leu Ala Arg Arg Lys Ile				
	115	120	125	
Thr Glu Leu Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala Arg Ala				
	130	135	140	
Leu Val Arg Asp Val Glu Val Tyr Leu Phe Asp Glu Pro Met Ala His				
	145	150	155	160
Leu Asp Gln Ala Leu Ala Arg Asp Ile Val Ala Asp Leu Arg Lys Ile				
	165	170	175	
Gln Gln Ser Leu Gly Leu Thr Phe Val Tyr Val Thr His Ser Lys Ser				
	180	185	190	

Glu Ala Phe Ala Leu Ala Asp Gln Ile Val Val Leu Val Asp Gly Gln
 195 200 205
 Val Ala Gln Val Gly Glu Ala Glu Glu Leu Val Glu Lys Pro Lys Thr
 210 215 220
 Leu Glu Ile Ala Glu Phe Leu Ser Pro Thr Glu Leu Asn Val Arg Arg
 225 230 235 240
 Arg Gly Asp Ala Val Glu Ala Trp Arg Pro Glu Asp Thr Gln Leu Ala
 245 250 255
 Arg Gly Gly Thr Ala Thr Val Glu Ala Val Thr Tyr Leu Gly Arg Glu
 260 265 270
 Trp Leu Val Gln Thr Thr Glu Gly His Ala Val Ser Glu Glu Lys Phe
 275 280 285
 Asp Val Gly Glu Ser Val Thr Leu Thr Gln Lys Lys Val Phe Ser Phe
 290 295 300

<210> 337
 <211> 491
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(468)
 <223> RXA02353

<400> 337
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 tac gaa gca gcc cgc gtc gat ggc gca acc gcg tgg cag caa ttc acc 96
 Tyr Glu Ala Ala Arg Val Asp Gly Ala Thr Ala Trp Gln Gln Phe Thr
 20 25 30
 aag atc acc ctc ccg ctg gtg cgc cca gct ttg atg gtg gca gta ctc 144
 Lys Ile Thr Leu Pro Leu Val Arg Pro Ala Leu Met Val Ala Val Leu
 35 40 45
 ttc cgc acc ctc gat gcg cta cgc atg tat gac ctc ccc gtc atc atg 192
 Phe Arg Thr Leu Asp Ala Leu Arg Met Tyr Asp Leu Pro Val Ile Met
 50 55 60
 atc tcc agc tcc tcc aac tcc ccc acc gct gtt atc tcc cag ctg gtt 240
 Ile Ser Ser Ser Ser Asn Ser Pro Thr Ala Val Ile Ser Gln Leu Val
 65 70 75 80
 gtg gaa gac atg cgc caa aac aac ttc aac tcc gct tcc gcc ctt tcc 288
 Val Glu Asp Met Arg Gln Asn Asn Phe Asn Ser Ala Ser Ala Leu Ser
 85 90 95
 aca ctg atc ttc ctg ctg atc ttc ttc gtg gcg ttc atc atg atc cga 336
 Thr Leu Ile Phe Leu Leu Ile Phe Phe Val Ala Phe Ile Met Ile Arg
 100 105 110

ttc ctc ggc gca gat gtt tcg ggc caa cgc gga ata aag aaa aag aaa 384
 Phe Leu Gly Ala Asp Val Ser Gly Gln Arg Gly Ile Lys Lys Lys Lys
 115 120 125

ctg ggc gga acc aag gat gag aaa ccc acc gct aag gat gct gtt gta 432
 Leu Gly Gly Thr Lys Asp Glu Lys Pro Thr Ala Lys Asp Ala Val Val
 130 135 140

aag gcc gat tct gct gtg aag gaa gcc gct aag cca tgactaaacg 478
 Lys Ala Asp Ser Ala Val Lys Glu Ala Ala Lys Pro
 145 150 155

aacaaaagga ctc 491

<210> 338

<211> 156

<212> PRT

<213> Corynebacterium glutamicum

<400> 338

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Tyr Glu Ala Ala Arg Val Asp Gly Ala Thr Ala Trp Gln Gln Phe Thr
 20 25 30

Lys Ile Thr Leu Pro Leu Val Arg Pro Ala Leu Met Val Ala Val Leu
 35 40 45

Phe Arg Thr Leu Asp Ala Leu Arg Met Tyr Asp Leu Pro Val Ile Met
 50 55 60

Ile Ser Ser Ser Ser Asn Ser Pro Thr Ala Val Ile Ser Gln Leu Val
 65 70 75 80

Val Glu Asp Met Arg Gln Asn Asn Phe Asn Ser Ala Ser Ala Leu Ser
 85 90 95

Thr Leu Ile Phe Leu Leu Ile Phe Phe Val Ala Phe Ile Met Ile Arg
 100 105 110

Phe Leu Gly Ala Asp Val Ser Gly Gln Arg Gly Ile Lys Lys Lys Lys
 115 120 125

Leu Gly Gly Thr Lys Asp Glu Lys Pro Thr Ala Lys Asp Ala Val Val
 130 135 140

Lys Ala Asp Ser Ala Val Lys Glu Ala Ala Lys Pro
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<210> 339

<211> 921

<212> DNA

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<220>

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<222> (101) .. (898)

<223> RXA01297

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Met Val Leu Ala Ile Leu Phe Ile Gly Leu Pro Leu Val Phe Ile Val
10 15 20

ctg act agc ttc aag cag cag tca gag att tac acc cag ccg gtc acg 211
Leu Thr Ser Phe Lys Gln Gln Ser Glu Ile Tyr Thr Gln Pro Val Thr
25 30 35

tgg ttc cct tcg gaa ttt aat ttc gat aac tat gca aat gtt ttc gag 259
 Trp Phe Pro Ser Glu Phe Asn Phe Asp Asn Tyr Ala Asn Val Phe Glu
 40 45 50

cgg gtt ccg ttc ctg aac tac ttc cgc aac tcg atc atc atc acg gtt 307
Arg Val Pro Phe Leu Asn Tyr Phe Arg Asn Ser Ile Ile Ile Thr Val
55 60 65

att ttg tgt ctg gtg aag att atc ttg ggt gtg atc tct gca tat gcg 355
Ile Leu Cys Leu Val Lys Ile Ile Leu Gly Val Ile Ser Ala Tyr Ala
70 75 80 85

ttg tcg att ttg cgc ttc ccg ggt cga aac ctt gtg ttc ttg ctg gtt 403
Leu Ser Ile Leu Arg Phe Pro Gly Arg Asn Leu Val Phe Leu Leu Val
90 95 100

atc tcc gcg ctg atg gtg cct tcc gaa gtg act gtt att tcc aac tat 451
Ile Ser Ala Leu Met Val Pro Ser Glu Val Thr Val Ile Ser Asn Tyr
105 110 115

gcg ttg gtc agt cag ctt ggt tgg cgc gat acc tac cag ggc atc atc 499
Ala Leu Val Ser Gln Leu Gly Trp Arg Asp Thr Tyr Gln Gly Ile Ile
120 125 130

ggt ccg cta gcg ggt att gct ttc gga acg ttc ctc atg cgt aac cac 547
Val Pro Leu Ala Gly Ile Ala Phe Gly Thr Phe Leu Met Arg Asn His
135 140 145

ttc	atg	tct	att	cct	tct	gag	ctc	att	gaa	gct	gcg	cga	atg	gat	cac	595
Phe	Met	Ser	Ile	Pro	Ser	Glu	Leu	Ile	Glu	Ala	Ala	Arg	Met	Asp	His	
150					155					160					165	

tgt	gga	cac	ttc	agg	ttg	ctc	tgg	aag	gtt	ttg	ctt	cca	atc	tct	atg	643
Cys	Gly	His	Phe	Arg	Leu	Leu	Trp	Lys	Val	Leu	Leu	Pro	Ile	Ser	Met	
				170					175					180		

cct acg ttg gtg gcg ttc tcc atg atc acc gtg gtg aat gaa tgg aac 691
Pro Thr Leu Val Ala Phe Ser Met Ile Thr Val Val Asn Glu Trp Asn
185 190 195

caa tac ctg tgg cct ttc ctg atg gca gaa acc gat aat tca gca act 739
Gln Tyr Leu Trp Pro Phe Leu Met Ala Glu Thr Asp Asn Ser Ala Thr
200 205 210

ctg ccc att ggt ttg acc atg ctt caa aac aat gag ggt gtc tcc aac 787

Leu Pro Ile Gly Leu Thr Met Leu Gln Asn Asn Glu Gly Val Ser Asn
 215 220 225
 tgg gga cct gtc atg gcc gca acg atc atg acc atg ttg cct gtg ctt 835
 Trp Gly Pro Val Met Ala Ala Thr Ile Met Thr Met Leu Pro Val Leu
 230 235 240 245
 gtg atg ttc ttg gca ctg cag gag tac atg atc aag gga ctt atc tcc 883
 Val Met Phe Leu Ala Leu Gln Glu Tyr Met Ile Lys Gly Leu Ile Ser
 250 255 260
 ggc gcc gtc aag ggc taaaaacttc tcgctaaaaa ctt 921
 Gly Ala Val Lys Gly
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<210> 340
 <211> 266
 <212> PRT
 <213> Corynebacterium glutamicum

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 Thr Gln Pro Val Thr Trp Phe Pro Ser Glu Phe Asn Phe Asp Asn Tyr
 35 40 45
 Ala Asn Val Phe Glu Arg Val Pro Phe Leu Asn Tyr Phe Arg Asn Ser
 50 55 60
 Ile Ile Ile Thr Val Ile Leu Cys Leu Val Lys Ile Ile Leu Gly Val
 65 70 75 80
 Ile Ser Ala Tyr Ala Leu Ser Ile Leu Arg Phe Pro Gly Arg Asn Leu
 85 90 95
 Val Phe Leu Leu Val Ile Ser Ala Leu Met Val Pro Ser Glu Val Thr
 100 105 110
 Val Ile Ser Asn Tyr Ala Leu Val Ser Gln Leu Gly Trp Arg Asp Thr
 115 120 125
 Tyr Gln Gly Ile Ile Val Pro Leu Ala Gly Ile Ala Phe Gly Thr Phe
 130 135 140
 Leu Met Arg Asn His Phe Met Ser Ile Pro Ser Glu Leu Ile Glu Ala
 145 150 155 160
 Ala Arg Met Asp His Cys Gly His Phe Arg Leu Leu Trp Lys Val Leu
 165 170 175
 Leu Pro Ile Ser Met Pro Thr Leu Val Ala Phe Ser Met Ile Thr Val
 180 185 190
 Val Asn Glu Trp Asn Gln Tyr Leu Trp Pro Phe Leu Met Ala Glu Thr
 195 200 205

Asp Asn Ser Ala Thr Leu Pro Ile Gly Leu Thr Met Leu Gln Asn Asn
 210 215 220

Glu Gly Val Ser Asn Trp Gly Pro Val Met Ala Ala Thr Ile Met Thr
 225 230 235 240

Met Leu Pro Val Leu Val Met Phe Leu Ala Leu Gln Glu Tyr Met Ile
 245 250 255

Lys Gly Leu Ile Ser Gly Ala Val Lys Gly
 260 265

<210> 341
 <211> 899
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(876)
 <223> RXS00088

<400> 341

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Val Ala Ala Thr Asp Asn Arg Ala Phe Glu Leu Leu Asp Arg Trp Gly	
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gta gag ctc gtt gca gct cca ctt cag ctg gtt cca ttt acc gtt acg	144
Val Glu Leu Val Ala Ala Pro Leu Gln Leu Val Pro Phe Thr Val Thr	
35 40 45	
ggc tac acc gaa gag ggc ggc gtc gct aac ctt ggc tcc cac cgc gag	192
Gly Tyr Thr Glu Glu Gly Gly Val Ala Asn Leu Gly Ser His Arg Glu	
50 55 60	
cca gac ctg gaa gca ctt gct gct gca cag cct tcc ctg atc atc aac	240
Pro Asp Leu Glu Ala Leu Ala Ala Ala Gln Pro Ser Leu Ile Ile Asn	
65 70 75 80	
ggc cag cgc ttc gct cag tac tac gat gac atc att gcc ctg aac cct	288
Gly Gln Arg Phe Ala Gln Tyr Tyr Asp Asp Ile Ile Ala Leu Asn Pro	
85 90 95	
gac gca acc gtt gtt gag cta gac cca cgc gat ggc gag cca ctt gac	336
Asp Ala Thr Val Val Glu Leu Asp Pro Arg Asp Gly Glu Pro Leu Asp	
100 105 110	
cag gag ctt atc cgc cag gct gaa acc ctg ggt gag atc ttc ggc gaa	384
Gln Glu Leu Ile Arg Gln Ala Glu Thr Leu Gly Glu Ile Phe Gly Glu	
115 120 125	
gaa gaa gat gct gca aag atc gtt gct gat ttc gag tcc gca ctt gag	432
Glu Glu Asp Ala Ala Lys Ile Val Ala Asp Phe Glu Ser Ala Leu Glu	
130 135 140	
cgc gct aag acc gca tac gca gca atc tcc gac cag acc gtc atg gca	480

Arg Ala Lys Thr Ala Tyr Ala Ala Ile Ser Asp Gln Thr Val Met Ala
 145 150 155 160
 gtt aac gtt tcc ggc gga aac att ggc tac atc gct cct tcc gtt gga 528
 Val Asn Val Ser Gly Gly Asn Ile Gly Tyr Ile Ala Pro Ser Val Gly
 165 170 175
 cgc acc tac ggt cca atc ttc gac ctg gtt gga ctc acc cca gca ctc 576
 Arg Thr Tyr Gly Pro Ile Phe Asp Leu Val Gly Leu Thr Pro Ala Leu
 180 185 190
 gag gtt ggc aac gcg tcc tcc gac cac gag ggc gac gac att aac gtc 624
 Glu Val Gly Asn Ala Ser Ser Asp His Glu Gly Asp Asp Ile Asn Val
 195 200 205
 gaa gca atc gca gct gca aac cca gac ctg atc ctg gtc atg gac cgc 672
 Glu Ala Ile Ala Ala Ala Asn Pro Asp Leu Ile Leu Val Met Asp Arg
 210 215 220
 gat ggt ggc acc agc acc cgc aac gaa gct gat tac gtt cca gca gag 720
 Asp Gly Gly Thr Ser Thr Arg Asn Glu Ala Asp Tyr Val Pro Ala Glu
 225 230 235 240
 cag atc gtc tcc gac aat gaa gca ctg gca aac gtc aag gct gtc acc 768
 Gln Ile Val Ser Asp Asn Glu Ala Leu Ala Asn Val Lys Ala Val Thr
 245 250 255
 gac gga tac gtt tac tac gca cct gca gat acc tac acc aac gaa aac 816
 Asp Gly Tyr Val Tyr Tyr Ala Pro Ala Asp Thr Tyr Thr Asn Glu Asn
 260 265 270
 atc atc acc tac acc gag atc ctc aac ggc atg gca gat atg ttc gag 864
 Ile Ile Thr Tyr Thr Glu Ile Leu Asn Gly Met Ala Asp Met Phe Glu
 275 280 285
 aag gca gct cag taggggatcg atccacact gac 899
 Lys Ala Ala Gln
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<210> 342

<211> 292

<212> PRT

<213> Corynebacterium glutamicum

<400> 342

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 20 25 30
 Val Glu Leu Val Ala Ala Pro Leu Gln Leu Val Pro Phe Thr Val Thr
 35 40 45
 Gly Tyr Thr Glu Glu Gly Gly Val Ala Asn Leu Gly Ser His Arg Glu
 50 55 60
 Pro Asp Leu Glu Ala Leu Ala Ala Ala Gln Pro Ser Leu Ile Ile Asn
 65 70 75 80


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<400> 343
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                                     Met Ser Ser Lys His
                                     1           5
cct ttg aag cgc act gcc gtt act gtt ttt gca ctc ggc gct tcc gct 163

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Pro	Leu	Lys	Arg	Thr	Ala	Val	Thr	Val	Phe	Ala	Leu	Gly	Ala	Ser	Ala		
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Ala	Leu	Leu	Val	Ala	Cys	Ser	Glu	Pro	Ser	Glu	Asp	Val	Ser	Thr	Ala		
			25					30					35				
gag	acc	acc	act	gca	agc	tct	tcc	gct	aac	gca	tcc	gat	gca	gcc	ggt	259	
Glu	Thr	Thr	Thr	Ala	Ser	Ser	Ser	Ala	Asn	Ala	Ser	Asp	Ala	Ala	Gly		
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Glu	Lys	Val	Thr	Ile	Thr	Val	Tyr	Thr	Ser	Glu	Pro	Glu	Glu	Lys	Val		
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Asp	Glu	Ile	Asn	Lys	Ala	Phe	Met	Glu	Ala	Asn	Pro	Asp	Ile	Glu	Val		
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Glu	Val	Tyr	Arg	Ala	Gly	Thr	Gly	Asp	Leu	Thr	Ala	Arg	Ile	Glu	Ala		
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gaa	aag	gca	tcc	ggg	tct	atc	gag	gct	gat	gtg	ttg	tgg	gct	gcg	gat	451	
Glu	Lys	Ala	Ser	Gly	Ser	Ile	Glu	Ala	Asp	Val	Leu	Trp	Ala	Ala	Asp		
			105					110					115				
gct	gca	acc	ttt	gaa	act	tat	gca	gca	cag	ggc	gac	ctt	gca	gag	ctg	499	
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			120				125					130					
gaa	gat	gtt	gag	act	tcc	gac	atc	att	gaa	gag	gct	ctg	gat	gct	gag	547	
Glu	Asp	Val	Glu	Thr	Ser	Asp	Ile	Ile	Glu	Glu	Ala	Leu	Asp	Ala	Glu		
	135					140					145						
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Asn	Phe	Tyr	Val	Gly	Thr	Arg	Ile	Ile	Pro	Thr	Val	Ile	Ala	Tyr	Asn		
	150				155					160					165		
act	gaa	gtt	gtt	gat	cag	gct	gag	ctt	cct	acg	tct	tgg	gct	gat	ctg	643	
Thr	Glu	Val	Val	Asp	Gln	Ala	Glu	Leu	Pro	Thr	Ser	Trp	Ala	Asp	Leu		
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act	gat	cct	aag	tat	gca	ggc	caa	ctg	gtc	atg	ccg	gat	cca	gct	gtg	691	
Thr	Asp	Pro	Lys	Tyr	Ala	Gly	Gln	Leu	Val	Met	Pro	Asp	Pro	Ala	Val		
			185				190						195				
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Leu	Gly	Glu	Ala	Trp	Ile	Thr	Ala	Leu	Gly	Glu	Asn	Gln	Pro	Met	Ile		
	215					220					225						
gct	cag	tcc	aac	ggc	cca	acc	tcc	cag	gag	atc	gct	ggc	ggg	ggc	cac	835	
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	230				235					240					245		
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Pro	Val	Gly	Ile	Val	Val	Asp	Tyr	Leu	Val	Arg	Asp	Leu	Ala	Ala	Ala		

250										255					260					
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Gly Ser Pro Ile Asp Thr Ile Tyr Ala Ser Glu Gly Ser Pro Tyr Ile																				
265 270 275																				
act gag cct gca ggt gtg ttc gct gat tct gaa aag aag gaa gca gcc	979																			
Thr Glu Pro Ala Gly Val Phe Ala Asp Ser Glu Lys Lys Glu Ala Ala																				
280 285 290																				
gag cgc tac atc aac ttc ctg ctg tct gtt gaa ggc cag gaa atc gca	1027																			
Glu Arg Tyr Ile Asn Phe Leu Leu Ser Val Glu Gly Gln Glu Ile Ala																				
295 300 305																				
gtt gag cag gca tac ctg cca gtg cgt gaa gat gtc gga act cca gag	1075																			
Val Glu Gln Ala Tyr Leu Pro Val Arg Glu Asp Val Gly Thr Pro Glu																				
310 315 320 325																				
ggc acc ccc gag ttg gct gac atc gag ctg atg acc cct gac ctg gag	1123																			
Gly Thr Pro Glu Leu Ala Asp Ile Glu Leu Met Thr Pro Asp Leu Glu																				
330 335 340																				
gtt gta acc gct gat aag gcg gct gct gtt gag ttc ttc caa aac gca	1171																			
Val Val Thr Ala Asp Lys Ala Ala Val Glu Phe Phe Gln Asn Ala																				
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atg aac tagttttcct atgcagitat ctc	1200																			
Met Asn																				

<210> 344

<211> 359

<212> PRT

<213> Corynebacterium glutamicum

<400> 344

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Leu Gly Ala Ser Ala Ala Leu Leu Val Ala Cys Ser Glu Pro Ser Glu	
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35 40 45	
Ser Asp Ala Ala Gly Glu Lys Val Thr Ile Thr Val Tyr Thr Ser Glu	
50 55 60	
Pro Glu Glu Lys Val Asp Glu Ile Asn Lys Ala Phe Met Glu Ala Asn	
65 70 75 80	
Pro Asp Ile Glu Val Glu Val Tyr Arg Ala Gly Thr Gly Asp Leu Thr	
85 90 95	
Ala Arg Ile Glu Ala Glu Lys Ala Ser Gly Ser Ile Glu Ala Asp Val	
100 105 110	
Leu Trp Ala Ala Asp Ala Ala Thr Phe Glu Thr Tyr Ala Ala Gln Gly	
115 120 125	

Asp Leu Ala Glu Leu Glu Asp Val Glu Thr Ser Asp Ile Ile Glu Glu
 130 135 140
 Ala Leu Asp Ala Glu Asn Phe Tyr Val Gly Thr Arg Ile Ile Pro Thr
 145 150 155 160
 Val Ile Ala Tyr Asn Thr Glu Val Val Asp Gln Ala Glu Leu Pro Thr
 165 170 175
 Ser Trp Ala Asp Leu Thr Asp Pro Lys Tyr Ala Gly Gln Leu Val Met
 180 185 190
 Pro Asp Pro Ala Val Ser Gly Ala Ala Ala Phe Asn Ala Ser Val Trp
 195 200 205
 Lys Asn Asp Pro Ala Leu Gly Glu Ala Trp Ile Thr Ala Leu Gly Glu
 210 215 220
 Asn Gln Pro Met Ile Ala Gln Ser Asn Gly Pro Thr Ser Gln Glu Ile
 225 230 235 240
 Ala Gly Gly Gly His Pro Val Gly Ile Val Val Asp Tyr Leu Val Arg
 245 250 255
 Asp Leu Ala Ala Ala Gly Ser Pro Ile Asp Thr Ile Tyr Ala Ser Glu
 260 265 270
 Gly Ser Pro Tyr Ile Thr Glu Pro Ala Gly Val Phe Ala Asp Ser Glu
 275 280 285
 Lys Lys Glu Ala Ala Glu Arg Tyr Ile Asn Phe Leu Leu Ser Val Glu
 290 295 300
 Gly Gln Glu Ile Ala Val Glu Gln Ala Tyr Leu Pro Val Arg Glu Asp
 305 310 315 320
 Val Gly Thr Pro Glu Gly Thr Pro Glu Leu Ala Asp Ile Glu Leu Met
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 Thr Pro Asp Leu Glu Val Val Thr Ala Asp Lys Ala Ala Ala Val Glu
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 Phe Phe Gln Asn Ala Met Asn
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<211> 1059

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1036)

<223> RXS02590

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 Met Gly Ile Ser Leu

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ttg	tca	tca	ctg	ttg	aaa	atc	cat	ggg	ttt	cca	gtc	gtc	gca	gat	ttc	163	
Leu	Ser	Ser	Leu	Leu	Lys	Ile	His	Gly	Phe	Pro	Val	Val	Ala	Asp	Phe		
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ttc	ttc	gcg	tta	gct	gtt	gtg	gtg	gca	att	gtc	att	att	ggc	ggg	tg	211	
Phe	Phe	Ala	Leu	Ala	Val	Val	Val	Ala	Ile	Val	Ile	Ile	Gly	Gly	Trp		
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cta	atc	tac	cgc	tct	cct	tca	ttc	aaa	act	gaa	gtc	atg	ccg	gca	tg	259	
Leu	Ile	Tyr	Arg	Ser	Pro	Ser	Phe	Lys	Thr	Glu	Val	Met	Pro	Ala	Trp		
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gca	atg	ctg	tcc	atg	ggg	ttg	atc	gca	ttg	gga	act	gca	agc	ccc	gta	307	
Ala	Met	Leu	Ser	Met	Gly	Leu	Ile	Ala	Leu	Gly	Thr	Ala	Ser	Pro	Val		
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gtt	ttg	ggg	gat	gat	ctg	tg	gga	ttt	atg	ttt	gtg	tgc	tg	tct	att	355	
Val	Leu	Gly	Asp	Asp	Leu	Trp	Gly	Phe	Met	Phe	Val	Cys	Trp	Ser	Ile		
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ggc	aca	gcc	gtg	gga	ctt	gtt	gcc	tat	tcc	tta	tat	ata	acg	gcc	att	403	
Gly	Thr	Ala	Val	Gly	Leu	Val	Ala	Tyr	Ser	Leu	Tyr	Ile	Thr	Ala	Ile		
				90					95					100			
ttg	cga	tct	aag	gcg	ggc	aca	cca	act	ttt	gcg	tg	ggg	ctt	cct	ctt	451	
Leu	Arg	Ser	Lys	Ala	Gly	Thr	Pro	Thr	Phe	Ala	Trp	Gly	Leu	Pro	Leu		
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gtc	acg	ccg	atg	gtt	gct	tcc	acc	tgc	gca	gca	caa	ctc	cat	gag	cac	499	
Val	Thr	Pro	Met	Val	Ala	Ser	Thr	Ser	Ala	Ala	Gln	Leu	His	Glu	His		
				120					125					130			
ttt	gaa	ctt	ccg	gcg	atg	ctg	tg	gtt	tct	ttc	ggg	ctc	ttc	ctt	tta	547	
Phe	Glu	Leu	Pro	Ala	Met	Leu	Trp	Val	Ser	Phe	Gly	Leu	Phe	Leu	Leu		
				135					140					145			
act	ttg	gcg	tct	gca	cca	gca	gtt	ttt	acc	cga	gtg	tat	ttc	tac	tat	595	
Thr	Leu	Ala	Ser	Ala	Pro	Ala	Val	Phe	Thr	Arg	Val	Tyr	Phe	Tyr	Tyr		
				150					155					160			
ttc	ggc	ccc	aag	gcg	cag	ggc	atc	cca	ctg	atg	gca	aca	cca	aca	tca	643	
Phe	Gly	Pro	Lys	Ala	Gln	Gly	Ile	Pro	Leu	Met	Ala	Thr	Pro	Thr	Ser		
				170					175					180			
tg	att	cct	ttg	ggg	atg	gtg	ggc	caa	tcc	act	gca	gca	gct	cag	ctc	691	
Trp	Ile	Pro	Leu	Gly	Met	Val	Gly	Gln	Ser	Thr	Ala	Ala	Ala	Gln	Leu		
				185					190					195			
atc	ggg	gcg	tcc	ttt	gga	tcc	aag	aca	gca	atc	aca	atg	ggc	att	att	739	
Ile	Gly	Ala	Ser	Phe	Gly	Ser	Lys	Thr	Ala	Ile	Thr	Met	Gly	Ile	Ile		
				200					205					210			
tac	ggc	atc	atc	atg	gga	att	ttt	acg	att	cct	ctg	gga	gcc	atc	gct	787	
Tyr	Gly	Ile	Ile	Met	Gly	Ile	Phe	Thr	Ile	Pro	Leu	Gly	Ala	Ile	Ala		
				215					220					225			
cac	ttt	gtg	ttc	tac	aga	gct	gtt	ttc	aaa	ggg	gcg	aca	tac	agc	ccc	835	
His	Phe	Val	Phe	Tyr	Arg	Ala	Val	Phe	Lys	Gly	Ala	Thr	Tyr	Ser	Pro		
				230					235					240			

aca tgg tgg gcc agt acc ttc cca gtt ggc act ttg agt ttg ggt gcg 883
 Thr Trp Trp Ala Ser Thr Phe Pro Val Gly Thr Leu Ser Leu Gly Ala
 250 255 260

cat ttt tta tca cag agc acc gga gtg gag tgg ttt aac tac ttc agc 931
 His Phe Leu Ser Gln Ser Thr Gly Val Glu Trp Phe Asn Tyr Phe Ser
 265 270 275

ctg tac ttg att gct tta atg ctc ttt cat gtc atc gtg tcc acc atc 979
 Leu Tyr Leu Ile Ala Leu Met Leu Phe His Val Ile Val Ser Thr Ile
 280 285 290

gcc ggt acg att gca gta atg aga aga atc gtc gga aag ctt aaa tct 1027
 Ala Gly Thr Ile Ala Val Met Arg Arg Ile Val Gly Lys Leu Lys Ser
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caa ctg gcc taaattgcag cgagaggtct aaa 1059
 Gln Leu Ala
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<210> 346

<211> 312

<212> PRT

<213> Corynebacterium glutamicum

<400> 346

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Ile Ile Gly Gly Trp Leu Ile Tyr Arg Ser Pro Ser Phe Lys Thr Glu
 35 40 45

Val Met Pro Ala Trp Ala Met Leu Ser Met Gly Leu Ile Ala Leu Gly
 50 55 60

Thr Ala Ser Pro Val Val Leu Gly Asp Asp Leu Trp Gly Phe Met Phe
 65 70 75 80

Val Cys Trp Ser Ile Gly Thr Ala Val Gly Leu Val Ala Tyr Ser Leu
 85 90 95

Tyr Ile Thr Ala Ile Leu Arg Ser Lys Ala Gly Thr Pro Thr Phe Ala
 100 105 110

Trp Gly Leu Pro Leu Val Thr Pro Met Val Ala Ser Thr Ser Ala Ala
 115 120 125

Gln Leu His Glu His Phe Glu Leu Pro Ala Met Leu Trp Val Ser Phe
 130 135 140

Gly Leu Phe Leu Leu Thr Leu Ala Ser Ala Pro Ala Val Phe Thr Arg
 145 150 155 160

Val Tyr Phe Tyr Tyr Phe Gly Pro Lys Ala Gln Gly Ile Pro Leu Met
 165 170 175

Ala Thr Pro Thr Ser Trp Ile Pro Leu Gly Met Val Gly Gln Ser Thr
 180 185 190

Ala Ala Ala Gln Leu Ile Gly Ala Ser Phe Gly Ser Lys Thr Ala Ile
 195 200 205

Thr Met Gly Ile Ile Tyr Gly Ile Ile Met Gly Ile Phe Thr Ile Pro
 210 215 220

Leu Gly Ala Ile Ala His Phe Val Phe Tyr Arg Ala Val Phe Lys Gly
 225 230 235 240

Ala Thr Tyr Ser Pro Thr Trp Trp Ala Ser Thr Phe Pro Val Gly Thr
 245 250 255

Leu Ser Leu Gly Ala His Phe Leu Ser Gln Ser Thr Gly Val Glu Trp
 260 265 270

Phe Asn Tyr Phe Ser Leu Tyr Leu Ile Ala Leu Met Leu Phe His Val
 275 280 285

Ile Val Ser Thr Ile Ala Gly Thr Ile Ala Val Met Arg Arg Ile Val
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Gly Lys Leu Lys Ser Gln Leu Ala
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 <212> DNA
 <213> *Corynebacterium glutamicum*

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 <222> (101)..(1702)
 <223> RXS00758

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 Met Thr Leu Lys Lys
 1 5

tct ctc gct gta acc acg gcg gct gca ctt gct ttg agc ctt gcc gct 163
 Ser Leu Ala Val Thr Thr Ala Ala Ala Leu Ala Leu Ser Leu Ala Ala
 10 15 20

tgc tcg tcc gac tcc tcg tcc gac agc tcc tca tcc tca tca ggc agc 211
 Cys Ser Ser Asp Ser Ser Ser Asp Ser Ser Ser Ser Ser Ser Gly Ser
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gaa ggc ggc gac aac tac gtc ctc gtc aac ggc act gag cca cag aac 259
 Glu Gly Gly Asp Asn Tyr Val Leu Val Asn Gly Thr Glu Pro Gln Asn
 40 45 50

ccg ctc gtc cca ggc aac acc aac gaa gta ggt ggc ggt cgc atc gtc 307
 Pro Leu Val Pro Gly Asn Thr Asn Glu Val Gly Gly Gly Arg Ile Val
 55 60 65

gac agc atc ttc tcc ggc ctg gtc tac tac gac gtc gac ggc tcc cct	355
Asp Ser Ile Phe Ser Gly Leu Val Tyr Tyr Asp Val Asp Gly Ser Pro	
70 75 80 85	
gtc aac gat gtt gca gag tcc atc gaa ctc gaa ggt gac aag acc tac	403
Val Asn Asp Val Ala Glu Ser Ile Glu Leu Glu Gly Asp Lys Thr Tyr	
90 95 100	
cgc atc acc atc aaa gac ggc cag acc ttc acc gat ggc acc cca gtt	451
Arg Ile Thr Ile Lys Asp Gly Gln Thr Phe Thr Asp Gly Thr Pro Val	
105 110 115	
acc gct gag agc ttt gtc aac gca tgg aac tac aac gta gct aac agc	499
Thr Ala Glu Ser Phe Val Asn Ala Trp Asn Tyr Asn Val Ala Asn Ser	
120 125 130	
acg ctg tcc tcc tac ttc ttt gag tcc atc ctc ggc tac gaa gaa ggc	547
Thr Leu Ser Ser Tyr Phe Phe Glu Ser Ile Leu Gly Tyr Glu Glu Gly	
135 140 145	
gtc gag tcc atg gaa ggc ctc cag gtc gtc gac gac acc acc ttc acc	595
Val Glu Ser Met Glu Gly Leu Gln Val Val Asp Asp Thr Thr Phe Thr	
150 155 160 165	
gtc gag ctc acc cag cct gag tcc gac ttc cca ctg cgc ctg gga tac	643
Val Glu Leu Thr Gln Pro Glu Ser Asp Phe Pro Leu Arg Leu Gly Tyr	
170 175 180	
tcc gca ttc ttc ccg ctt cct gaa tcc gca ttt gac gac atg gac gca	691
Ser Ala Phe Phe Pro Leu Pro Glu Ser Ala Phe Asp Asp Met Asp Ala	
185 190 195	
ttc ggt gag aac cca atc ggc aac ggt cca tac aag ctc caa gag tgg	739
Phe Gly Glu Asn Pro Ile Gly Asn Gly Pro Tyr Lys Leu Gln Glu Trp	
200 205 210	
aac cac aac cag gac gcc acc atc gtt cct aac gcg gac tac acc ggt	787
Asn His Asn Gln Asp Ala Thr Ile Val Pro Asn Ala Asp Tyr Thr Gly	
215 220 225	
gga cgc cag gct cag aac gac ggc gtg aag ttc atc ttc tac cca acc	835
Gly Arg Gln Ala Gln Asn Asp Gly Val Lys Phe Ile Phe Tyr Pro Thr	
230 235 240 245	
ttc gac tcc gct tac gcg gac ctg ctc tcc gac aac ttg gat gtg ctg	883
Phe Asp Ser Ala Tyr Ala Asp Leu Leu Ser Asp Asn Leu Asp Val Leu	
250 255 260	
gac gct atc cca gac tcc gcg ttc tcc tcc ttc gag gac gag ctc tct	931
Asp Ala Ile Pro Asp Ser Ala Phe Ser Ser Phe Glu Asp Glu Leu Ser	
265 270 275	
ggc cgt tcc atc aac cag cct tcc gct gtg ttc cag tcc ttc acc atc	979
Gly Arg Ser Ile Asn Gln Pro Ser Ala Val Phe Gln Ser Phe Thr Ile	
280 285 290	
ccg gag agc ctt gag cac ttc tcc ggc gaa gaa ggc gtg ctg cgt cgc	1027
Pro Glu Ser Leu Glu His Phe Ser Gly Glu Glu Gly Val Leu Arg Arg	
295 300 305	
cag gcc atc tcc ttg gcc gtc aac cgc gac gag atc acc caa acc atc	1075

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Phe	Glu	Gly	Thr	Arg	Thr	Pro	Ala	Thr	Asp	Phe	Thr	Ser	Pro	Val	Ile		
				330					335					340			
gac	gga	cac	tct	gat	tcc	ctc	cag	ggc	gca	gat	gtc	ttg	acc	tac	gat	1171	
Asp	Gly	His	Ser	Asp	Ser	Leu	Gln	Gly	Ala	Asp	Val	Leu	Thr	Tyr	Asp		
			345					350					355				
cca	gag	cgc	gct	cag	gaa	ctg	tgg	gca	cag	gca	gac	gag	atc	agc	cct	1219	
Pro	Glu	Arg	Ala	Gln	Glu	Leu	Trp	Ala	Gln	Ala	Asp	Glu	Ile	Ser	Pro		
		360					365					370					
tgg	tcc	ggc	gag	ttc	tcc	atc	tcc	tac	aac	gca	gac	ggt	gga	cac	cag	1267	
Trp	Ser	Gly	Glu	Phe	Ser	Ile	Ser	Tyr	Asn	Ala	Asp	Gly	Gly	His	Gln		
	375					380					385						
gca	tgg	gtg	gac	gca	acc	gcc	aat	tcc	atc	cgc	aac	acc	ctg	ggt	atc	1315	
Ala	Trp	Val	Asp	Ala	Thr	Ala	Asn	Ser	Ile	Arg	Asn	Thr	Leu	Gly	Ile		
390					395					400					405		
gac	gcc	atc	ggc	aac	cca	tac	cca	gac	ttc	aag	tcc	ctg	cgt	gac	gat	1363	
Asp	Ala	Ile	Gly	Asn	Pro	Tyr	Pro	Asp	Phe	Lys	Ser	Leu	Arg	Asp	Asp		
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gtc	acc	aac	cgc	acc	atc	aac	ggc	gca	ttc	cgc	acc	ggc	tgg	cag	gca	1411	
Val	Thr	Asn	Arg	Thr	Ile	Asn	Gly	Ala	Phe	Arg	Thr	Gly	Trp	Gln	Ala		
			425				430						435				
gac	tac	ccg	tcc	ttg	ggc	aac	ttc	ctc	gga	cct	ttg	tac	ggc	acc	ggt	1459	
Asp	Tyr	Pro	Ser	Leu	Gly	Asn	Phe	Leu	Gly	Pro	Leu	Tyr	Gly	Thr	Gly		
		440				445						450					
gca	ggc	tcc	aac	gat	ggt	gac	tac	tcc	aac	cca	gat	ttc	gat	gcc	aag	1507	
Ala	Gly	Ser	Asn	Asp	Gly	Asp	Tyr	Ser	Asn	Pro	Asp	Phe	Asp	Ala	Lys		
	455				460					465							
ctc	gcc	gaa	gca	gca	aac	gcg	gcc	gat	gtt	gac	gca	tca	acc	ccg	cta	1555	
Leu	Ala	Glu	Ala	Ala	Asn	Ala	Ala	Asp	Val	Asp	Ala	Ser	Thr	Pro	Leu		
470					475					480					485		
tac	aac	gaa	gca	cag	gaa	atc	ctg	ctc	cag	gat	ctc	cca	gcg	atc	cca	1603	
Tyr	Asn	Glu	Ala	Gln	Glu	Ile	Leu	Leu	Gln	Asp	Leu	Pro	Ala	Ile	Pro		
				490					495					500			
act	tgg	tac	tcc	aac	gca	gtt	ggt	gga	tac	tcc	acc	aac	gtg	gac	aac	1651	
Thr	Trp	Tyr	Ser	Asn	Ala	Val	Gly	Gly	Tyr	Ser	Thr	Asn	Val	Asp	Asn		
			505				510						515				
gtg	gaa	ttc	cag	tgg	aac	tcg	caa	cct	gcg	tac	tac	cag	atc	acc	aag	1699	
Val	Glu	Phe	Gln	Trp	Asn	Ser	Gln	Pro	Ala	Tyr	Tyr	Gln	Ile	Thr	Lys		
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Asn																	

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<212> PRT

<213> *Corynebacterium glutamicum*

<400> 348

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Ser Ser Ser Gly Ser Glu Gly Gly Asp Asn Tyr Val Leu Val Asn Gly
      35           40           45

Thr Glu Pro Gln Asn Pro Leu Val Pro Gly Asn Thr Asn Glu Val Gly
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Gly Gly Arg Ile Val Asp Ser Ile Phe Ser Gly Leu Val Tyr Tyr Asp
      65           70           75           80

Val Asp Gly Ser Pro Val Asn Asp Val Ala Glu Ser Ile Glu Leu Glu
      85           90           95

Gly Asp Lys Thr Tyr Arg Ile Thr Ile Lys Asp Gly Gln Thr Phe Thr
      100           105           110

Asp Gly Thr Pro Val Thr Ala Glu Ser Phe Val Asn Ala Trp Asn Tyr
      115           120           125

Asn Val Ala Asn Ser Thr Leu Ser Ser Tyr Phe Phe Glu Ser Ile Leu
      130           135           140

Gly Tyr Glu Glu Gly Val Glu Ser Met Glu Gly Leu Gln Val Val Asp
      145           150           155           160

Asp Thr Thr Phe Thr Val Glu Leu Thr Gln Pro Glu Ser Asp Phe Pro
      165           170           175

Leu Arg Leu Gly Tyr Ser Ala Phe Phe Pro Leu Pro Glu Ser Ala Phe
      180           185           190

Asp Asp Met Asp Ala Phe Gly Glu Asn Pro Ile Gly Asn Gly Pro Tyr
      195           200           205

Lys Leu Gln Glu Trp Asn His Asn Gln Asp Ala Thr Ile Val Pro Asn
      210           215           220

Ala Asp Tyr Thr Gly Gly Arg Gln Ala Gln Asn Asp Gly Val Lys Phe
      225           230           235           240

Ile Phe Tyr Pro Thr Phe Asp Ser Ala Tyr Ala Asp Leu Leu Ser Asp
      245           250           255

Asn Leu Asp Val Leu Asp Ala Ile Pro Asp Ser Ala Phe Ser Ser Phe
      260           265           270

Glu Asp Glu Leu Ser Gly Arg Ser Ile Asn Gln Pro Ser Ala Val Phe
      275           280           285

Gln Ser Phe Thr Ile Pro Glu Ser Leu Glu His Phe Ser Gly Glu Glu
      290           295           300

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Gly Val Leu Arg Arg Gln Ala Ile Ser Leu Ala Val Asn Arg Asp Glu
 305 310 315 320
 Ile Thr Gln Thr Ile Phe Glu Gly Thr Arg Thr Pro Ala Thr Asp Phe
 325 330 335
 Thr Ser Pro Val Ile Asp Gly His Ser Asp Ser Leu Gln Gly Ala Asp
 340 345 350
 Val Leu Thr Tyr Asp Pro Glu Arg Ala Gln Glu Leu Trp Ala Gln Ala
 355 360 365
 Asp Glu Ile Ser Pro Trp Ser Gly Glu Phe Ser Ile Ser Tyr Asn Ala
 370 375 380
 Asp Gly Gly His Gln Ala Trp Val Asp Ala Thr Ala Asn Ser Ile Arg
 385 390 395 400
 Asn Thr Leu Gly Ile Asp Ala Ile Gly Asn Pro Tyr Pro Asp Phe Lys
 405 410 415
 Ser Leu Arg Asp Asp Val Thr Asn Arg Thr Ile Asn Gly Ala Phe Arg
 420 425 430
 Thr Gly Trp Gln Ala Asp Tyr Pro Ser Leu Gly Asn Phe Leu Gly Pro
 435 440 445
 Leu Tyr Gly Thr Gly Ala Gly Ser Asn Asp Gly Asp Tyr Ser Asn Pro
 450 455 460
 Asp Phe Asp Ala Lys Leu Ala Glu Ala Ala Asn Ala Ala Asp Val Asp
 465 470 475 480
 Ala Ser Thr Pro Leu Tyr Asn Glu Ala Gln Glu Ile Leu Leu Gln Asp
 485 490 495
 Leu Pro Ala Ile Pro Thr Trp Tyr Ser Asn Ala Val Gly Gly Tyr Ser
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 Tyr Gln Ile Thr Lys Asn
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<210> 349

<211> 1698

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1675)

<223> RXS01346

<400> 349

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ggcacgttgc aaacagcaac gctcacccat aggagattta atg cgc aca gcc aca 115

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Lys Val Ile Ala Thr Val Met Ala Ser Thr Leu Ala Ile Gly Leu Ala						
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tct tgt tcc agc tct agt ggc acc cca gac gtg aat tac gta tcc gtc						211
Ser Cys Ser Ser Ser Ser Ser Gly Thr Pro Asp Val Asn Tyr Val Ser Val						
	25		30		35	
aac ggc acc gaa cct cag cgc gga ctc atc ccg ggc gac acc aat gaa						259
Asn Gly Thr Glu Pro Gln Arg Gly Leu Ile Pro Gly Asp Thr Asn Glu						
	40		45		50	
aac ggc ggt ggg cga gtg gtg gac atg ctg tac tct ggg ctc gtc tac						307
Asn Gly Gly Gly Arg Val Val Asp Met Leu Tyr Ser Gly Leu Val Tyr						
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ttt gat gaa gct ggc gtt gct caa aat gac ctg gcg gca tca att gac						355
Phe Asp Glu Ala Gly Val Ala Gln Asn Asp Leu Ala Ala Ser Ile Asp						
	70		75		80	85
cag gaa aca gac acc acc tac aaa atc act ttg cgt gat ggc atc aaa						403
Gln Glu Thr Asp Thr Thr Tyr Lys Ile Thr Leu Arg Asp Gly Ile Lys						
	90		95		100	
ttc agt gac gga tgc gat att act gcc act gat ttt gtg gat acc tgg						451
Phe Ser Asp Gly Ser Asp Ile Thr Ala Thr Asp Phe Val Asp Thr Trp						
	105		110		115	
aat ttt gta gtg gaa aat gga ctg ctc aac act tct ttc ttc tca ccg						499
Asn Phe Val Val Glu Asn Gly Leu Leu Asn Thr Ser Phe Phe Ser Pro						
	120		125		130	
att aaa ggg tat gag gag ggc gtg gaa acg ctc gag ggt ttg aat gtg						547
Ile Lys Gly Tyr Glu Glu Gly Val Glu Thr Leu Glu Gly Leu Asn Val						
	135		140		145	
gtg gat gat cgc aca ttt acc atc gag ctt gcc caa ccg gat tct gag						595
Val Asp Asp Arg Thr Phe Thr Ile Glu Leu Ala Gln Pro Asp Ser Glu						
	150		155		160	165
ttc acc caa cgc att ggc tac tac ggt ttt gca ccg atg cca gct tgc						643
Phe Thr Gln Arg Ile Gly Tyr Tyr Gly Phe Ala Pro Met Pro Ala Ser						
	170		175		180	
gct cgc gat gat att gac gcc ttt ggt gaa aac ccc gtg tcc tct ggc						691
Ala Arg Asp Asp Ile Asp Ala Phe Gly Glu Asn Pro Val Ser Ser Gly						
	185		190		195	
cct tac aaa cta gag cag tgg gat cac aac gca gaa ctg aaa gtg gtg						739
Pro Tyr Lys Leu Glu Gln Trp Asp His Asn Ala Glu Leu Lys Val Val						
	200		205		210	
gcc aat gaa cac tac gat ggc ccg cgc gca gcc aac aac gat ggc ttg						787
Ala Asn Glu His Tyr Asp Gly Pro Arg Ala Ala Asn Asn Asp Gly Leu						
	215		220		225	
aag tac gtg ttc tac gcc caa aat gat gca gct tat tca gat ctg ttg						835
Lys Tyr Val Phe Tyr Ala Gln Asn Asp Ala Ala Tyr Ser Asp Leu Leu						

230	235	240	245	
gct gga aac cta gat gtg ctg gat ctc att cca cca tcg gcg tac acc				883
Ala Gly Asn Leu Asp Val Leu Asp Leu Ile Pro Pro Ser Ala Tyr Thr	250	255	260	
acc tat gaa gag gaa ctg tcg ggt cga tcc att aat caa cct gcg gcc				931
Thr Tyr Glu Glu Glu Leu Ser Gly Arg Ser Ile Asn Gln Pro Ala Ala	265	270	275	
tcc tat ctg gaa ctc tcc att cgc atg gaa tcc ccc aac ttt gaa ggg				979
Ser Tyr Leu Glu Leu Ser Ile Arg Met Glu Ser Pro Asn Phe Glu Gly	280	285	290	
caa cag gga cag ttg cgt cga caa gca att tct atg gcg att aac cgt				1027
Gln Gln Gly Gln Leu Arg Arg Gln Ala Ile Ser Met Ala Ile Asn Arg	295	300	305	
gaa gaa atc gct gag cag atc ttc gcc ggc acc tac acg cct gcg ctc				1075
Glu Glu Ile Ala Glu Gln Ile Phe Ala Gly Thr Tyr Thr Pro Ala Leu	310	315	320	325
gac ttc acc gcg ccc gtg ctc gac ggc tgg cgc gat gat ttg aac ggc				1123
Asp Phe Thr Ala Pro Val Leu Asp Gly Trp Arg Asp Asp Leu Asn Gly	330	335	340	
aat gac gtg ctg act ttc cag cct gac aag gcc cgt gag ctg tgg gaa				1171
Asn Asp Val Leu Thr Phe Gln Pro Asp Lys Ala Arg Glu Leu Trp Glu	345	350	355	
gac gct gag gag atc gca cct ttt gag ggc gaa ttg cag atc agt tac				1219
Asp Ala Glu Glu Ile Ala Pro Phe Glu Gly Glu Leu Gln Ile Ser Tyr	360	365	370	
aac gcg gat gtt ccc aac cgg gaa tgg gtg gat gcg gta gca aac agc				1267
Asn Ala Asp Val Pro Asn Arg Glu Trp Val Asp Ala Val Ala Asn Ser	375	380	385	
atc agc aac gaa tta gac gtc aac gcc act ggc aat cct ttc ccc gat				1315
Ile Ser Asn Glu Leu Asp Val Asn Ala Thr Gly Asn Pro Phe Pro Asp	390	395	400	405
ttt aaa tcc ttc cgc gac aca tac cgc acc acc gga ttg gat ggc gcc				1363
Phe Lys Ser Phe Arg Asp Thr Tyr Arg Thr Thr Gly Leu Asp Gly Ala	410	415	420	
tac cgc acc gcg tgg ttt gcg gac tac cca agc atc ggc aac ttc ctt				1411
Tyr Arg Thr Ala Trp Phe Ala Asp Tyr Pro Ser Ile Gly Asn Phe Leu	425	430	435	
gga cct aac tac acc tcg ggc gtg gcc tcc aac gat gcc aag tac gaa				1459
Gly Pro Asn Tyr Thr Ser Gly Val Ala Ser Asn Asp Ala Lys Tyr Glu	440	445	450	
aac cca gaa ttt gat caa ttg att gcc gac gcc gca gca gcc tcc acc				1507
Asn Pro Glu Phe Asp Gln Leu Ile Ala Asp Ala Ala Ala Ser Thr	455	460	465	
aag gag gaa acc ttc cag gca tat gcg cag gcc cag gaa atg ttg ttg				1555
Lys Glu Glu Thr Phe Gln Ala Tyr Ala Gln Ala Gln Glu Met Leu Leu	470	475	480	485

cgc gat ctt ccc gca atc cca ctg tgg tac ccg aat gtg gtt ggc ggc 1603
 Arg Asp Leu Pro Ala Ile Pro Leu Trp Tyr Pro Asn Val Val Gly Gly
 490 495 500

tac tca gaa tcc gtg gac aac gtc tcc gta aac tgg aag gcc ata cct 1651
 Tyr Ser Glu Ser Val Asp Asn Val Ser Val Asn Trp Lys Ala Ile Pro
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<212> PRT

<213> Corynebacterium glutamicum

<400> 350

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Asn Tyr Val Ser Val Asn Gly Thr Glu Pro Gln Arg Gly Leu Ile Pro
 35 40 45

Gly Asp Thr Asn Glu Asn Gly Gly Gly Arg Val Val Asp Met Leu Tyr
 50 55 60

Ser Gly Leu Val Tyr Phe Asp Glu Ala Gly Val Ala Gln Asn Asp Leu
 65 70 75 80

Ala Ala Ser Ile Asp Gln Glu Thr Asp Thr Thr Tyr Lys Ile Thr Leu
 85 90 95

Arg Asp Gly Ile Lys Phe Ser Asp Gly Ser Asp Ile Thr Ala Thr Asp
 100 105 110

Phe Val Asp Thr Trp Asn Phe Val Val Glu Asn Gly Leu Leu Asn Thr
 115 120 125

Ser Phe Phe Ser Pro Ile Lys Gly Tyr Glu Glu Gly Val Glu Thr Leu
 130 135 140

Glu Gly Leu Asn Val Val Asp Asp Arg Thr Phe Thr Ile Glu Leu Ala
 145 150 155 160

Gln Pro Asp Ser Glu Phe Thr Gln Arg Ile Gly Tyr Tyr Gly Phe Ala
 165 170 175

Pro Met Pro Ala Ser Ala Arg Asp Asp Ile Asp Ala Phe Gly Glu Asn
 180 185 190

Pro Val Ser Ser Gly Pro Tyr Lys Leu Glu Gln Trp Asp His Asn Ala
 195 200 205

Glu Leu Lys Val Val Ala Asn Glu His Tyr Asp Gly Pro Arg Ala Ala
 210 215 220

Asn Asn Asp Gly Leu Lys Tyr Val Phe Tyr Ala Gln Asn Asp Ala Ala
 225 230 235 240
 Tyr Ser Asp Leu Leu Ala Gly Asn Leu Asp Val Leu Asp Leu Ile Pro
 245 250 255
 Pro Ser Ala Tyr Thr Thr Tyr Glu Glu Glu Leu Ser Gly Arg Ser Ile
 260 265 270
 Asn Gln Pro Ala Ala Ser Tyr Leu Glu Leu Ser Ile Arg Met Glu Ser
 275 280 285
 Pro Asn Phe Glu Gly Gln Gln Gly Gln Leu Arg Arg Gln Ala Ile Ser
 290 295 300
 Met Ala Ile Asn Arg Glu Glu Ile Ala Glu Gln Ile Phe Ala Gly Thr
 305 310 315 320
 Tyr Thr Pro Ala Leu Asp Phe Thr Ala Pro Val Leu Asp Gly Trp Arg
 325 330 335
 Asp Asp Leu Asn Gly Asn Asp Val Leu Thr Phe Gln Pro Asp Lys Ala
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 Arg Glu Leu Trp Glu Asp Ala Glu Glu Ile Ala Pro Phe Glu Gly Glu
 355 360 365
 Leu Gln Ile Ser Tyr Asn Ala Asp Val Pro Asn Arg Glu Trp Val Asp
 370 375 380
 Ala Val Ala Asn Ser Ile Ser Asn Glu Leu Asp Val Asn Ala Thr Gly
 385 390 395 400
 Asn Pro Phe Pro Asp Phe Lys Ser Phe Arg Asp Thr Tyr Arg Thr Thr
 405 410 415
 Gly Leu Asp Gly Ala Tyr Arg Thr Ala Trp Phe Ala Asp Tyr Pro Ser
 420 425 430
 Ile Gly Asn Phe Leu Gly Pro Asn Tyr Thr Ser Gly Val Ala Ser Asn
 435 440 445
 Asp Ala Lys Tyr Glu Asn Pro Glu Phe Asp Gln Leu Ile Ala Asp Ala
 450 455 460
 Ala Ala Ala Ser Thr Lys Glu Glu Thr Phe Gln Ala Tyr Ala Gln Ala
 465 470 475 480
 Gln Glu Met Leu Leu Arg Asp Leu Pro Ala Ile Pro Leu Trp Tyr Pro
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 Trp Lys Ala Ile Pro Val Tyr Trp Ala Ile Thr Lys Gln
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<223> RXS00912

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Leu Thr Ile Ala Ala Ala Phe Phe Met Leu Ser Phe Ile Phe Thr Ile
  10                      15                      20                      25

tac cgc atc atc gtc ggg ccc aac tcc atc gat cgc cta ctc ggc ctg      148
Tyr Arg Ile Ile Val Gly Pro Asn Ser Ile Asp Arg Leu Leu Gly Leu
                      30                      35                      40

gac gga acc gtc tcc atg att caa tgc tcc atg gcc acc tac atc tgc      196
Asp Gly Thr Val Ser Met Ile Gln Cys Ser Met Ala Thr Tyr Ile Cys
                      45                      50                      55

tgg aca ctc gac acc acc gtc acc aac ttc atg atg gtc atc gca ctc      244
Trp Thr Leu Asp Thr Thr Val Thr Asn Phe Met Met Val Ile Ala Leu
                      60                      65                      70

tta gga ttc atc agc tct gta tcc gta gcc cgc ttc cgc aag agg gat      292
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<213> Corynebacterium glutamicum

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Asn Ser Ile Asp Arg Leu Leu Gly Leu Asp Gly Thr Val Ser Met Ile
  35                      40                      45

Gln Cys Ser Met Ala Thr Tyr Ile Cys Trp Thr Leu Asp Thr Thr Val
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<div style="display: flex; justify-content: space-between;"> Leu Leu Ile Leu Ala Ile Val Gly Gly Leu Ala Leu Thr Met Gln Lys 10 15 20 </div>																	
ggg ttc agt aac tct ttc act att gaa gac acc cct tcg att gat gcc																	211
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185	190	195																		
atc atc ggt att ggc atc gcg ttc atc gtg ttg att ttc acc ttt ggt	739																			
Ile Ile Gly Ile Gly Ile Ala Phe Ile Val Leu Ile Phe Thr Phe Gly																				
200	205	210																		
tct ttg att gct gca ggc ttg cct ttg att acc gcg gtg atc ggc gtg	787																			
Ser Leu Ile Ala Ala Gly Leu Pro Leu Ile Thr Ala Val Ile Gly Val																				
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230	235	240	245																	
aac aat gtg act cca gtg ctc gca gtg atg att ggc ctg gcc gtg ggc	883																			
Asn Asn Val Thr Pro Val Leu Ala Val Met Ile Gly Leu Ala Val Gly																				
250	255	260																		
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265	270	275																		
cgc atg cca cgt gcc gat gct gcc gga atg gcg gtg ggc aca gct ggt	979																			
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280	285	290																		
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Ser Ala Val Val Phe Ala Gly Ala Thr Val Ile Ile Ala Leu Val Ala																				
295	300	305																		
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Leu Ile Ile Ala Asp Ile Gly Phe Leu Thr Ala Met Gly Ile Ser Ala																				
310	315	320	325																	
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Ala Phe Thr Val Phe Val Ala Val Leu Ile Ala Leu Thr Phe Ile Pro																				
330	335	340																		
gcg ctg ttg ggt gtg ttt ggt ggt cat gcg ttc aag ggc aag atc cct	1171																			
Ala Leu Leu Gly Val Phe Gly Gly His Ala Phe Lys Gly Lys Ile Pro																				
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Gly Ile Gly Gly Asn Pro Thr Pro Lys Gln Thr Trp Glu Gln Ala Leu																				
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aat cgt cgt tcc aag ggt cgc tca tgg gtc aag ctt gta cag aaa gca	1267																			
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410	415	420																		

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Glu Val Asn Ala Asp Ser Thr Ala Leu Gln Pro Leu Ile Glu Ala Gln	
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Glu Pro Glu Glu Gly Glu Phe Asp Arg Glu Gln Ala Ala Arg Phe Ala	
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Leu Val Thr Pro Tyr Thr Gly Pro Ala Asp Lys Glu Thr Pro Glu Leu	
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 730 735 740

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<211> 783

<212> PRT

<213> Corynebacterium glutamicum

<400> 354

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Pro Ser Ile Asp Ala Thr Val Ser Leu Val Glu Asn Phe Pro Asp Gln
 35 40 45

Thr Asn Pro Val Thr Ala Ala Gly Val Asn Val Val Phe Gln Ser Pro
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Glu Gly Thr Thr Leu Asp Asp Pro Gln Met Met Thr Ala Met Asp Ala
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Val Val Asp Tyr Ile Glu Asp Asn Leu Pro Asp Phe Gly Gly Gly Glu
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Arg Phe Gly Asn Pro Val Glu Val Ser Pro Ala Leu Glu Glu Met Val
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Ile Glu Gln Met Thr Ser Met Gly Leu Pro Glu Glu Thr Ala Ala Lys
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 Asp Ala Ala Asn Leu Ala Val Leu Ser Glu Asp Lys Thr Ile Gly Tyr
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 145 150 155 160
 His Arg Asp Val Ile Asn Glu Ala Met Gln Ile Gly Glu Asp Leu Gly
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 Val Arg Val Glu Ala Gly Gly Pro Ala Phe Gly Asp Pro Ile Gln Ile
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 Glu Thr Thr Ser Glu Ile Ile Gly Ile Gly Ile Ala Phe Ile Val Leu
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 260 265 270
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 Ile Ala Leu Val Ala Leu Ile Ile Ala Asp Ile Gly Phe Leu Thr Ala
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 Glu Thr Pro Glu Leu Met His Val Leu Arg Ala Gln Glu Ala Gln Ile
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 Ala Val Val Val Gly Leu Ala Ile Phe Leu Leu Ile Leu Val Phe Arg
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 Ser Leu Leu Val Pro Leu Val Ala Gly Leu Gly Phe Leu Leu Ser Val
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 Leu Ile Gly Val Thr Phe Gly Leu Ala Met Asp Tyr Gln Val Phe Leu
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Ser Asp Pro Ser Glu Lys Pro His Thr Phe Phe Asp Lys Ile Leu Ala																			
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Leu Glu Asp Leu Asp																
				90												

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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 360
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 Lys Ala Tyr Thr Val Met Gly His Gly Ser Glu Val Glu Glu Ala Pro
 20 25 30
 Arg Pro Thr Thr Arg Arg Leu Asn Asp Asp Glu Glu Val Thr Val His
 35 40 45
 Glu Ala Val Val Ala Gly Asp Thr Val Ala Ser Arg Gly Gly Leu Ser
 50 55 60
 Thr Gln Glu Asn Arg Asp Leu Val Ser Phe Val Glu Leu Lys Ala Arg
 65 70 75 80
 Leu Glu Lys Arg Arg Leu Glu Asp Leu Asp
 85 90

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 <222> (101)..(2191)
 <223> RXS02587

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 ttgttatcca accgccacaa ttcccaggag taatccaccc gtg ttt tct aaa tgg 115
 Val Phe Ser Lys Trp
 1 5
 ggc cac ttt gct tac aga ttt agg cgc att gtt ccg tta gtc gtc atc 163
 Gly His Phe Ala Tyr Arg Phe Arg Arg Ile Val Pro Leu Val Val Ile
 10 15 20
 gcc gcg att ttg gct ttg ttt gtc att ttc ggc acc aag ctg ggc gac 211
 Ala Ala Ile Leu Ala Leu Phe Val Ile Phe Gly Thr Lys Leu Gly Asp
 25 30 35
 cgc atg agc cag gaa gga tgg gat gat cct ggt tct tcc tcg acc gct 259
 Arg Met Ser Gln Glu Gly Trp Asp Asp Pro Gly Ser Ser Ser Thr Ala
 40 45 50
 gcg gcg cgc atc gag ttg gag acc ttt ggg cgt gac aat gac ggc gat 307
 Ala Ala Arg Ile Glu Leu Glu Thr Phe Gly Arg Asp Asn Asp Gly Asp
 55 60 65
 gtc gtg ttg ctg ttt act gcg cct gaa ggc act tct ttc gat gat gca 355

Val	Val	Leu	Leu	Phe	Thr	Ala	Pro	Glu	Gly	Thr	Ser	Phe	Asp	Asp	Ala		
70					75					80					85		
gag	gtg	ttc	tcc	agc	atc	tct	ggc	tac	tta	gat	ggg	cta	atc	gag	aac	403	
Glu	Val	Phe	Ser	Ser	Ile	Ser	Gly	Tyr	Leu	Asp	Gly	Leu	Ile	Glu	Asn		
			90					95						100			
aac	cct	gat	gaa	gtc	agc	cac	atc	aac	agc	tac	ttt	gac	act	cgt	aat	451	
Asn	Pro	Asp	Glu	Val	Ser	His	Ile	Asn	Ser	Tyr	Phe	Asp	Thr	Arg	Asn		
			105					110					115				
caa	aat	ctc	ctc	agc	aaa	gac	ggc	acc	caa	acc	ttt	gca	gct	ctc	ggg	499	
Gln	Asn	Leu	Leu	Ser	Lys	Asp	Gly	Thr	Gln	Thr	Phe	Ala	Ala	Leu	Gly		
		120					125					130					
ctc	aaa	ggt	gac	ggc	gag	caa	acg	ctg	aag	gac	ttc	cgg	gag	att	gaa	547	
Leu	Lys	Gly	Asp	Gly	Glu	Gln	Thr	Leu	Lys	Asp	Phe	Arg	Glu	Ile	Glu		
	135					140					145						
gat	cag	ctc	cat	ccg	gac	aac	ctt	gcc	ggt	ggc	gtc	acc	act	gag	gtc	595	
Asp	Gln	Leu	His	Pro	Asp	Asn	Leu	Ala	Gly	Gly	Val	Thr	Thr	Glu	Val		
150					155					160					165		
gcg	ggt	gcc	acc	gct	gta	gcc	gac	gca	ctc	gat	gag	ggc	atg	gct	ggc	643	
Ala	Gly	Ala	Thr	Ala	Val	Ala	Asp	Ala	Leu	Asp	Glu	Gly	Met	Ala	Gly		
			170						175					180			
gat	att	tca	cgc	gcc	gaa	gtt	ttt	gcg	ctg	cct	ttc	gtg	gct	atc	ttg	691	
Asp	Ile	Ser	Arg	Ala	Glu	Val	Phe	Ala	Leu	Pro	Phe	Val	Ala	Ile	Leu		
			185					190					195				
ctg	ctc	atc	gtg	ttt	ggc	tca	gtt	gtt	gcc	gcg	gcg	atg	cca	ttg	atc	739	
Leu	Leu	Ile	Val	Phe	Gly	Ser	Val	Val	Ala	Ala	Ala	Met	Pro	Leu	Ile		
		200					205					210					
gtg	ggc	att	ttg	tcc	atc	ttg	ggt	tcg	ctg	ggc	atc	ttg	gca	att	ttg	787	
Val	Gly	Ile	Leu	Ser	Ile	Leu	Gly	Ser	Leu	Gly	Ile	Leu	Ala	Ile	Leu		
	215					220					225						
gct	gga	ttc	ttc	cag	gtc	aac	gta	ttt	gca	caa	tct	gtt	gtg	acc	ctt	835	
Ala	Gly	Phe	Phe	Gln	Val	Asn	Val	Phe	Ala	Gln	Ser	Val	Val	Thr	Leu		
230					235					240					245		
ctg	ggc	ttg	ggt	ctt	gcc	att	gac	tat	ggc	tta	ttc	atg	gtc	tct	cgt	883	
Leu	Gly	Leu	Gly	Leu	Ala	Ile	Asp	Tyr	Gly	Leu	Phe	Met	Val	Ser	Arg		
			250						255					260			
ttc	cgt	gag	gaa	atg	gat	aag	ggc	acc	ccg	gtt	gaa	cag	gct	gtt	gcc	931	
Phe	Arg	Glu	Glu	Met	Asp	Lys	Gly	Thr	Pro	Val	Glu	Gln	Ala	Val	Ala		
			265					270					275				
acc	act	acg	gcg	acc	gcg	ggt	aag	act	gtg	gtg	ttc	tct	gca	gcg	atg	979	
Thr	Thr	Thr	Ala	Thr	Ala	Gly	Lys	Thr	Val	Val	Phe	Ser	Ala	Ala	Met		
			280				285					290					
gtg	gct	gtg	gcg	ctg	tcc	ggg	ttg	ttt	gtt	ttc	cca	cag	gct	ttc	ttg	1027	
Val	Ala	Val	Ala	Leu	Ser	Gly	Leu	Phe	Val	Phe	Pro	Gln	Ala	Phe	Leu		
	295					300					305						
aag	tcg	gtg	gca	ttc	ggt	gcg	att	tcc	gcg	gtt	ggc	ctt	gct	gct	ttg	1075	
Lys	Ser	Val	Ala	Phe	Gly	Ala	Ile	Ser	Ala	Val	Gly	Leu	Ala	Ala	Leu		

310	315	320	325	
atg tcg gtg acg gtg ttg ccg tcg ctg ttc agc atg ttg ggt aag aat				1123
Met Ser Val Thr Val Leu Pro Ser Leu Phe Ser Met Leu Gly Lys Asn	330	335	340	
atc gat aag tgg agt ttg cgt cgc act gct cga aca gcg cgc cgt ttg				1171
Ile Asp Lys Trp Ser Leu Arg Arg Thr Ala Arg Thr Ala Arg Arg Leu	345	350	355	
gaa gac acc att tgg tac cgc gtg ccg gca tgg gca atg cgc cat gcc				1219
Glu Asp Thr Ile Trp Tyr Arg Val Pro Ala Trp Ala Met Arg His Ala	360	365	370	
aag gca gtg acc gtg ggc gtc gta ttg ctc ttg ctt gct ctt aca gtg				1267
Lys Ala Val Thr Val Gly Val Val Leu Leu Leu Leu Ala Leu Thr Val	375	380	385	
ccg ttg acg ggc gtg aaa ttc ggc ggc atc aat gaa acg tat ctg cca				1315
Pro Leu Thr Gly Val Lys Phe Gly Gly Ile Asn Glu Thr Tyr Leu Pro	390	395	400	405
cca gct aac gac acc cgc gtc gcc caa gag cgt ttc gac gag gcg ttt				1363
Pro Ala Asn Asp Thr Arg Val Ala Gln Glu Arg Phe Asp Glu Ala Phe	410	415	420	
ccc gcc ttc cgc acc gag ccg gtc aag ctt gtg gtc acc ggg gcg gac				1411
Pro Ala Phe Arg Thr Glu Pro Val Lys Leu Val Val Thr Gly Ala Asp	425	430	435	
aac aac cag ctg atc gat atc tat gtt cag gcc aac gaa gtt gag gga				1459
Asn Asn Gln Leu Ile Asp Ile Tyr Val Gln Ala Asn Glu Val Glu Gly	440	445	450	
ctg aca gat cgt ttc acc gca ggt gcg act acc gat gat ggc acc acg				1507
Leu Thr Asp Arg Phe Thr Ala Gly Ala Thr Thr Asp Asp Gly Thr Thr	455	460	465	
gtg ttg tct act ggt att cag gat cgt tcc ctc aat gag cag gta gtg				1555
Val Leu Ser Thr Gly Ile Gln Asp Arg Ser Leu Asn Glu Gln Val Val	470	475	480	485
gag cag ctt cgc gct att tcc gtc cct gag ggc gtt gag gtg cag atc				1603
Glu Gln Leu Arg Ala Ile Ser Val Pro Glu Gly Val Glu Val Gln Ile	490	495	500	
ggt ggc act cca gcc atg gag atc gaa tcc att gag gcg ctc ttt gaa				1651
Gly Gly Thr Pro Ala Met Glu Ile Glu Ser Ile Glu Ala Leu Phe Glu	505	510	515	
aag ctc ctc tgg atg gct ctc tac att gtg ctg gcc act ttc atc ctc				1699
Lys Leu Leu Trp Met Ala Leu Tyr Ile Val Leu Ala Thr Phe Ile Leu	520	525	530	
atg gca ttg gta ttt ggt tcg gtg att ttg ccg gcg aag gcc atc atc				1747
Met Ala Leu Val Phe Gly Ser Val Ile Leu Pro Ala Lys Ala Ile Ile	535	540	545	
atg acc att ctg ggt atg ggt gcc acc ttg ggt att ctc acc ttg atg				1795
Met Thr Ile Leu Gly Met Gly Ala Thr Leu Gly Ile Leu Thr Leu Met	550	555	560	565

ttc gtc gat ggc gtg ggt gcc agc gca ttg aac ttc tcc cct ggc cca 1843
 Phe Val Asp Gly Val Gly Ala Ser Ala Leu Asn Phe Ser Pro Gly Pro
 570 575 580

ctg atg agt cca gtg ctg gtg ctg atc atg gct att att tac gga ctt 1891
 Leu Met Ser Pro Val Leu Val Leu Ile Met Ala Ile Ile Tyr Gly Leu
 585 590 595

tcc acc gac tat gag gtg ttc ctg gta tct cgc atg gtg gag gcc cgc 1939
 Ser Thr Asp Tyr Glu Val Phe Leu Val Ser Arg Met Val Glu Ala Arg
 600 605 610

gat aaa ggc gaa tcc acc gac gac gcc atc aga tac ggc act gca cac 1987
 Asp Lys Gly Glu Ser Thr Asp Asp Ala Ile Arg Tyr Gly Thr Ala His
 615 620 625

acc gga tct atc atc acc gcg gcc gca ctg atc atg att gtg gtc tgt 2035
 Thr Gly Ser Ile Ile Thr Ala Ala Ala Leu Ile Met Ile Val Val Cys
 630 635 640 645

gga gcg ttt ggt ttc tct gag atc gtc atg atg aag tac atc gcg ttc 2083
 Gly Ala Phe Gly Phe Ser Glu Ile Val Met Met Lys Tyr Ile Ala Phe
 650 655 660

ggc atg atc gca gcg ctg att ctg gat gcc acc atc atc cgc atg ctg 2131
 Gly Met Ile Ala Ala Leu Ile Leu Asp Ala Thr Ile Ile Arg Met Leu
 665 670 675

ctt gtc ccc cgc cgt gat gca cct gct tcg cga cga caa ctg gtg ggc 2179
 Leu Val Pro Arg Arg Asp Ala Pro Ala Ser Arg Arg Gln Leu Val Gly
 680 685 690

acc cgg ctt cgt taaaaaggcc tacaccgtca tgg 2214
 Thr Arg Leu Arg
 695

<210> 362

<211> 697

<212> PRT

<213> Corynebacterium glutamicum

<400> 362

Val Phe Ser Lys Trp Gly His Phe Ala Tyr Arg Phe Arg Arg Ile Val
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Pro Leu Val Val Ile Ala Ala Ile Leu Ala Leu Phe Val Ile Phe Gly
 20 25 30

Thr Lys Leu Gly Asp Arg Met Ser Gln Glu Gly Trp Asp Asp Pro Gly
 35 40 45

Ser Ser Ser Thr Ala Ala Ala Arg Ile Glu Leu Glu Thr Phe Gly Arg
 50 55 60

Asp Asn Asp Gly Asp Val Val Leu Leu Phe Thr Ala Pro Glu Gly Thr
 65 70 75 80

Ser Phe Asp Asp Ala Glu Val Phe Ser Ser Ile Ser Gly Tyr Leu Asp
 85 90 95

Gly Leu Ile Glu Asn Asn Pro Asp Glu Val Ser His Ile Asn Ser Tyr
 100 105 110
 Phe Asp Thr Arg Asn Gln Asn Leu Leu Ser Lys Asp Gly Thr Gln Thr
 115 120 125
 Phe Ala Ala Leu Gly Leu Lys Gly Asp Gly Glu Gln Thr Leu Lys Asp
 130 135 140
 Phe Arg Glu Ile Glu Asp Gln Leu His Pro Asp Asn Leu Ala Gly Gly
 145 150 155 160
 Val Thr Thr Glu Val Ala Gly Ala Thr Ala Val Ala Asp Ala Leu Asp
 165 170 175
 Glu Gly Met Ala Gly Asp Ile Ser Arg Ala Glu Val Phe Ala Leu Pro
 180 185 190
 Phe Val Ala Ile Leu Leu Leu Ile Val Phe Gly Ser Val Val Ala Ala
 195 200 205
 Ala Met Pro Leu Ile Val Gly Ile Leu Ser Ile Leu Gly Ser Leu Gly
 210 215 220
 Ile Leu Ala Ile Leu Ala Gly Phe Phe Gln Val Asn Val Phe Ala Gln
 225 230 235 240
 Ser Val Val Thr Leu Leu Gly Leu Gly Leu Ala Ile Asp Tyr Gly Leu
 245 250 255
 Phe Met Val Ser Arg Phe Arg Glu Glu Met Asp Lys Gly Thr Pro Val
 260 265 270
 Glu Gln Ala Val Ala Thr Thr Thr Ala Thr Ala Gly Lys Thr Val Val
 275 280 285
 Phe Ser Ala Ala Met Val Ala Val Ala Leu Ser Gly Leu Phe Val Phe
 290 295 300
 Pro Gln Ala Phe Leu Lys Ser Val Ala Phe Gly Ala Ile Ser Ala Val
 305 310 315 320
 Gly Leu Ala Ala Leu Met Ser Val Thr Val Leu Pro Ser Leu Phe Ser
 325 330 335
 Met Leu Gly Lys Asn Ile Asp Lys Trp Ser Leu Arg Arg Thr Ala Arg
 340 345 350
 Thr Ala Arg Arg Leu Glu Asp Thr Ile Trp Tyr Arg Val Pro Ala Trp
 355 360 365
 Ala Met Arg His Ala Lys Ala Val Thr Val Gly Val Val Leu Leu Leu
 370 375 380
 Leu Ala Leu Thr Val Pro Leu Thr Gly Val Lys Phe Gly Gly Ile Asn
 385 390 395 400
 Glu Thr Tyr Leu Pro Pro Ala Asn Asp Thr Arg Val Ala Gln Glu Arg
 405 410 415

Phe Asp Glu Ala Phe Pro Ala Phe Arg Thr Glu Pro Val Lys Leu Val
 420 425 430
 Val Thr Gly Ala Asp Asn Asn Gln Leu Ile Asp Ile Tyr Val Gln Ala
 435 440 445
 Asn Glu Val Glu Gly Leu Thr Asp Arg Phe Thr Ala Gly Ala Thr Thr
 450 455 460
 Asp Asp Gly Thr Thr Val Leu Ser Thr Gly Ile Gln Asp Arg Ser Leu
 465 470 475 480
 Asn Glu Gln Val Val Glu Gln Leu Arg Ala Ile Ser Val Pro Glu Gly
 485 490 495
 Val Glu Val Gln Ile Gly Gly Thr Pro Ala Met Glu Ile Glu Ser Ile
 500 505 510
 Glu Ala Leu Phe Glu Lys Leu Leu Trp Met Ala Leu Tyr Ile Val Leu
 515 520 525
 Ala Thr Phe Ile Leu Met Ala Leu Val Phe Gly Ser Val Ile Leu Pro
 530 535 540
 Ala Lys Ala Ile Ile Met Thr Ile Leu Gly Met Gly Ala Thr Leu Gly
 545 550 555 560
 Ile Leu Thr Leu Met Phe Val Asp Gly Val Gly Ala Ser Ala Leu Asn
 565 570 575
 Phe Ser Pro Gly Pro Leu Met Ser Pro Val Leu Val Leu Ile Met Ala
 580 585 590
 Ile Ile Tyr Gly Leu Ser Thr Asp Tyr Glu Val Phe Leu Val Ser Arg
 595 600 605
 Met Val Glu Ala Arg Asp Lys Gly Glu Ser Thr Asp Asp Ala Ile Arg
 610 615 620
 Tyr Gly Thr Ala His Thr Gly Ser Ile Ile Thr Ala Ala Ala Leu Ile
 625 630 635 640
 Met Ile Val Val Cys Gly Ala Phe Gly Phe Ser Glu Ile Val Met Met
 645 650 655
 Lys Tyr Ile Ala Phe Gly Met Ile Ala Ala Leu Ile Leu Asp Ala Thr
 660 665 670
 Ile Ile Arg Met Leu Leu Val Pro Arg Arg Asp Ala Pro Ala Ser Arg
 675 680 685
 Arg Gln Leu Val Gly Thr Arg Leu Arg
 690 695

<210> 363

<211> 729

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(706)

<223> RXS03042

<400> 363

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tcgcctcggc gacgtcctgg ttccttacgt tctgatcggt ttg gtt cta gcg ttc 115
                                   Leu Val Leu Ala Phe
                                   1           5

ctc gtg ctg ttg ctc gtg ttc cgg tcc att tgg gtc cca ttg atc gcg 163
Leu Val Leu Leu Leu Val Phe Arg Ser Ile Trp Val Pro Leu Ile Ala
                        10                        15                        20

gct ctg ggc ttt ggc ttg tca gtt ctg gct acc ttt ggt gct acc gtg 211
Ala Leu Gly Phe Gly Leu Ser Val Leu Ala Thr Phe Gly Ala Thr Val
                        25                        30                        35

gcg atc ttc caa gaa ggt gct ttc ggc atc atc gac gat cct cag cca 259
Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile Asp Asp Pro Gln Pro
                        40                        45                        50

ctg ctg tcc ttc ttg ccg atc atg ctc atc ggc ctg gta ttt ggt ctg 307
Leu Leu Ser Phe Leu Pro Ile Met Leu Ile Gly Leu Val Phe Gly Leu
                        55                        60                        65

gcc atg gat tac cag atc ttc ctc gtt act cgt atg cgt gag ggc ttc 355
Ala Met Asp Tyr Gln Ile Phe Leu Val Thr Arg Met Arg Glu Gly Phe
                        70                        75                        80                        85

acc aag ggc aag act gcg ggc aac gca acg tcg aat ggt ttc aag cac 403
Thr Lys Gly Lys Thr Ala Gly Asn Ala Thr Ser Asn Gly Phe Lys His
                        90                        95                        100

ggg gcc cgc gtg gtc act gct gcg gcg ctg atc atg gtg tct gtg ttc 451
Gly Ala Arg Val Val Thr Ala Ala Ala Leu Ile Met Val Ser Val Phe
                        105                        110                        115

gcg gca ttc ata gcg cag gac atg gcg ttt att aag acc atg ggc ttt 499
Ala Ala Phe Ile Ala Gln Asp Met Ala Phe Ile Lys Thr Met Gly Phe
                        120                        125                        130

gct ctg gcc gtt gct gtg ttc ttc gat gcc ttc gtt gtt cgc atg atg 547
Ala Leu Ala Val Ala Val Phe Phe Asp Ala Phe Val Val Arg Met Met
                        135                        140                        145

att atc cct gca aca atg ttc ctg ctt gat gac aag gct tgg tgg cta 595
Ile Ile Pro Ala Thr Met Phe Leu Leu Asp Asp Lys Ala Trp Trp Leu
                        150                        155                        160                        165

cct aag tgg ttg gat aag att ctt ccc aac gtt gat gtt gaa ggt gag 643
Pro Lys Trp Leu Asp Lys Ile Leu Pro Asn Val Asp Val Glu Gly Glu
                        170                        175                        180

ggg ctt agt gaa cta cat gag gct cgc acc gag gaa ctg aag gaa aat 691
Gly Leu Ser Glu Leu His Glu Ala Arg Thr Glu Glu Leu Lys Glu Asn
                        185                        190                        195

gta ggt gtc ggg gct tagagaaaca aaaaaggctg cta 729
Val Gly Val Gly Ala

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200

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 <211> 202
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 364

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 1 5 10 15

Val Pro Leu Ile Ala Ala Leu Gly Phe Gly Leu Ser Val Leu Ala Thr
 20 25 30

Phe Gly Ala Thr Val Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile
 35 40 45

Asp Asp Pro Gln Pro Leu Leu Ser Phe Leu Pro Ile Met Leu Ile Gly
 50 55 60

Leu Val Phe Gly Leu Ala Met Asp Tyr Gln Ile Phe Leu Val Thr Arg
 65 70 75 80

Met Arg Glu Gly Phe Thr Lys Gly Lys Thr Ala Gly Asn Ala Thr Ser
 85 90 95

Asn Gly Phe Lys His Gly Ala Arg Val Val Thr Ala Ala Ala Leu Ile
 100 105 110

Met Val Ser Val Phe Ala Ala Phe Ile Ala Gln Asp Met Ala Phe Ile
 115 120 125

Lys Thr Met Gly Phe Ala Leu Ala Val Ala Val Phe Phe Asp Ala Phe
 130 135 140

Val Val Arg Met Met Ile Ile Pro Ala Thr Met Phe Leu Leu Asp Asp
 145 150 155 160

Lys Ala Trp Trp Leu Pro Lys Trp Leu Asp Lys Ile Leu Pro Asn Val
 165 170 175

Asp Val Glu Gly Glu Gly Leu Ser Glu Leu His Glu Ala Arg Thr Glu
 180 185 190

Glu Leu Lys Glu Asn Val Gly Val Gly Ala
 195 200

<210> 365
 <211> 826
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(826)

<223> RXS03075

<400> 365

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	Val Ala Lys Phe Leu	
	1 5	
tat aag tta ggc tcc acg gcc tat caa aag aaa tgg ccg ttt ctt gcg	163	
Tyr Lys Leu Gly Ser Thr Ala Tyr Gln Lys Lys Trp Pro Phe Leu Ala		
10 15 20		
gtc tgg ctc gtg att ctc ata ggt atc acg acg ctg gcg ggg ctg tat	211	
Val Trp Leu Val Ile Leu Ile Gly Ile Thr Thr Leu Ala Gly Leu Tyr		
25 30 35		
gcc aag cca acg tcg agt agc ttc tct atc cct ggt ctt gat tct gtc	259	
Ala Lys Pro Thr Ser Ser Ser Phe Ser Ile Pro Gly Leu Asp Ser Val		
40 45 50		
acg acc atg gag aag atg cag gag cgt ttc cct ggt tcg gat gat gca	307	
Thr Thr Met Glu Lys Met Gln Glu Arg Phe Pro Gly Ser Asp Asp Ala		
55 60 65		
aca tcg gct ccc act ggt tct gtc gtc att cag gca ccg gaa ggc aag	355	
Thr Ser Ala Pro Thr Gly Ser Val Val Ile Gln Ala Pro Glu Gly Lys		
70 75 80 85		
acc ctc act gat cct gag gtt ggg gct gaa gta aac cag atg ctt gat	403	
Thr Leu Thr Asp Pro Glu Val Gly Ala Glu Val Asn Gln Met Leu Asp		
90 95 100		
gag gtt cgg gcg act ggt gtg ctg aag gat gct gat tcc gtt gtg gat	451	
Glu Val Arg Ala Thr Gly Val Leu Lys Asp Ala Asp Ser Val Val Asp		
105 110 115		
cct gtg ttg gct gcg cag ggt gtg gct gct cag atg acc cca gcc ctg	499	
Pro Val Leu Ala Ala Gln Gly Val Ala Ala Gln Met Thr Pro Ala Leu		
120 125 130		
gag gct cag ggt gta cct gcg gag aag atc gcc gca gat att gag tcg	547	
Glu Ala Gln Gly Val Pro Ala Glu Lys Ile Ala Ala Asp Ile Glu Ser		
135 140 145		
att agt cca ctg agt gca gat gag act acc ggc atc atc tcg atg act	595	
Ile Ser Pro Leu Ser Ala Asp Glu Thr Thr Gly Ile Ile Ser Met Thr		
150 155 160 165		
ttt gat gca gat tct gcc atg gat ata tcc gca gag gat cgt gag aag	643	
Phe Asp Ala Asp Ser Ala Met Asp Ile Ser Ala Glu Asp Arg Glu Lys		
170 175 180		
gtc acc aat att ctt gat gaa tac gat gac ggc gat ctg act gtt gtc	691	
Val Thr Asn Ile Leu Asp Glu Tyr Asp Asp Gly Asp Leu Thr Val Val		
185 190 195		
tac aac ggc aac gtg ttt ggc gca gct gca acc agc ttg gac atg acc	739	
Tyr Asn Gly Asn Val Phe Gly Ala Ala Ala Thr Ser Leu Asp Met Thr		
200 205 210		
tct gag ctc atc ggc ctg ctg gtg gct gcg gtc gtt ctt atc gtg acc	787	
Ser Glu Leu Ile Gly Leu Leu Val Ala Ala Val Val Leu Ile Val Thr		
215 220 225		

ttc ggt tgc ttc atc gct gcc ggt atg ccg ctg atc tct
 Phe Gly Ser Phe Ile Ala Ala Gly Met Pro Leu Ile Ser
 230 235 240

826

<210> 366

<211> 242

<212> PRT

<213> Corynebacterium glutamicum

<400> 366

Val Ala Lys Phe Leu Tyr Lys Leu Gly Ser Thr Ala Tyr Gln Lys Lys
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Trp Pro Phe Leu Ala Val Trp Leu Val Ile Leu Ile Gly Ile Thr Thr
 20 25 30

Leu Ala Gly Leu Tyr Ala Lys Pro Thr Ser Ser Ser Phe Ser Ile Pro
 35 40 45

Gly Leu Asp Ser Val Thr Thr Met Glu Lys Met Gln Glu Arg Phe Pro
 50 55 60

Gly Ser Asp Asp Ala Thr Ser Ala Pro Thr Gly Ser Val Val Ile Gln
 65 70 75 80

Ala Pro Glu Gly Lys Thr Leu Thr Asp Pro Glu Val Gly Ala Glu Val
 85 90 95

Asn Gln Met Leu Asp Glu Val Arg Ala Thr Gly Val Leu Lys Asp Ala
 100 105 110

Asp Ser Val Val Asp Pro Val Leu Ala Ala Gln Gly Val Ala Ala Gln
 115 120 125

Met Thr Pro Ala Leu Glu Ala Gln Gly Val Pro Ala Glu Lys Ile Ala
 130 135 140

Ala Asp Ile Glu Ser Ile Ser Pro Leu Ser Ala Asp Glu Thr Thr Gly
 145 150 155 160

Ile Ile Ser Met Thr Phe Asp Ala Asp Ser Ala Met Asp Ile Ser Ala
 165 170 175

Glu Asp Arg Glu Lys Val Thr Asn Ile Leu Asp Glu Tyr Asp Asp Gly
 180 185 190

Asp Leu Thr Val Val Tyr Asn Gly Asn Val Phe Gly Ala Ala Ala Thr
 195 200 205

Ser Leu Asp Met Thr Ser Glu Leu Ile Gly Leu Leu Val Ala Ala Val
 210 215 220

Val Leu Ile Val Thr Phe Gly Ser Phe Ile Ala Ala Gly Met Pro Leu
 225 230 235 240

Ile Ser

<210> 367

<211> 983
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(960)
 <223> RXS03124

<400> 367
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 tac gcg cta ttt atc gtg tcc cgt ttc cgc aat gag ttg att tct cag 96
 Tyr Ala Leu Phe Ile Val Ser Arg Phe Arg Asn Glu Leu Ile Ser Gln
 20 25 30
 act ggc gct aat gat ctg gag cca aag gaa ttg gct gag cgt ctg cgc 144
 Thr Gly Ala Asn Asp Leu Glu Pro Lys Glu Leu Ala Glu Arg Leu Arg
 35 40 45
 acc atg ccg ttg gct gct cgt gcg cat gcg atg gga atg gct gtg ggc 192
 Thr Met Pro Leu Ala Ala Arg Ala His Ala Met Gly Met Ala Val Gly
 50 55 60
 act gcg ggt tct gcg gtt gta ttc gcg ggt acc acg gtg ctg atc gct 240
 Thr Ala Gly Ser Ala Val Val Phe Ala Gly Thr Thr Val Leu Ile Ala
 65 70 75 80
 ctg gtt gct ctg tcg atc att aat att cca ttt cta acc gtg atg gcc 288
 Leu Val Ala Leu Ser Ile Ile Asn Ile Pro Phe Leu Thr Val Met Ala
 85 90 95
 att gct gcc gca atc acc gtt gcc atc gca gtt ctg gtt gct ctg tcc 336
 Ile Ala Ala Ala Ile Thr Val Ala Ile Ala Val Leu Val Ala Leu Ser
 100 105 110
 ttc ctg cca gct ctg ctt ggc ctg ctt ggc act cgc atc ttc gca gca 384
 Phe Leu Pro Ala Leu Leu Gly Leu Leu Gly Thr Arg Ile Phe Ala Ala
 115 120 125
 cgc gtg cct gga cct aag gtt ccg gat cct gag gac gag aag cca acg 432
 Arg Val Pro Gly Pro Lys Val Pro Asp Pro Glu Asp Glu Lys Pro Thr
 130 135 140
 atg ggt ctg aag tgg gtc cgc ctt gtg cgc aag atg ccg gtg gct tac 480
 Met Gly Leu Lys Trp Val Arg Leu Val Arg Lys Met Pro Val Ala Tyr
 145 150 155 160
 ctg ctg gtt ggc gtc gtt ttg ctt ggt gca atc gca att cct gcg acc 528
 Leu Leu Val Gly Val Val Leu Leu Gly Ala Ile Ala Ile Pro Ala Thr
 165 170 175
 aat atg cgc ctg gcc atg ccg act gat ggc acc tcc acg ctg ggc acc 576
 Asn Met Arg Leu Ala Met Pro Thr Asp Gly Thr Ser Thr Leu Gly Thr
 180 185 190
 gcg ccg cgc acg ggg tat gac atg acg gca gat gcg ttc ggc ccg ggc 624
 Ala Pro Arg Thr Gly Tyr Asp Met Thr Ala Asp Ala Phe Gly Pro Gly
 195 200 205

cgc aac gcg ccc atg att gcg ctt atc gac gca acc gac gtc cct gag 672
 Arg Asn Ala Pro Met Ile Ala Leu Ile Asp Ala Thr Asp Val Pro Glu
 210 215 220

 gaa gaa cgc cca ttg gtg ttt gga cag gcg gtg gag caa ttc ttg aac 720
 Glu Glu Arg Pro Leu Val Phe Gly Gln Ala Val Glu Gln Phe Leu Asn
 225 230 235 240

 act gat ggt gtg aag aat gct cag atc act cag acc acg gag aat ttc 768
 Thr Asp Gly Val Lys Asn Ala Gln Ile Thr Gln Thr Thr Glu Asn Phe
 245 250 255

 gat acc gcg cag atc ctg tta ccc cag aat ttg atg cga tcg atg agc 816
 Asp Thr Ala Gln Ile Leu Leu Pro Gln Asn Leu Met Arg Ser Met Ser
 260 265 270

 gca cct ctg aga ctc tcg caa ctc ttc gtg cag atg ctg aga cct tcg 864
 Ala Pro Leu Arg Leu Ser Gln Leu Phe Val Gln Met Leu Arg Pro Ser
 275 280 285

 ctg atg aca ccg gcg cga cgt atg gca tta ctg gcg tca ccc caa ttt 912
 Leu Met Thr Pro Ala Arg Arg Met Ala Leu Leu Ala Ser Pro Gln Phe
 290 295 300

 acg atg aca tct ctg ctc gcc tcg gcg acg tcc tgg ttc ctt acg ttc 960
 Thr Met Thr Ser Leu Leu Ala Ser Ala Thr Ser Trp Phe Leu Thr Phe
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<210> 368

<211> 320

<212> PRT

<213> Corynebacterium glutamicum

<400> 368

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 Thr Gly Ala Asn Asp Leu Glu Pro Lys Glu Leu Ala Glu Arg Leu Arg
 35 40 45

 Thr Met Pro Leu Ala Ala Arg Ala His Ala Met Gly Met Ala Val Gly
 50 55 60

 Thr Ala Gly Ser Ala Val Val Phe Ala Gly Thr Thr Val Leu Ile Ala
 65 70 75 80

 Leu Val Ala Leu Ser Ile Ile Asn Ile Pro Phe Leu Thr Val Met Ala
 85 90 95

 Ile Ala Ala Ala Ile Thr Val Ala Ile Ala Val Leu Val Ala Leu Ser
 100 105 110

 Phe Leu Pro Ala Leu Leu Gly Leu Leu Gly Thr Arg Ile Phe Ala Ala
 115 120 125

Arg Val Pro Gly Pro Lys Val Pro Asp Pro Glu Asp Glu Lys Pro Thr
 130 135 140
 Met Gly Leu Lys Trp Val Arg Leu Val Arg Lys Met Pro Val Ala Tyr
 145 150 155 160
 Leu Leu Val Gly Val Val Leu Leu Gly Ala Ile Ala Ile Pro Ala Thr
 165 170 175
 Asn Met Arg Leu Ala Met Pro Thr Asp Gly Thr Ser Thr Leu Gly Thr
 180 185 190
 Ala Pro Arg Thr Gly Tyr Asp Met Thr Ala Asp Ala Phe Gly Pro Gly
 195 200 205
 Arg Asn Ala Pro Met Ile Ala Leu Ile Asp Ala Thr Asp Val Pro Glu
 210 215 220
 Glu Glu Arg Pro Leu Val Phe Gly Gln Ala Val Glu Gln Phe Leu Asn
 225 230 235 240
 Thr Asp Gly Val Lys Asn Ala Gln Ile Thr Gln Thr Thr Glu Asn Phe
 245 250 255
 Asp Thr Ala Gln Ile Leu Leu Pro Gln Asn Leu Met Arg Ser Met Ser
 260 265 270
 Ala Pro Leu Arg Leu Ser Gln Leu Phe Val Gln Met Leu Arg Pro Ser
 275 280 285
 Leu Met Thr Pro Ala Arg Arg Met Ala Leu Leu Ala Ser Pro Gln Phe
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<210> 369

<211> 271

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(271)

<223> RXS03125

<400> 369

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 Leu Val Leu Ala Phe
 1 5

ctc gtg ctg ttg ctc gtg ttc cgg tcc att tgg gtc cca ttg atc gcg 163
 Leu Val Leu Leu Val Phe Arg Ser Ile Trp Val Pro Leu Ile Ala
 10 15 20

gct ctg ggc ttt ggc ttg tca gtt ctg gct acc ttt ggt gct acc gtg 211
 Ala Leu Gly Phe Gly Leu Ser Val Leu Ala Thr Phe Gly Ala Thr Val

25 30 35
 gcg atc ttc caa gaa ggt gct ttc ggc atc atc gac gat cct cag cca 259
 Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile Asp Asp Pro Gln Pro
 40 45 50
 ctg ctg tgc ttc 271
 Leu Leu Cys Phe
 55
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 <211> 57
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 370
 Leu Val Leu Ala Phe Leu Val Leu Leu Leu Val Phe Arg Ser Ile Trp
 1 5 10 15
 Val Pro Leu Ile Ala Ala Leu Gly Phe Gly Leu Ser Val Leu Ala Thr
 20 25 30
 Phe Gly Ala Thr Val Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile
 35 40 45
 Asp Asp Pro Gln Pro Leu Leu Cys Phe
 50 55
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 <212> DNA
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 <222> (101)..(553)
 <223> RXA00596
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 ccacgggagt gccaaagccct agctaccagg gaggaacta atg ctt aac gcc ctg 115
 Met Leu Asn Ala Leu
 1 5
 aaa ttc atc cca tgg ctg atc ggc cag att ttc ctc tct ggc ttc agc 163
 Lys Phe Ile Pro Trp Leu Ile Gly Gln Ile Phe Leu Ser Gly Phe Ser
 10 15 20
 gtg atc acc gct gcg gta aaa aag gac acc ggc ttc aac ccc gtt gtt 211
 Val Ile Thr Ala Ala Val Lys Lys Asp Thr Gly Phe Asn Pro Val Val
 25 30 35
 atc cgc tac cca ctt cga gtg acc acg gac ttc cag atc gca gcc ctg 259
 Ile Arg Tyr Pro Leu Arg Val Thr Thr Asp Phe Gln Ile Ala Ala Leu
 40 45 50
 tca acg tgc atc acc gcg act cct tcc acc ctg tcc ctt ggc cta cgc 307
 Ser Thr Cys Ile Thr Ala Thr Pro Ser Thr Leu Ser Leu Gly Leu Arg

55	60	65	
gaa ccc cgc aag ccc ggc gac ccc acc att ttg ctg atc caa gca gtg Glu Pro Arg Lys Pro Gly Asp Pro Thr Ile Leu Leu Ile Gln Ala Val 70 75 80 85			355
ttt ggt tcc gat cca gta gaa gtt ttt gaa tcc atc gcc gat atg gaa Phe Gly Ser Asp Pro Val Glu Val Phe Glu Ser Ile Ala Asp Met Glu 90 95 100			403
caa cgc ctc gtc cct tcg gtc gct tca att gac cac ggc gtc cca ggc Gln Arg Leu Val Pro Ser Val Ala Ser Ile Asp His Gly Val Pro Gly 105 110 115			451
caa ggc cct tac aag gag atc cgc ccc agc gat gct gag tgg cca agt Gln Gly Pro Tyr Lys Glu Ile Arg Pro Ser Asp Ala Glu Trp Pro Ser 120 125 130			499
cgc gag atc gct gac acc gcc caa aac acc gtc agc caa gac aag agg Arg Glu Ile Ala Asp Thr Ala Gln Asn Thr Val Ser Gln Asp Lys Arg 135 140 145			547
gag ttt taaaacaaca tgactgcttt tgg Glu Phe 150			576
<210> 372			
<211> 151			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 372			
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Leu Ser Gly Phe Ser Val Ile Thr Ala Ala Val Lys Lys Asp Thr Gly 20 25 30			
Phe Asn Pro Val Val Ile Arg Tyr Pro Leu Arg Val Thr Thr Asp Phe 35 40 45			
Gln Ile Ala Ala Leu Ser Thr Cys Ile Thr Ala Thr Pro Ser Thr Leu 50 55 60			
Ser Leu Gly Leu Arg Glu Pro Arg Lys Pro Gly Asp Pro Thr Ile Leu 65 70 75 80			
Leu Ile Gln Ala Val Phe Gly Ser Asp Pro Val Glu Val Phe Glu Ser 85 90 95			
Ile Ala Asp Met Glu Gln Arg Leu Val Pro Ser Val Ala Ser Ile Asp 100 105 110			
His Gly Val Pro Gly Gln Gly Pro Tyr Lys Glu Ile Arg Pro Ser Asp 115 120 125			
Ala Glu Trp Pro Ser Arg Glu Ile Ala Asp Thr Ala Gln Asn Thr Val 130 135 140			
Ser Gln Asp Lys Arg Glu Phe			

150

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<221> CDS
<222> (101)..(715)
<223> RXA02079
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gat gca acc aaa gtg cgc aaa gct gtg ctc acc gtc gcg ctg ctt aac 163
Asp Ala Thr Lys Val Arg Lys Ala Val Leu Thr Val Ala Leu Leu Asn
10 15 20

gtt tct cta ctg gct gac agt gtc gat ttt ctt gaa gac acc tcc atc 259
Val Ser Leu Leu Ala Asp Ser Val Asp Phe Leu Glu Asp Thr Ser Ile
40 45 50

gtg	atg	ggc	aaa	ctt	atg	gcg	att	gtg	att	ctt	gca	cct	gct	gct	ttt	355
Val	Met	Gly	Lys	Leu	Met	Ala	Ile	Val	Ile	Leu	Ala	Pro	Ala	Ala	Phe	
70					75					80					85	

gtg ttt ccg atc gtc gct tct ctg ggc gcc gtc gtg atc aac ggc 451
Val Phe Pro Ile Ile Val Ala Ser Leu Gly Ala Val Val Ile Asn Gly
105 110 115

ggc caa gct gcc ttc cta tcc gcc cga aat gac gtc ctg atc aac att 547
Gly Gln Ala Ala Phe Leu Ser Ala Arg Asn Asp Val Leu Ile Asn Ile
135 140 145

cca gat ttg atc cta ggt tgt ttc atc att ctg ctc gca ctg cac gcc 643

Pro Asp Leu Ile Leu Gly Cys Phe Ile Ile Leu Leu Ala Leu His Ala
 170 175 180

gct cac gag gtg tgg gaa gtc agt gag gaa gaa cgc ctc gcc tcc aaa 691
 Ala His Glu Val Trp Glu Val Ser Glu Glu Glu Arg Leu Ala Ser Lys
 185 190 195

gcc ctt gct ggg gaa gcc atc gat taggggagca gtatgagctt ttc 738
 Ala Leu Ala Gly Glu Ala Ile Asp
 200 205

<210> 374

<211> 205

<212> PRT

<213> Corynebacterium glutamicum

<400> 374

Met Ser Glu Ala Phe Asp Ala Thr Lys Val Arg Lys Ala Val Leu Thr
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 20 25 30

Leu Ser Ala Gly Ser Val Ser Leu Leu Ala Asp Ser Val Asp Phe Leu
 35 40 45

Glu Asp Thr Ser Ile Asn Leu Leu Ile Phe Ile Ala Leu Gly Trp Pro
 50 55 60

Leu Ala Arg Arg Ala Val Met Gly Lys Leu Met Ala Ile Val Ile Leu
 65 70 75 80

Ala Pro Ala Ala Phe Ala Ala Trp Ala Ala Ile Gln Arg Phe Ser Ala
 85 90 95

Pro Gln Ala Pro Glu Val Phe Pro Ile Ile Val Ala Ser Leu Gly Ala
 100 105 110

Val Val Ile Asn Gly Ala Ser Ala Ile Ile Ile Ser Arg Val Arg Gln
 115 120 125

His Gly Gly Ser Leu Gly Gln Ala Ala Phe Leu Ser Ala Arg Asn Asp
 130 135 140

Val Leu Ile Asn Ile Ala Ile Ile Met Met Ala Leu Ile Thr Ala Trp
 145 150 155 160

Thr Thr Ser Gly Trp Pro Asp Leu Ile Leu Gly Cys Phe Ile Ile Leu
 165 170 175

Leu Ala Leu His Ala Ala His Glu Val Trp Glu Val Ser Glu Glu Glu
 180 185 190

Arg Leu Ala Ser Lys Ala Leu Ala Gly Glu Ala Ile Asp
 195 200 205

<210> 375

<211> 1458

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1435)

<223> RXA01303

<400> 375

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tgacggaaag cctttccgcg taaccatgaa gaggcatacac gtg aca caa ctc aac 115
                               Val Thr Gln Leu Asn
                               1           5

acc aaa ggc gtt gtt ctg caa ggg tgg gat cca gaa gat cct gaa cat 163
Thr Lys Gly Val Val Leu Gln Gly Trp Asp Pro Glu Asp Pro Glu His
                10                15                20

tgg gac tcg aaa att gca tgg cga acc ctg tgg att acc acc ttc tcc 211
Trp Asp Ser Lys Ile Ala Trp Arg Thr Leu Trp Ile Thr Thr Phe Ser
                25                30                35

atg att att ggg ttc tgc gtg tgg tat ttg gtt tct gcc atc gct ccc 259
Met Ile Ile Gly Phe Cys Val Trp Tyr Leu Val Ser Ala Ile Ala Pro
                40                45                50

cta ctc aat cga att gga ttt gat ctc tca gca ggt cag ctt tat tgg 307
Leu Leu Asn Arg Ile Gly Phe Asp Leu Ser Ala Gly Gln Leu Tyr Trp
                55                60                65

ctc gca tct atc ccc ggt ttg gcc ggc gga tta atc cga ttg att tac 355
Leu Ala Ser Ile Pro Gly Leu Ala Gly Gly Leu Ile Arg Leu Ile Tyr
                70                75                80                85

atg ttc ctt cca ccg att ctt gga acc cgc aaa ttg gtc gga att tcc 403
Met Phe Leu Pro Pro Ile Leu Gly Thr Arg Lys Leu Val Gly Ile Ser
                90                95                100

tcc ggt cta ttt ttg atc ccc atg ttt ggg tgg ttc ctg gct gtc caa 451
Ser Gly Leu Phe Leu Ile Pro Met Phe Gly Trp Phe Leu Ala Val Gln
                105                110                115

gat tca agc act ccc tac tgg tgg ctt ctc aca ctc gct gca ctc act 499
Asp Ser Ser Thr Pro Tyr Trp Trp Leu Leu Thr Leu Ala Ala Leu Thr
                120                125                130

ggc att ggt ggt ggc gtg ttc tct gga tat atg ccg tcc acg gga tac 547
Gly Ile Gly Gly Gly Val Phe Ser Gly Tyr Met Pro Ser Thr Gly Tyr
                135                140                145

ttc ttc ccc aag gca aaa tcg ggc act gcg ctg ggc att cag gca ggt 595
Phe Phe Pro Lys Ala Lys Ser Gly Thr Ala Leu Gly Ile Gln Ala Gly
                150                155                160                165

atc ggc aac ctc ggc gtc tcg ata att cag ttc atg ggc cca tgg gtc 643
Ile Gly Asn Leu Gly Val Ser Ile Ile Gln Phe Met Gly Pro Trp Val
                170                175                180

atg ggt ttc ggt ctg ctg ggc att ggt ttc ctc acc ccg cag cgc acc 691
Met Gly Phe Gly Leu Leu Gly Ile Gly Phe Leu Thr Pro Gln Arg Thr
                185                190                195

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att gaa ggc acc acg gtg ttt gtg cac aat gct gcg att gtg ttg gtc Ile Glu Gly Thr Thr Val Phe Val His Asn Ala Ala Ile Val Leu Val 200 205 210	739
ccg tgg act att ctc gcg gcc gtt tta tcc ttc ctg ttt ctt aaa gat Pro Trp Thr Ile Leu Ala Ala Val Leu Ser Phe Leu Phe Leu Lys Asp 215 220 225	787
gtc cca gtc acc gca aat ttc cgg caa cag atc gat atc ttt ggc aac Val Pro Val Thr Ala Asn Phe Arg Gln Gln Ile Asp Ile Phe Gly Asn 230 235 240 245	835
aag aac aca tgg att ttg tcc att atc tac ttg atg aca ttc ggt gcc Lys Asn Thr Trp Ile Leu Ser Ile Ile Tyr Leu Met Thr Phe Gly Ala 250 255 260	883
ttc gcc ggt ttc gcc gcg cag ttc ggt ctg atc atc aac aac aac ttc Phe Ala Gly Phe Ala Ala Gln Phe Gly Leu Ile Ile Asn Asn Asn Phe 265 270 275	931
ggc atc gct tcc ccg atg gca gag act tat cca gct gag atg ctt cac Gly Ile Ala Ser Pro Met Ala Glu Thr Tyr Pro Ala Glu Met Leu His 280 285 290	979
gcc ggt gct acg ttc gcg ttt ctt gga cct ttg att ggt gct ttg gtg Ala Gly Ala Thr Phe Ala Phe Leu Gly Pro Leu Ile Gly Ala Leu Val 295 300 305	1027
cgt gct gca tgg ggt cca ctg tgt gac aga ttc ggt gga gct atc tgg Arg Ala Ala Trp Gly Pro Leu Cys Asp Arg Phe Gly Gly Ala Ile Trp 310 315 320 325	1075
acc ttt gtc ggt ggc atc gga atg act atc gcc act gca gct gcc gca Thr Phe Val Gly Gly Ile Gly Met Thr Ile Ala Thr Ala Ala Ala Ala 330 335 340	1123
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tgg tcc atg ctt gcc ctg ttc ttc ttc acc ggt ctg ggc aat gct ggc Trp Ser Met Leu Ala Leu Phe Phe Phe Thr Gly Leu Gly Asn Ala Gly 360 365 370	1219
acc ttc aaa caa atg ccc atg att ttg cct aaa cgc caa gca ggt ggc Thr Phe Lys Gln Met Pro Met Ile Leu Pro Lys Arg Gln Ala Gly Gly 375 380 385	1267
gtg atc ggc tgg acc ggt gcc att ggt gcc ttc ggc ccc ttc att gtc Val Ile Gly Trp Thr Gly Ala Ile Gly Ala Phe Gly Pro Phe Ile Val 390 395 400 405	1315
ggt gtc ttg ctc tcc ttc act cca act gtc gcg ttc ttc tgg ggc tgc Gly Val Leu Leu Ser Phe Thr Pro Thr Val Ala Phe Phe Trp Gly Cys 410 415 420	1363
gtg gtg ttc ttc atc atc gcc acc gct ttg acc tgg atc tac tac gcc Val Val Phe Phe Ile Ile Ala Thr Ala Leu Thr Trp Ile Tyr Tyr Ala 425 430 435	1411

cgc ccg aac gct cca ttc ccg gga taaaccgaaa ggccaatcca tga
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1458

<210> 376

<211> 445

<212> PRT

<213> Corynebacterium glutamicum

<400> 376

Val Thr Gln Leu Asn Thr Lys Gly Val Val Leu Gln Gly Trp Asp Pro
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Ile Thr Thr Phe Ser Met Ile Ile Gly Phe Cys Val Trp Tyr Leu Val
 35 40 45

Ser Ala Ile Ala Pro Leu Leu Asn Arg Ile Gly Phe Asp Leu Ser Ala
 50 55 60

Gly Gln Leu Tyr Trp Leu Ala Ser Ile Pro Gly Leu Ala Gly Gly Leu
 65 70 75 80

Ile Arg Leu Ile Tyr Met Phe Leu Pro Pro Ile Leu Gly Thr Arg Lys
 85 90 95

Leu Val Gly Ile Ser Ser Gly Leu Phe Leu Ile Pro Met Phe Gly Trp
 100 105 110

Phe Leu Ala Val Gln Asp Ser Ser Thr Pro Tyr Trp Trp Leu Leu Thr
 115 120 125

Leu Ala Ala Leu Thr Gly Ile Gly Gly Gly Val Phe Ser Gly Tyr Met
 130 135 140

Pro Ser Thr Gly Tyr Phe Phe Pro Lys Ala Lys Ser Gly Thr Ala Leu
 145 150 155 160

Gly Ile Gln Ala Gly Ile Gly Asn Leu Gly Val Ser Ile Ile Gln Phe
 165 170 175

Met Gly Pro Trp Val Met Gly Phe Gly Leu Leu Gly Ile Gly Phe Leu
 180 185 190

Thr Pro Gln Arg Thr Ile Glu Gly Thr Thr Val Phe Val His Asn Ala
 195 200 205

Ala Ile Val Leu Val Pro Trp Thr Ile Leu Ala Ala Val Leu Ser Phe
 210 215 220

Leu Phe Leu Lys Asp Val Pro Val Thr Ala Asn Phe Arg Gln Gln Ile
 225 230 235 240

Asp Ile Phe Gly Asn Lys Asn Thr Trp Ile Leu Ser Ile Ile Tyr Leu
 245 250 255

Met Thr Phe Gly Ala Phe Ala Gly Phe Ala Ala Gln Phe Gly Leu Ile
 260 265 270

Ile Asn Asn Asn Phe Gly Ile Ala Ser Pro Met Ala Glu Thr Tyr Pro
 275 280 285
 Ala Glu Met Leu His Ala Gly Ala Thr Phe Ala Phe Leu Gly Pro Leu
 290 295 300
 Ile Gly Ala Leu Val Arg Ala Ala Trp Gly Pro Leu Cys Asp Arg Phe
 305 310 315 320
 Gly Gly Ala Ile Trp Thr Phe Val Gly Gly Ile Gly Met Thr Ile Ala
 325 330 335
 Thr,Ala Ala Ala Ala Ile Phe Leu Ser Arg Ala Glu Thr Pro Asp Asp
 340 345 350
 Phe Trp Pro Phe Leu Trp Ser Met Leu Ala Leu Phe Phe Phe Thr Gly
 355 360 365
 Leu Gly Asn Ala Gly Thr Phe Lys Gln Met Pro Met Ile Leu Pro Lys
 370 375 380
 Arg Gln Ala Gly Gly Val Ile Gly Trp Thr Gly Ala Ile Gly Ala Phe
 385 390 395 400
 Gly Pro Phe Ile Val Gly Val Leu Leu Ser Phe Thr Pro Thr Val Ala
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<210> 377
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(715)
 <223> RXA02079

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 Met Ser Glu Ala Phe
 1 5
 gat gca acc aaa gtg cgc aaa gct gtg ctc acc gtc gcg ctg ctt aac 163
 Asp Ala Thr Lys Val Arg Lys Ala Val Leu Thr Val Ala Leu Leu Asn
 10 15 20
 ttc gct tat ttc ttt gta gaa ttc ttt att gca tta agc gca ggc tcc 211
 Phe Ala Tyr Phe Phe Val Glu Phe Phe Ile Ala Leu Ser Ala Gly Ser
 25 30 35
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      20             25             30
Leu Ser Ala Gly Ser Val Ser Leu Leu Ala Asp Ser Val Asp Phe Leu
      35             40             45
Glu Asp Thr Ser Ile Asn Leu Leu Ile Phe Ile Ala Leu Gly Trp Pro
  50             55             60

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Leu Ala Arg Arg Ala Val Met Gly Lys Leu Met Ala Ile Val Ile Leu
65 70 75 80

Ala Pro Ala Ala Phe Ala Ala Trp Ala Ala Ile Gln Arg Phe Ser Ala
85 90 95

Pro Gln Ala Pro Glu Val Phe Pro Ile Ile Val Ala Ser Leu Gly Ala
100 105 110

Val Val Ile Asn Gly Ala Ser Ala Ile Ile Ile Ser Arg Val Arg Gln
115 120 125

His Gly Gly Ser Leu Gly Gln Ala Ala Phe Leu Ser Ala Arg Asn Asp
130 135 140

Val Leu Ile Asn Ile Ala Ile Ile Met Met Ala Leu Ile Thr Ala Trp
145 150 155 160

Thr Thr Ser Gly Trp Pro Asp Leu Ile Leu Gly Cys Phe Ile Ile Leu
165 170 175

Leu Ala Leu His Ala Ala His Glu Val Trp Glu Val Ser Glu Glu Glu
180 185 190

Arg Leu Ala Ser Lys Ala Leu Ala Gly Glu Ala Ile Asp
195 200 205

<210> 379

<211> 1173

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1150)

<223> RXN00832

<400> 379

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ggaacggccc agagttctta agaaagtttg actagagaac atg ccg ttt tct tgg 115
Met Pro Phe Ser Trp
1 5

cta aaa cca att gat tat gcc cgc atc ttt gtc ggc tgg gca tcg att 163
Leu Lys Pro Ile Asp Tyr Ala Arg Ile Phe Val Gly Trp Ala Ser Ile
10 15 20

ttt atc atc ccc ctc atc aca ctg cca tca att att gag ttg gcg ctg 211
Phe Ile Ile Pro Leu Ile Thr Leu Pro Ser Ile Ile Glu Leu Ala Leu
25 30 35

atc gtg gca gtc atc cta ttc tgc gca ttt ggc gtg gtg aag atg gcg 259
Ile Val Ala Val Ile Leu Phe Cys Ala Phe Gly Val Val Lys Met Ala
40 45 50

gag cgt ttg gct cat att ttg ggt gat cct ttt gga tcg ttg atc ctt 307
Glu Arg Leu Ala His Ile Leu Gly Asp Pro Phe Gly Ser Leu Ile Leu
55 60 65

acc ttg tgg atc gtg atc att gaa gtg att ttg atc tgt gcg gtg atg	355
Thr Leu Ser Ile Val Ile Ile Glu Val Ile Leu Ile Cys Ala Val Met	
70 75 80 85	
ctg ggg cct gct gat tca acc act gct ggt cgg gat tcc gtg atg gca	403
Leu Gly Pro Ala Asp Ser Thr Thr Ala Gly Arg Asp Ser Val Met Ala	
90 95 100	
gtg tcc atg atc atc atg ggt ttg gtc gtg gga ttg tgc cta ctc att	451
Val Ser Met Ile Ile Met Gly Leu Val Val Gly Leu Cys Leu Leu Ile	
105 110 115	
ggg ggt tta agg cat gga agc atg cca cac aat ggg gtg gga act ccg	499
Gly Gly Leu Arg His Gly Ser Met Pro His Asn Gly Val Gly Thr Pro	
120 125 130	
acc tac ttg gtg ctg atc gca act ttt tcc gta atc gcc ttt gcg gtt	547
Thr Tyr Leu Val Leu Ile Ala Thr Phe Ser Val Ile Ala Phe Ala Val	
135 140 145	
cca gct ttc agg gga gaa tac tcc act ggg cag gca ctt gtt att tca	595
Pro Ala Phe Arg Gly Glu Tyr Ser Thr Gly Gln Ala Leu Val Ile Ser	
150 155 160 165	
aca ctg aca gca gtg gtg tac ggg ttc ttc ctg ttt cgc caa atg ggt	643
Thr Leu Thr Ala Val Val Tyr Gly Phe Phe Leu Phe Arg Gln Met Gly	
170 175 180	
gcc caa gct ggt gaa ttt caa gag gtc gag gtc gca gaa aag gca gac	691
Ala Gln Ala Gly Glu Phe Gln Glu Val Glu Val Ala Glu Lys Ala Asp	
185 190 195	
gac gca gca aaa tgg gag gtc cca ttt aga ggc tta atc ttg att atc	739
Asp Ala Ala Lys Trp Glu Val Pro Phe Arg Gly Leu Ile Leu Ile Ile	
200 205 210	
act gtg ctc ccc atc gtg ttg ctg tcc cat gac atg gcc acg gtg atg	787
Thr Val Leu Pro Ile Val Leu Leu Ser His Asp Met Ala Thr Val Met	
215 220 225	
gat gaa gtc ctg gca agc ctt ggt gca ccc gta gca atg gct gga tta	835
Asp Glu Val Leu Ala Ser Leu Gly Ala Pro Val Ala Met Ala Gly Leu	
230 235 240 245	
att att gcc acc att gtc ttc ttg cca gag acc atc acc tcc ttg aaa	883
Ile Ile Ala Thr Ile Val Phe Leu Pro Glu Thr Ile Thr Ser Leu Lys	
250 255 260	
gct gcg tgg aca gga gag att cag cga gta agc aac ctc gcg cat gga	931
Ala Ala Trp Thr Gly Glu Ile Gln Arg Val Ser Asn Leu Ala His Gly	
265 270 275	
gcc caa gta tca acg gtg ggg ctg aca atc cca gct gtt cta gtg atc	979
Ala Gln Val Ser Thr Val Gly Leu Thr Ile Pro Ala Val Leu Val Ile	
280 285 290	
ggc gtg atc aca ggt caa gat gta gtt ttg ggg gag acc ccg atc aac	1027
Gly Val Ile Thr Gly Gln Asp Val Val Leu Gly Glu Thr Pro Ile Asn	
295 300 305	

ttg ttg ctg ctg gga acc acc att gcg gtg aca gcc att gcg ttt agc 1075
 Leu Leu Leu Leu Gly Thr Thr Ile Ala Val Thr Ala Ile Ala Phe Ser
 310 315 320 325

tcc aag aaa gtc agt gct gtg cat ggc tgc gtg ctg ctc atg ctt ttc 1123
 Ser Lys Lys Val Ser Ala Val His Gly Ser Val Leu Leu Met Leu Phe
 330 335 340

ggt gtt tac atg atg agc atg ttc gcc tgatttaggt agcctggtgg 1170
 Gly Val Tyr Met Met Ser Met Phe Ala
 345 350

gaa 1173

<210> 380

<211> 350

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 380

Met Pro Phe Ser Trp Leu Lys Pro Ile Asp Tyr Ala Arg Ile Phe Val
 1 5 10 15

Gly Trp Ala Ser Ile Phe Ile Ile Pro Leu Ile Thr Leu Pro Ser Ile
 20 25 30

Ile Glu Leu Ala Leu Ile Val Ala Val Ile Leu Phe Cys Ala Phe Gly
 35 40 45

Val Val Lys Met Ala Glu Arg Leu Ala His Ile Leu Gly Asp Pro Phe
 50 55 60

Gly Ser Leu Ile Leu Thr Leu Ser Ile Val Ile Ile Glu Val Ile Leu
 65 70 75 80

Ile Cys Ala Val Met Leu Gly Pro Ala Asp Ser Thr Thr Ala Gly Arg
 85 90 95

Asp Ser Val Met Ala Val Ser Met Ile Ile Met Gly Leu Val Val Gly
 100 105 110

Leu Cys Leu Leu Ile Gly Gly Leu Arg His Gly Ser Met Pro His Asn
 115 120 125

Gly Val Gly Thr Pro Thr Tyr Leu Val Leu Ile Ala Thr Phe Ser Val
 130 135 140

Ile Ala Phe Ala Val Pro Ala Phe Arg Gly Glu Tyr Ser Thr Gly Gln
 145 150 155 160

Ala Leu Val Ile Ser Thr Leu Thr Ala Val Val Tyr Gly Phe Phe Leu
 165 170 175

Phe Arg Gln Met Gly Ala Gln Ala Gly Glu Phe Gln Glu Val Glu Val
 180 185 190

Ala Glu Lys Ala Asp Asp Ala Ala Lys Trp Glu Val Pro Phe Arg Gly
 195 200 205

Leu Ile Leu Ile Ile Thr Val Leu Pro Ile Val Leu Leu Ser His Asp

210	215	220
Met Ala Thr Val Met	Asp Glu Val Leu Ala	Ser Leu Gly Ala Pro Val
225	230	235 240
Ala Met Ala Gly Leu	Ile Ile Ala Thr	Ile Val Phe Leu Pro Glu Thr
245	250	255
Ile Thr Ser Leu Lys	Ala Ala Trp Thr	Gly Glu Ile Gln Arg Val Ser
260	265	270
Asn Leu Ala His Gly	Ala Gln Val Ser Thr	Val Gly Leu Thr Ile Pro
275	280	285
Ala Val Leu Val Ile	Gly Val Ile Thr	Gly Gln Asp Val Val Leu Gly
290	295	300
Glu Thr Pro Ile Asn	Leu Leu Leu Leu	Gly Thr Thr Ile Ala Val Thr
305	310	315 320
Ala Ile Ala Phe Ser	Ser Lys Lys Val	Ser Ala Val His Gly Ser Val
325	330	335
Leu Leu Met Leu Phe	Gly Val Tyr Met	Met Ser Met Phe Ala
340	345	350

<210> 381
 <211> 578
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(555)
 <223> FRXA00832

<400> 381

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Thr Leu Thr Ala Val Val Tyr Gly Phe Phe Leu Phe Arg Gln Met Gly	
1 5 10 15	
gcc caa gct ggt gaa ttt caa gag gtc gag gtc gca gaa aag gca gac	96
Ala Gln Ala Gly Glu Phe Gln Glu Val Glu Val Ala Glu Lys Ala Asp	
20 25 30	
gac gca gca aaa tgg gag gtc cca ttt aga ggc tta atc ttg att atc	144
Asp Ala Ala Lys Trp Glu Val Pro Phe Arg Gly Leu Ile Leu Ile Ile	
35 40 45	
act gtg ctc ccc atc gtg ttg ctg tcc cat gac atg gcc acg gtg atg	192
Thr Val Leu Pro Ile Val Leu Leu Ser His Asp Met Ala Thr Val Met	
50 55 60	
gat gaa gtc ctg gca agc ctt ggt gca ccc gta gca atg gct gga tta	240
Asp Glu Val Leu Ala Ser Leu Gly Ala Pro Val Ala Met Ala Gly Leu	
65 70 75 80	
att att gcc acc att gtc ttc ttg cca gag acc atc acc tcc ttg aaa	288
Ile Ile Ala Thr Ile Val Phe Leu Pro Glu Thr Ile Thr Ser Leu Lys	
85 90 95	

gct gcg tgg aca gga gag att cag cga gta agc aac ctc gcg cat gga 336
 Ala Ala Trp Thr Gly Glu Ile Gln Arg Val Ser Asn Leu Ala His Gly
 100 105 110

gcc caa gta tca acg gtg ggg ctg aca atc cca gct gtt cta gtg atc 384
 Ala Gln Val Ser Thr Val Gly Leu Thr Ile Pro Ala Val Leu Val Ile
 115 120 125

ggc gtg atc aca ggt caa gat gta gtt ttg ggg gag acc ccg atc aac 432
 Gly Val Ile Thr Gly Gln Asp Val Val Leu Gly Glu Thr Pro Ile Asn
 130 135 140

ttg ttg ctg ctg gga acc acc att gcg gtg aca gcc att gcg ttt agc 480
 Leu Leu Leu Leu Gly Thr Thr Ile Ala Val Thr Ala Ile Ala Phe Ser
 145 150 155 160

tcc aag aaa gtc agt gct gtg cat ggc tcg gtg ctg ctc atg ctt ttc 528
 Ser Lys Lys Val Ser Ala Val His Gly Ser Val Leu Leu Met Leu Phe
 165 170 175

ggt gtt tac atg atg agc atg ttc gcc tgatttaggt agcctggtgg 575
 Gly Val Tyr Met Met Ser Met Phe Ala
 180 185

gaa 578

<210> 382

<211> 185

<212> PRT

<213> Corynebacterium glutamicum

<400> 382

Thr Leu Thr Ala Val Val Tyr Gly Phe Phe Leu Phe Arg Gln Met Gly
 1 5 10 15

Ala Gln Ala Gly Glu Phe Gln Glu Val Glu Val Ala Glu Lys Ala Asp
 20 25 30

Asp Ala Ala Lys Trp Glu Val Pro Phe Arg Gly Leu Ile Leu Ile Ile
 35 40 45

Thr Val Leu Pro Ile Val Leu Leu Ser His Asp Met Ala Thr Val Met
 50 55 60

Asp Glu Val Leu Ala Ser Leu Gly Ala Pro Val Ala Met Ala Gly Leu
 65 70 75 80

Ile Ile Ala Thr Ile Val Phe Leu Pro Glu Thr Ile Thr Ser Leu Lys
 85 90 95

Ala Ala Trp Thr Gly Glu Ile Gln Arg Val Ser Asn Leu Ala His Gly
 100 105 110

Ala Gln Val Ser Thr Val Gly Leu Thr Ile Pro Ala Val Leu Val Ile
 115 120 125

Gly Val Ile Thr Gly Gln Asp Val Val Leu Gly Glu Thr Pro Ile Asn
 130 135 140

Leu Leu Leu Leu Gly Thr Thr Ile Ala Val Thr Ala Ile Ala Phe Ser
 145 150 155 160

Ser Lys Lys Val Ser Ala Val His Gly Ser Val Leu Leu Met Leu Phe
 165 170 175

Gly Val Tyr Met Met Ser Met Phe Ala
 180 185

<210> 383

<211> 2733

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(2710)

<223> RXN00378

<400> 383

accgtgagcc ttatactgtg aggacattaa aagtgacacc tctttttcta tcttttacaa 60

cccaagaagg tttatcgtga gcacaccgga ttcttcctcg gtg gac aag gcc gta 115
 Val Asp Lys Ala Val
 1 5

aac act gct atc tct gac gcc aaa aca gcg gcg ctc aag gca ggt gtt 163
 Asn Thr Ala Ile Ser Asp Ala Lys Thr Ala Ala Leu Lys Ala Gly Val
 10 15 20

gga ttg aac cga gcc acc gcc tca gaa gaa gag gaa gat tta agc tca 211
 Gly Leu Asn Arg Ala Thr Ala Ser Glu Glu Glu Glu Asp Leu Ser Ser
 25 30 35

agc att aag gtt tct ttg gcc ttt gag ctc gag ggg tta agc aat gca 259
 Ser Ile Lys Val Ser Leu Ala Phe Glu Leu Glu Gly Leu Ser Asn Ala
 40 45 50

cca tcg ttg atg gtg gtg gaa aaa gcc cta gag aag atc ccc ggt gta 307
 Pro Ser Leu Met Val Val Glu Lys Ala Leu Glu Lys Ile Pro Gly Val
 55 60 65

tcc gcg gat ctg att tac cct tca caa act gca tgg att aca gca act 355
 Ser Ala Asp Leu Ile Tyr Pro Ser Gln Thr Ala Trp Ile Thr Ala Thr
 70 75 80 85

gat cgg gta cat ccc gaa acc ctc att gag gtg ttt gag cag ttc ggc 403
 Asp Arg Val His Pro Glu Thr Leu Ile Glu Val Phe Glu Gln Phe Gly
 90 95 100

atc aaa gca cac ctt tct aat tca tcg ctg ctg cgc agg cat caa cag 451
 Ile Lys Ala His Leu Ser Asn Ser Ser Leu Leu Arg Arg His Gln Gln
 105 110 115

ctc agc gcg gaa gta aat agg gaa gca cgc ctt gat cgt tac cgc tcc 499
 Leu Ser Ala Glu Val Asn Arg Glu Ala Arg Leu Asp Arg Tyr Arg Ser
 120 125 130

cga atg gat gcc aag cga atc tcg cct cgt gtg cga agg cat aac cga 547
 Arg Met Asp Ala Lys Arg Ile Ser Pro Arg Val Arg Arg His Asn Arg

135	140	145	
caa gaa atg gta cat gcg gta cgc gct cgt gaa agt ggt tgg att aaa			595
Gln Glu Met Val His Ala Val Arg Ala Arg Glu Ser Gly Trp Ile Lys			
150	155	160	165
cgc agg aat cac acc acc tcg cag cat gaa gac cca atg tcg ggc gat			643
Arg Arg Asn His Thr Thr Ser Gln His Glu Asp Pro Met Ser Gly Asp			
	170	175	180
gtg ctg ttc acc gcc cgc gca ctg att aca cct aag cgt ttg tgg gtg			691
Val Leu Phe Thr Ala Arg Ala Leu Ile Thr Pro Lys Arg Leu Trp Val			
	185	190	195
tcg ttg ccg ttt gcg ctc atc gta ttg gcg tta tcg ttg aat cct tcg			739
Ser Leu Pro Phe Ala Leu Ile Val Leu Ala Leu Ser Leu Asn Pro Ser			
	200	205	210
tgg cag ttt gat tat tgg cag tgg ttg tcc gct gtg ttg gct att cct			787
Trp Gln Phe Asp Tyr Trp Gln Trp Leu Ser Ala Val Leu Ala Ile Pro			
	215	220	225
gtg gtg gtg tgg ggt gcc tgg ccg ttt cac cgc gct gca gca ggc ggt			835
Val Val Val Trp Gly Ala Trp Pro Phe His Arg Ala Ala Ala Gly Gly			
	230	235	240
att cgt cga gga att tcc gct ctt gat gcg acc agc tca atc gct att			883
Ile Arg Arg Gly Ile Ser Ala Leu Asp Ala Thr Ser Ser Ile Ala Ile			
	250	255	260
gct gct gca tac gcg tgg tct atc gcc atg ctg ttg ttt gaa acc cca			931
Ala Ala Ala Tyr Ala Trp Ser Ile Ala Met Leu Leu Phe Glu Thr Pro			
	265	270	275
gga ggt aaa tcc tgg cgg tca tat ccg tcc tgg ttc gct ttt gac cac			979
Gly Gly Lys Ser Trp Arg Ser Tyr Pro Ser Trp Phe Ala Phe Asp His			
	280	285	290
ggc acg ttg acc caa aac gag att tat ttt gat gtg gcc tgc gga atc			1027
Gly Thr Leu Thr Gln Asn Glu Ile Tyr Phe Asp Val Ala Cys Gly Ile			
	295	300	305
acc gtg ttg ctt ctt gcc gga cgg ctg ctg aca agg cgt cga agc caa			1075
Thr Val Leu Leu Leu Ala Gly Arg Leu Leu Thr Arg Arg Arg Ser Gln			
	310	315	320
tcc agt ttg tta gcg gaa ctt ggt cgc ctc caa atc gat cca cag cgc			1123
Ser Ser Leu Leu Ala Glu Leu Gly Arg Leu Gln Ile Asp Pro Gln Arg			
	330	335	340
att gtc act gtg gtg cgt aaa cac cga ttg aag cgc gta gtc cag gaa			1171
Ile Val Thr Val Val Arg Lys His Arg Leu Lys Arg Val Val Gln Glu			
	345	350	355
ctg aac att cca gtg cag gaa gtc cgt gtc aat gac gat gtg aaa gtt			1219
Leu Asn Ile Pro Val Gln Glu Val Arg Val Asn Asp Asp Val Lys Val			
	360	365	370
cca cct aat acc acg atc cct gtg gat ggc act gtc atc ggt ggc ggt			1267
Pro Pro Asn Thr Thr Ile Pro Val Asp Gly Thr Val Ile Gly Gly Gly			
	375	380	385

tcg cgg atc gca gct agc atc atc atg gga caa gac cag cgt gat gta	1315
Ser Arg Ile Ala Ala Ser Ile Ile Met Gly Gln Asp Gln Arg Asp Val	
390 395 400 405	
aaa gta aat gac aaa gtt ttc gcc ggc agc ctc aac ctc gaa tcc gaa	1363
Lys Val Asn Asp Lys Val Phe Ala Gly Ser Leu Asn Leu Glu Ser Glu	
410 415 420	
atc aag gtt cgt gtt att cgc act ggt cac cgc acc cgc atc gcc gcg	1411
Ile Lys Val Arg Val Ile Arg Thr Gly His Arg Thr Arg Ile Ala Ala	
425 430 435	
gta cat agg tgg gtt aaa gaa gcg acg ttg aag gaa aac cgc cac aat	1459
Val His Arg Trp Val Lys Glu Ala Thr Leu Lys Glu Asn Arg His Asn	
440 445 450	
agg gca gcg atc cgt tcg gcc ggt aac ctt gtg ccc atc acg ttc acc	1507
Arg Ala Ala Ile Arg Ser Ala Gly Asn Leu Val Pro Ile Thr Phe Thr	
455 460 465	
ctt gct gtg gtg gac ttc tgt ctg tgg gca ctg atc tct gga aac atc	1555
Leu Ala Val Val Asp Phe Cys Leu Trp Ala Leu Ile Ser Gly Asn Ile	
470 475 480 485	
aac gct gca ttt acc act acc ttg gct gtc ctt gcg tgc gtg gct ccg	1603
Asn Ala Ala Phe Thr Thr Thr Leu Ala Val Leu Ala Cys Val Ala Pro	
490 495 500	
gtg gcc tta gcg ttg tct gct cca ctt gcc acg agg aat tcc atc gaa	1651
Val Ala Leu Ala Leu Ser Ala Pro Leu Ala Thr Arg Asn Ser Ile Glu	
505 510 515	
gct gca gca cga cac ggt att ttg gtc cgc tct ggt gaa att ttc cga	1699
Ala Ala Ala Arg His Gly Ile Leu Val Arg Ser Gly Glu Ile Phe Arg	
520 525 530	
gtt ctc gat gat gtg gat act gcc gta ttt aat cgt gtg ggc aca cta	1747
Val Leu Asp Asp Val Asp Thr Ala Val Phe Asn Arg Val Gly Thr Leu	
535 540 545	
acc gat ggc gaa atg aca gtg gaa acc gtc aca gca gac aaa ggc gag	1795
Thr Asp Gly Glu Met Thr Val Glu Thr Val Thr Ala Asp Lys Gly Glu	
550 555 560 565	
gac cca gaa cta gtg ctg cgt gtc gcc ggg gcg ttg gcc atg gaa tcc	1843
Asp Pro Glu Leu Val Leu Arg Val Ala Gly Ala Leu Ala Met Glu Ser	
570 575 580	
cac cac gcg att tcc aaa gca ctg gtg aaa gca tcc cgt gaa gct cgt	1891
His His Ala Ile Ser Lys Ala Leu Val Lys Ala Ser Arg Glu Ala Arg	
585 590 595	
gat acc ggc gcc ggt ggt gaa gat gtc cca cac tgg att gaa gta ggc	1939
Asp Thr Gly Ala Gly Gly Glu Asp Val Pro His Trp Ile Glu Val Gly	
600 605 610	
aac gtg gaa atc acc gaa gcc ggc tca ttc caa gca acc atc gag ctg	1987
Asn Val Glu Ile Thr Glu Ala Gly Ser Phe Gln Ala Thr Ile Glu Leu	
615 620 625	

cca ctg atc aaa cca tct ggc gaa aaa atc atg cgc acc aca gaa gca Pro Leu Ile Lys Pro Ser Gly Glu Lys Ile Met Arg Thr Thr Glu Ala 630 635 640 645	2035
ctc ctg tgg cga cca cga tcc atg aca gaa gtc cgt gag cac tta agc Leu Leu Trp Arg Pro Arg Ser Met Thr Glu Val Arg Glu His Leu Ser 650 655 660	2083
ccc cga cta gtg gca gca gca acc tca ggt ggc gca cca ctg atc gtg Pro Arg Leu Val Ala Ala Ala Thr Ser Gly Gly Ala Pro Leu Ile Val 665 670 675	2131
cga tgg aaa ggc aaa gac cgc gga gtt atc act cta agt gac cac gtg Arg Trp Lys Gly Lys Asp Arg Gly Val Ile Thr Leu Ser Asp His Val 680 685 690	2179
aga tca gat tcc tcc gat gcg att att gcg att gaa gaa caa ggc atc Arg Ser Asp Ser Ser Asp Ala Ile Ile Ala Ile Glu Glu Gln Gly Ile 695 700 705	2227
gag acc atg atg ctt tca cgt gat act tac ccg gtg gca cgt cga tac Glu Thr Met Met Leu Ser Arg Asp Thr Tyr Pro Val Ala Arg Arg Tyr 710 715 720 725	2275
gca gac agc tta ggc atc acc cac gtc ttg gcc ggc atc gcg ccg ggc Ala Asp Ser Leu Gly Ile Thr His Val Leu Ala Gly Ile Ala Pro Gly 730 735 740	2323
aag aaa gcc cag gtc gtc cgt gca gtc cac acc cgc gga tcc act gtc Lys Lys Ala Gln Val Val Arg Ala Val His Thr Arg Gly Ser Thr Val 745 750 755	2371
gcg atg atc ggc gat gaa tca gta atg gac tgt ttg aaa gtc gct gac Ala Met Ile Gly Asp Glu Ser Val Met Asp Cys Leu Lys Val Ala Asp 760 765 770	2419
gtg ggt gta ctg atg ggc gtc gat cgt ccc tca gat ctg cgt gat gat Val Gly Val Leu Met Gly Val Asp Arg Pro Ser Asp Leu Arg Asp Asp 775 780 785	2467
tcc gat gac ccg gca gct gac gtt gtg gtc atg cgc gaa gag gtc atg Ser Asp Asp Pro Ala Ala Asp Val Val Met Arg Glu Glu Val Met 790 795 800 805	2515
agc gtg ccg acg ctg ttt aaa ctg gct cga cgc tac gcc aag ttg gtc Ser Val Pro Thr Leu Phe Lys Leu Ala Arg Arg Tyr Ala Lys Leu Val 810 815 820	2563
aat ggc aat att gct ctg gcc tgg atc tat aac ggt gtt gcc atg gtg Asn Gly Asn Ile Ala Leu Ala Trp Ile Tyr Asn Gly Val Ala Met Val 825 830 835	2611
ctt gca gtg tct ggc ttg ctg cat cca atg gct gcg acc gtg gct atg Leu Ala Val Ser Gly Leu Leu His Pro Met Ala Ala Thr Val Ala Met 840 845 850	2659
ctg gcg tct tcg ctg ctt att gaa tgg cgc tcg ggc agg gcg cgc aag Leu Ala Ser Ser Leu Leu Ile Glu Trp Arg Ser Gly Arg Ala Arg Lys 855 860 865	2707
tac taaccagcaa ttcccaagcc caa	2733

Tyr
870

<210> 384
<211> 870
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 384
Val Asp Lys Ala Val Asn Thr Ala Ile Ser Asp Ala Lys Thr Ala Ala
1 5 10 15
Leu Lys Ala Gly Val Gly Leu Asn Arg Ala Thr Ala Ser Glu Glu Glu
20 25 30
Glu Asp Leu Ser Ser Ser Ile Lys Val Ser Leu Ala Phe Glu Leu Glu
35 40 45
Gly Leu Ser Asn Ala Pro Ser Leu Met Val Val Glu Lys Ala Leu Glu
50 55 60
Lys Ile Pro Gly Val Ser Ala Asp Leu Ile Tyr Pro Ser Gln Thr Ala
65 70 75 80
Trp Ile Thr Ala Thr Asp Arg Val His Pro Glu Thr Leu Ile Glu Val
85 90 95
Phe Glu Gln Phe Gly Ile Lys Ala His Leu Ser Asn Ser Ser Leu Leu
100 105 110
Arg Arg His Gln Gln Leu Ser Ala Glu Val Asn Arg Glu Ala Arg Leu
115 120 125
Asp Arg Tyr Arg Ser Arg Met Asp Ala Lys Arg Ile Ser Pro Arg Val
130 135 140
Arg Arg His Asn Arg Gln Glu Met Val His Ala Val Arg Ala Arg Glu
145 150 155 160
Ser Gly Trp Ile Lys Arg Arg Asn His Thr Thr Ser Gln His Glu Asp
165 170 175
Pro Met Ser Gly Asp Val Leu Phe Thr Ala Arg Ala Leu Ile Thr Pro
180 185 190
Lys Arg Leu Trp Val Ser Leu Pro Phe Ala Leu Ile Val Leu Ala Leu
195 200 205
Ser Leu Asn Pro Ser Trp Gln Phe Asp Tyr Trp Gln Trp Leu Ser Ala
210 215 220
Val Leu Ala Ile Pro Val Val Val Trp Gly Ala Trp Pro Phe His Arg
225 230 235 240
Ala Ala Ala Gly Gly Ile Arg Arg Gly Ile Ser Ala Leu Asp Ala Thr
245 250 255
Ser Ser Ile Ala Ile Ala Ala Ala Tyr Ala Trp Ser Ile Ala Met Leu
260 265 270

Leu Phe Glu Thr Pro Gly Gly Lys Ser Trp Arg Ser Tyr Pro Ser Trp
 275 280 285
 Phe Ala Phe Asp His Gly Thr Leu Thr Gln Asn Glu Ile Tyr Phe Asp
 290 295 300
 Val Ala Cys Gly Ile Thr Val Leu Leu Leu Ala Gly Arg Leu Leu Thr
 305 310 315 320
 Arg Arg Arg Ser Gln Ser Ser Leu Leu Ala Glu Leu Gly Arg Leu Gln
 325 330 335
 Ile Asp Pro Gln Arg Ile Val Thr Val Val Arg Lys His Arg Leu Lys
 340 345 350
 Arg Val Val Gln Glu Leu Asn Ile Pro Val Gln Glu Val Arg Val Asn
 355 360 365
 Asp Asp Val Lys Val Pro Pro Asn Thr Thr Ile Pro Val Asp Gly Thr
 370 375 380
 Val Ile Gly Gly Gly Ser Arg Ile Ala Ala Ser Ile Ile Met Gly Gln
 385 390 395 400
 Asp Gln Arg Asp Val Lys Val Asn Asp Lys Val Phe Ala Gly Ser Leu
 405 410 415
 Asn Leu Glu Ser Glu Ile Lys Val Arg Val Ile Arg Thr Gly His Arg
 420 425 430
 Thr Arg Ile Ala Ala Val His Arg Trp Val Lys Glu Ala Thr Leu Lys
 435 440 445
 Glu Asn Arg His Asn Arg Ala Ala Ile Arg Ser Ala Gly Asn Leu Val
 450 455 460
 Pro Ile Thr Phe Thr Leu Ala Val Val Asp Phe Cys Leu Trp Ala Leu
 465 470 475 480
 Ile Ser Gly Asn Ile Asn Ala Ala Phe Thr Thr Thr Leu Ala Val Leu
 485 490 495
 Ala Cys Val Ala Pro Val Ala Leu Ala Leu Ser Ala Pro Leu Ala Thr
 500 505 510
 Arg Asn Ser Ile Glu Ala Ala Ala Arg His Gly Ile Leu Val Arg Ser
 515 520 525
 Gly Glu Ile Phe Arg Val Leu Asp Asp Val Asp Thr Ala Val Phe Asn
 530 535 540
 Arg Val Gly Thr Leu Thr Asp Gly Glu Met Thr Val Glu Thr Val Thr
 545 550 555 560
 Ala Asp Lys Gly Glu Asp Pro Glu Leu Val Leu Arg Val Ala Gly Ala
 565 570 575
 Leu Ala Met Glu Ser His His Ala Ile Ser Lys Ala Leu Val Lys Ala
 580 585 590
 Ser Arg Glu Ala Arg Asp Thr Gly Ala Gly Gly Glu Asp Val Pro His

595	600	605
Trp Ile Glu Val Gly Asn Val Glu Ile Thr Glu Ala Gly Ser Phe Gln 610 615 620		
Ala Thr Ile Glu Leu Pro Leu Ile Lys Pro Ser Gly Glu Lys Ile Met 625 630 635 640		
Arg Thr Thr Glu Ala Leu Leu Trp Arg Pro Arg Ser Met Thr Glu Val 645 650 655		
Arg Glu His Leu Ser Pro Arg Leu Val Ala Ala Ala Thr Ser Gly Gly 660 665 670		
Ala Pro Leu Ile Val Arg Trp Lys Gly Lys Asp Arg Gly Val Ile Thr 675 680 685		
Leu Ser Asp His Val Arg Ser Asp Ser Ser Asp Ala Ile Ile Ala Ile 690 695 700		
Glu Glu Gln Gly Ile Glu Thr Met Met Leu Ser Arg Asp Thr Tyr Pro 705 710 715 720		
Val Ala Arg Arg Tyr Ala Asp Ser Leu Gly Ile Thr His Val Leu Ala 725 730 735		
Gly Ile Ala Pro Gly Lys Lys Ala Gln Val Val Arg Ala Val His Thr 740 745 750		
Arg Gly Ser Thr Val Ala Met Ile Gly Asp Glu Ser Val Met Asp Cys 755 760 765		
Leu Lys Val Ala Asp Val Gly Val Leu Met Gly Val Asp Arg Pro Ser 770 775 780		
Asp Leu Arg Asp Asp Ser Asp Asp Pro Ala Ala Asp Val Val Val Met 785 790 795 800		
Arg Glu Glu Val Met Ser Val Pro Thr Leu Phe Lys Leu Ala Arg Arg 805 810 815		
Tyr Ala Lys Leu Val Asn Gly Asn Ile Ala Leu Ala Trp Ile Tyr Asn 820 825 830		
Gly Val Ala Met Val Leu Ala Val Ser Gly Leu Leu His Pro Met Ala 835 840 845		
Ala Thr Val Ala Met Leu Ala Ser Ser Leu Leu Ile Glu Trp Arg Ser 850 855 860		
Gly Arg Ala Arg Lys Tyr 865 870		

<210> 385

<211> 1796

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1773)

<223> FRXA00378

<400> 385

aaa tcc tgg cgg tca tat ccg tcc tgg ttc gct ttt gac cac ggc acg	48
Lys Ser Trp Arg Ser Tyr Pro Ser Trp Phe Ala Phe Asp His Gly Thr	
1 5 10 15	
ttg acc caa aac gag att tat ttt gat gtg gcc tgc gga atc acc gtg	96
Leu Thr Gln Asn Glu Ile Tyr Phe Asp Val Ala Cys Gly Ile Thr Val	
20 25 30	
ttg ctt ctt gcc gga cgg ctg ctg aca agg cgt cga agc caa tcc agt	144
Leu Leu Leu Ala Gly Arg Leu Leu Thr Arg Arg Arg Ser Gln Ser Ser	
35 40 45	
ttg tta gcg gaa ctt ggt cgc ctc caa atc gat cca cag cgc att gtc	192
Leu Leu Ala Glu Leu Gly Arg Leu Gln Ile Asp Pro Gln Arg Ile Val	
50 55 60	
act gtg gtg cgt aaa cac cga ttg aag cgc gta gtc cag gaa ctg aac	240
Thr Val Val Arg Lys His Arg Leu Lys Arg Val Val Gln Glu Leu Asn	
65 70 75 80	
att cca gtg cag gaa gtc cgt gtc aat gac gat gtg aaa gtt cca cct	288
Ile Pro Val Gln Glu Val Arg Val Asn Asp Asp Val Lys Val Pro Pro	
85 90 95	
aat acc acg atc cct gtg gat ggc act gtc atc ggt ggc ggt tcg cgg	336
Asn Thr Thr Ile Pro Val Asp Gly Thr Val Ile Gly Gly Gly Ser Arg	
100 105 110	
atc gca gct agc atc atc atg gga caa gac cag cgt gat gta aaa gta	384
Ile Ala Ala Ser Ile Ile Met Gly Gln Asp Gln Arg Asp Val Lys Val	
115 120 125	
aat gac aaa gtt ttc gcc ggc agc ctc aac ctc gaa tcc gaa atc aag	432
Asn Asp Lys Val Phe Ala Gly Ser Leu Asn Leu Glu Ser Glu Ile Lys	
130 135 140	
gtt cgt gtt att cgc act ggt cac cgc acc cgc atc gcc gcg gta cat	480
Val Arg Val Ile Arg Thr Gly His Arg Thr Arg Ile Ala Ala Val His	
145 150 155 160	
agg tgg gtt aaa gaa gcg acg ttg aag gaa aac cgc cac aat agg gca	528
Arg Trp Val Lys Glu Ala Thr Leu Lys Glu Asn Arg His Asn Arg Ala	
165 170 175	
gcg atc cgt tcg gcc ggt aac ctt gtg ccc atc acg ttc acc ctt gct	576
Ala Ile Arg Ser Ala Gly Asn Leu Val Pro Ile Thr Phe Thr Leu Ala	
180 185 190	
gtg gtg gac ttc tgt ctg tgg gca ctg atc tct gga aac atc aac gct	624
Val Val Asp Phe Cys Leu Trp Ala Leu Ile Ser Gly Asn Ile Asn Ala	
195 200 205	
gca ttt acc act acc ttg gct gtc ctt gcg tgc gtg gct ccg gtg gcc	672
Ala Phe Thr Thr Thr Leu Ala Val Leu Ala Cys Val Ala Pro Val Ala	
210 215 220	
tta gcg ttg tct gct cca ctt gcc acg agg aat tcc atc gaa gct gca	720

Leu Ala Leu Ser Ala Pro Leu Ala Thr Arg Asn Ser Ile Glu Ala Ala	
225	230 235 240
gca cga cac ggt att ttg gtc cgc tct ggt gaa att ttc cga gtt ctc	768
Ala Arg His Gly Ile Leu Val Arg Ser Gly Glu Ile Phe Arg Val Leu	
245	250 255
gat gat gtg gat act gcc gta ttt aat cgt gtg ggc aca cta acc gat	816
Asp Asp Val Asp Thr Ala Val Phe Asn Arg Val Gly Thr Leu Thr Asp	
260	265 270
ggc gaa atg aca gtg gaa acc gtc aca gca gac aaa ggc gag gac cca	864
Gly Glu Met Thr Val Glu Thr Val Thr Ala Asp Lys Gly Glu Asp Pro	
275	280 285
gaa cta gtg ctg cgt gtc gcc ggg gcg ttg gcc atg gaa tcc cac cac	912
Glu Leu Val Leu Arg Val Ala Gly Ala Leu Ala Met Glu Ser His His	
290	295 300
gcg att tcc aaa gca ctg gtg aaa gca tcc cgt gaa gct cgt gat acc	960
Ala Ile Ser Lys Ala Leu Val Lys Ala Ser Arg Glu Ala Arg Asp Thr	
305	310 315 320
ggc gcc ggt ggt gaa gat gtc cca cac tgg att gaa gta ggc aac gtg	1008
Gly Ala Gly Gly Glu Asp Val Pro His Trp Ile Glu Val Gly Asn Val	
325	330 335
gaa atc acc gaa gcc ggc tca ttc caa gca acc atc gag ctg cca ctg	1056
Glu Ile Thr Glu Ala Gly Ser Phe Gln Ala Thr Ile Glu Leu Pro Leu	
340	345 350
atc aaa cca tct ggc gaa aaa atc atg cgc acc aca gaa gca ctc ctg	1104
Ile Lys Pro Ser Gly Glu Lys Ile Met Arg Thr Thr Glu Ala Leu Leu	
355	360 365
tgg cga cca cga tcc atg aca gaa gtc cgt gag cac tta agc ccc cga	1152
Trp Arg Pro Arg Ser Met Thr Glu Val Arg Glu His Leu Ser Pro Arg	
370	375 380
cta gtg gca gca gca acc tca ggt ggc gca cca ctg atc gtg cga tgg	1200
Leu Val Ala Ala Ala Thr Ser Gly Gly Ala Pro Leu Ile Val Arg Trp	
385	390 395 400
aaa ggc aaa gac cgc gga gtt atc act cta agt gac cac gtg aga tca	1248
Lys Gly Lys Asp Arg Gly Val Ile Thr Leu Ser Asp His Val Arg Ser	
405	410 415
gat tcc tcc gat gcg att att gcg att gaa gaa caa ggc atc gag acc	1296
Asp Ser Ser Asp Ala Ile Ile Ala Ile Glu Glu Gln Gly Ile Glu Thr	
420	425 430
atg atg ctt tca cgt gat act tac ccg gtg gca cgt cga tac gca gac	1344
Met Met Leu Ser Arg Asp Thr Tyr Pro Val Ala Arg Arg Tyr Ala Asp	
435	440 445
agc tta ggc atc acc cac gtc ttg gcc ggc atc gcg ccg ggc aag aaa	1392
Ser Leu Gly Ile Thr His Val Leu Ala Gly Ile Ala Pro Gly Lys Lys	
450	455 460
gcc cag gtc gtc cgt gca gtc cac acc cgc gga tcc act gtc gcg atg	1440
Ala Gln Val Val Arg Ala Val His Thr Arg Gly Ser Thr Val Ala Met	

465	470	475	480	
atc ggc gat gaa tca gta atg gac tgt ttg aaa gtc gct gac gtg ggt				1488
Ile Gly Asp Glu Ser Val Met Asp Cys Leu Lys Val Ala Asp Val Gly	485	490	495	
gta ctg atg ggc gtc gat cgt ccc tca gat ctg cgt gat gat tcc gat				1536
Val Leu Met Gly Val Asp Arg Pro Ser Asp Leu Arg Asp Asp Ser Asp	500	505	510	
gac ccg gca gct gac gtt gtg gtc atg cgc gaa gag gtc atg agc gtg				1584
Asp Pro Ala Ala Asp Val Val Val Met Arg Glu Glu Val Met Ser Val	515	520	525	
ccg acg ctg ttt aaa ctg gct cga cgc tac gcc aag ttg gtc aat ggc				1632
Pro Thr Leu Phe Lys Leu Ala Arg Arg Tyr Ala Lys Leu Val Asn Gly	530	535	540	
aat att gct ctg gcc tgg atc tat aac ggt gtt gcc atg gtg ctt gca				1680
Asn Ile Ala Leu Ala Trp Ile Tyr Asn Gly Val Ala Met Val Leu Ala	545	550	555	560
gtg tct ggc ttg ctg cat cca atg gct gcg acc gtg gct atg ctg gcg				1728
Val Ser Gly Leu Leu His Pro Met Ala Ala Thr Val Ala Met Leu Ala	565	570	575	
tct tcg ctg ctt att gaa tgg cgc tcg ggc agg gcg cgc aag tac				1773
Ser Ser Leu Leu Ile Glu Trp Arg Ser Gly Arg Ala Arg Lys Tyr	580	585	590	
taaccagcaa ttccaagcc caa				1796
 <210> 386				
<211> 591				
<212> PRT				
<213> Corynebacterium glutamicum				
 <400> 386				
Lys Ser Trp Arg Ser Tyr Pro Ser Trp Phe Ala Phe Asp His Gly Thr	1	5	10	15
Leu Thr Gln Asn Glu Ile Tyr Phe Asp Val Ala Cys Gly Ile Thr Val	20	25	30	
Leu Leu Leu Ala Gly Arg Leu Leu Thr Arg Arg Arg Ser Gln Ser Ser	35	40	45	
Leu Leu Ala Glu Leu Gly Arg Leu Gln Ile Asp Pro Gln Arg Ile Val	50	55	60	
Thr Val Val Arg Lys His Arg Leu Lys Arg Val Val Gln Glu Leu Asn	65	70	75	80
Ile Pro Val Gln Glu Val Arg Val Asn Asp Asp Val Lys Val Pro Pro	85	90	95	
Asn Thr Thr Ile Pro Val Asp Gly Thr Val Ile Gly Gly Gly Ser Arg	100	105	110	
Ile Ala Ala Ser Ile Ile Met Gly Gln Asp Gln Arg Asp Val Lys Val				

115	120	125
Asn Asp Lys Val Phe Ala Gly Ser Leu Asn Leu Glu Ser Glu Ile Lys		
130	135	140
Val Arg Val Ile Arg Thr Gly His Arg Thr Arg Ile Ala Ala Val His		
145	150	155
		160
Arg Trp Val Lys Glu Ala Thr Leu Lys Glu Asn Arg His Asn Arg Ala		
	165	170
		175
Ala Ile Arg Ser Ala Gly Asn Leu Val Pro Ile Thr Phe Thr Leu Ala		
	180	185
		190
Val Val Asp Phe Cys Leu Trp Ala Leu Ile Ser Gly Asn Ile Asn Ala		
	195	200
		205
Ala Phe Thr Thr Thr Leu Ala Val Leu Ala Cys Val Ala Pro Val Ala		
	210	215
		220
Leu Ala Leu Ser Ala Pro Leu Ala Thr Arg Asn Ser Ile Glu Ala Ala		
	225	230
		235
		240
Ala Arg His Gly Ile Leu Val Arg Ser Gly Glu Ile Phe Arg Val Leu		
	245	250
		255
Asp Asp Val Asp Thr Ala Val Phe Asn Arg Val Gly Thr Leu Thr Asp		
	260	265
		270
Gly Glu Met Thr Val Glu Thr Val Thr Ala Asp Lys Gly Glu Asp Pro		
	275	280
		285
Glu Leu Val Leu Arg Val Ala Gly Ala Leu Ala Met Glu Ser His His		
	290	295
		300
Ala Ile Ser Lys Ala Leu Val Lys Ala Ser Arg Glu Ala Arg Asp Thr		
	305	310
		315
		320
Gly Ala Gly Gly Glu Asp Val Pro His Trp Ile Glu Val Gly Asn Val		
	325	330
		335
Glu Ile Thr Glu Ala Gly Ser Phe Gln Ala Thr Ile Glu Leu Pro Leu		
	340	345
		350
Ile Lys Pro Ser Gly Glu Lys Ile Met Arg Thr Thr Glu Ala Leu Leu		
	355	360
		365
Trp Arg Pro Arg Ser Met Thr Glu Val Arg Glu His Leu Ser Pro Arg		
	370	375
		380
Leu Val Ala Ala Ala Thr Ser Gly Gly Ala Pro Leu Ile Val Arg Trp		
	385	390
		395
		400
Lys Gly Lys Asp Arg Gly Val Ile Thr Leu Ser Asp His Val Arg Ser		
	405	410
		415
Asp Ser Ser Asp Ala Ile Ile Ala Ile Glu Glu Gln Gly Ile Glu Thr		
	420	425
		430
Met Met Leu Ser Arg Asp Thr Tyr Pro Val Ala Arg Arg Tyr Ala Asp		
	435	440
		445

Ser Leu Gly Ile Thr His Val Leu Ala Gly Ile Ala Pro Gly Lys Lys
 450 455 460
 Ala Gln Val Val Arg Ala Val His Thr Arg Gly Ser Thr Val Ala Met
 465 470 475 480
 Ile Gly Asp Glu Ser Val Met Asp Cys Leu Lys Val Ala Asp Val Gly
 485 490 495
 Val Leu Met Gly Val Asp Arg Pro Ser Asp Leu Arg Asp Asp Ser Asp
 500 505 510
 Asp Pro Ala Ala Asp Val Val Val Met Arg Glu Glu Val Met Ser Val
 515 520 525
 Pro Thr Leu Phe Lys Leu Ala Arg Arg Tyr Ala Lys Leu Val Asn Gly
 530 535 540
 Asn Ile Ala Leu Ala Trp Ile Tyr Asn Gly Val Ala Met Val Leu Ala
 545 550 555 560
 Val Ser Gly Leu Leu His Pro Met Ala Ala Thr Val Ala Met Leu Ala
 565 570 575
 Ser Ser Leu Leu Ile Glu Trp Arg Ser Gly Arg Ala Arg Lys Tyr
 580 585 590

<210> 387

<211> 327

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(304)

<223> RXA00942

<400> 387

cattgaccgg cagctcgctt gattcactgc acatcgtaga ttggacgggtg gacacgtttc 60
 agagtccgct ggatttcac acatcggaag gaagagaatt ttg agt acc aaa aat 115
 Leu Ser Thr Lys Asn
 1 5
 tac cac gtc gag ggt ttg acc tgc gca aac ggt gta gct tcc gta gag 163
 Tyr His Val Glu Gly Leu Thr Cys Ala Asn Gly Val Ala Ser Val Glu
 10 15 20
 gat gaa atc ggc att gtt gcg ggc acc cag ggt gtg gat att gat att 211
 Asp Glu Ile Gly Ile Val Ala Gly Thr Gln Gly Val Asp Ile Asp Ile
 25 30 35
 gag acc ggc cgc gtc acg gtg act ggt gaa ggt ttc act gac gag gaa 259
 Glu Thr Gly Arg Val Thr Val Thr Gly Glu Gly Phe Thr Asp Glu Glu
 40 45 50
 atc att gag gct gtc gcg aac gcg ggc tac aaa gtt tct ggg cgg 304
 Ile Ile Glu Ala Val Ala Asn Ala Gly Tyr Lys Val Ser Gly Arg
 55 60 65

tagcacaatt acacattcat ctc

327

<210> 388

<211> 68

<212> PRT

<213> Corynebacterium glutamicum

<400> 388

Leu Ser Thr Lys Asn Tyr His Val Glu Gly Leu Thr Cys Ala Asn Gly
 1 5 10 15

Val Ala Ser Val Glu Asp Glu Ile Gly Ile Val Ala Gly Thr Gln Gly
 20 25 30

Val Asp Ile Asp Ile Glu Thr Gly Arg Val Thr Val Thr Gly Glu Gly
 35 40 45

Phe Thr Asp Glu Glu Ile Ile Glu Ala Val Ala Asn Ala Gly Tyr Lys
 50 55 60

Val Ser Gly Arg
 65

<210> 389

<211> 1925

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1902)

<223> RXN01338

<400> 389

aaa act tat acc cca aat ccc tgg atg tta ttc atc cgc tca ttt gat 48
 Lys Thr Tyr Thr Pro Asn Pro Trp Met Leu Phe Ile Arg Ser Phe Asp
 1 5 10 15

ggc atc atc act gtc gca gcc ctt gtt gcc atc gca ata cat ctc att 96
 Gly Ile Ile Thr Val Ala Ala Leu Val Ala Ile Ala Ile His Leu Ile
 20 25 30

tta tgg ctg gct cta gat cta gat ggc ctt gct aaa aac tgg cct tta 144
 Leu Trp Leu Ala Leu Asp Leu Asp Gly Leu Ala Lys Asn Trp Pro Leu
 35 40 45

ata gcc atc gtt atc gta ggt ggc att ccg ttg atg tgg gat gtg ctg 192
 Ile Ala Ile Val Ile Val Gly Gly Ile Pro Leu Met Trp Asp Val Leu
 50 55 60

aaa tca gcc att aaa act cgc ggt ggc gcg gat act tta gca gca gtc 240
 Lys Ser Ala Ile Lys Thr Arg Gly Gly Ala Asp Thr Leu Ala Ala Val
 65 70 75 80

tcc atc att act tct gtg ttg tta ggg gag tgg ttg gtt gcc gcg atc 288
 Ser Ile Ile Thr Ser Val Leu Leu Gly Glu Trp Leu Val Ala Ala Ile
 85 90 95

atc gtg ctc atg ctc tct ggt ggt gaa gcg cta gaa gag gca gca tca Ile Val Leu Met Leu Ser Gly Gly Glu Ala Leu Glu Glu Ala Ala Ser 100 105 110	336
cgg cga gcc agt ggc acc ttg gac gca ctt gcc cgg cgc gca cca agt Arg Arg Ala Ser Gly Thr Leu Asp Ala Leu Ala Arg Arg Ala Pro Ser 115 120 125	384
aca gct cac cgc ctg ttg ggt gca acc att ctt gat gga acc gaa gag Thr Ala His Arg Leu Leu Gly Ala Thr Ile Leu Asp Gly Thr Glu Glu 130 135 140	432
atc gcc gtg gaa gag atc acg gtt ggt gat tta gtg gcg gtg ctc ccg Ile Ala Val Glu Glu Ile Thr Val Gly Asp Leu Val Ala Val Leu Pro 145 150 155 160	480
cat gaa ctt tgt ccc gtg gat ggt gaa atc gtg gca ggc cac ggc acc His Glu Leu Cys Pro Val Asp Gly Glu Ile Val Ala Gly His Gly Thr 165 170 175	528
atg gat gag tct tat ctc acg ggt gag ccc tat gtg gtg agt aaa tct Met Asp Glu Ser Tyr Leu Thr Gly Glu Pro Tyr Val Val Ser Lys Ser 180 185 190	576
aaa ggt tcg caa gca atg tcg ggt gca gtc aat ggt gat act ccg ctg Lys Gly Ser Gln Ala Met Ser Gly Ala Val Asn Gly Asp Thr Pro Leu 195 200 205	624
acg att gtt gcc aca aag ctt gcc cat gat tcc aga tac gcc caa att Thr Ile Val Ala Thr Lys Leu Ala His Asp Ser Arg Tyr Ala Gln Ile 210 215 220	672
gtt ggt gta ctc cat gaa gca gaa aac aac cgc cca gaa atg cgc agg Val Gly Val Leu His Glu Ala Glu Asn Asn Arg Pro Glu Met Arg Arg 225 230 235 240	720
atg gct gac cgt ctt ggc gcg tgg tat acg gtg att gca ctt gcc ctc Met Ala Asp Arg Leu Gly Ala Trp Tyr Thr Val Ile Ala Leu Ala Leu 245 250 255	768
ggt ggt ctt ggc tgg att gtc tcc ggc gac cca gtg agg ttc ttg gct Gly Gly Leu Gly Trp Ile Val Ser Gly Asp Pro Val Arg Phe Leu Ala 260 265 270	816
gtt gtc gtt gtc gcc acc cca tgt cca ttg ctc att gca gtg cca gtg Val Val Val Val Ala Thr Pro Cys Pro Leu Leu Ile Ala Val Pro Val 275 280 285	864
gcg atc atc ggt gcg att tct ctt gcg gct cgt cgg ggc atc atc gtg Ala Ile Ile Gly Ala Ile Ser Leu Ala Ala Arg Arg Gly Ile Ile Val 290 295 300	912
aag aac cct gga atg ctg gaa aac gct tca gga gta aag aca gtg atg Lys Asn Pro Gly Met Leu Glu Asn Ala Ser Gly Val Lys Thr Val Met 305 310 315 320	960
ttc gat aag act gga acg ctc acc tat ggc agg cca gtg att act gat Phe Asp Lys Thr Gly Thr Leu Thr Tyr Gly Arg Pro Val Ile Thr Asp 325 330 335	1008
atc cac act gct ccc gga gtt gag gaa gat aca gtc cta gct ttg gct	1056

Ile His Thr Ala Pro Gly Val Glu Glu Asp Thr Val Leu Ala Leu Ala	
340	345 350
gct tca gta gag cgc tac tcc aga cac ccg ttg gct gac gcg att cgt	1104
Ala Ser Val Glu Arg Tyr Ser Arg His Pro Leu Ala Asp Ala Ile Arg	
355	360 365
gag ggc gca aaa gcc agg gaa ctt cat ctg cct gat gta gtg gaa gta	1152
Glu Gly Ala Lys Ala Arg Glu Leu His Leu Pro Asp Val Val Glu Val	
370	375 380
tcg gaa cgt cca gga cag gga cta acc ggc acg gtg ggc gag cac ctg	1200
Ser Glu Arg Pro Gly Gln Gly Leu Thr Gly Thr Val Gly Glu His Leu	
385	390 395 400
gtt cga ata acc aat agg cgc agc aca cta gaa att gat cca gac agc	1248
Val Arg Ile Thr Asn Arg Arg Ser Thr Leu Glu Ile Asp Pro Asp Ser	
405	410 415
aag aac tac att ccg gtg aca agt tcc ggc atg gaa tct gtg gtg ctt	1296
Lys Asn Tyr Ile Pro Val Thr Ser Ser Gly Met Glu Ser Val Val Leu	
420	425 430
gtt gat gat aaa tat gca gca ctc att cgc ctc cgg gat gaa cct cgt	1344
Val Asp Asp Lys Tyr Ala Ala Leu Ile Arg Leu Arg Asp Glu Pro Arg	
435	440 445
gca tct gcc agt gag ttc atc gcg cac ttg ccc aag aag cac aaa gtg	1392
Ala Ser Ala Ser Glu Phe Ile Ala His Leu Pro Lys Lys His Lys Val	
450	455 460
gac aag ctc atg att atc tct ggt gat cgc gca tct gag gtt cgt tac	1440
Asp Lys Leu Met Ile Ile Ser Gly Asp Arg Ala Ser Glu Val Arg Tyr	
465	470 475 480
ctt gcg gac aag gtt ggc att gat gag gta cac gca gag gcc tca ccg	1488
Leu Ala Asp Lys Val Gly Ile Asp Glu Val His Ala Glu Ala Ser Pro	
485	490 495
gaa gac aag ctg aac att gtt aat cgg cat aat gag cac ggc gcc acc	1536
Glu Asp Lys Leu Asn Ile Val Asn Arg His Asn Glu His Gly Ala Thr	
500	505 510
atg ttc tta ggt gat gga atc aac gat gcg cca gcc atg gcc gtt gcc	1584
Met Phe Leu Gly Asp Gly Ile Asn Asp Ala Pro Ala Met Ala Val Ala	
515	520 525
acc gtt ggt gtc gcg atg gga gca gac tcc gat gtc acg tcc gaa gca	1632
Thr Val Gly Val Ala Met Gly Ala Asp Ser Asp Val Thr Ser Glu Ala	
530	535 540
gca gat gct gtg att ttg gat tct tcc ctg gaa cgt ctc gac gat ctg	1680
Ala Asp Ala Val Ile Leu Asp Ser Ser Leu Glu Arg Leu Asp Asp Leu	
545	550 555 560
ctc cac atc agt gca cgg atg cgt cga ata gcg ttg caa tct gcg ggc	1728
Leu His Ile Ser Ala Arg Met Arg Arg Ile Ala Leu Gln Ser Ala Gly	
565	570 575
ggt ggc atg gcg ttg agt gtc ata gga atg atc ctc gcg gta ttt gga	1776
Gly Gly Met Ala Leu Ser Val Ile Gly Met Ile Leu Ala Val Phe Gly	

580	585	590	
ttc ttg acg cca ctg atg ggt gcg atc ttc caa gag gtc att gac gtg			1824
Phe Leu Thr Pro Leu Met Gly Ala Ile Phe Gln Glu Val Ile Asp Val			
595	600	605	
ctg gct atc ctc aat tcc gct cgg gtc gca ctg cca cgc gga gcg att			1872
Leu Ala Ile Leu Asn Ser Ala Arg Val Ala Leu Pro Arg Gly Ala Ile			
610	615	620	
agt gat ttt gat acg caa gaa aaa gtt tct tagcagggta acctaaatgt			1922
Ser Asp Phe Asp Thr Gln Glu Lys Val Ser			
625	630		
cgt			1925
<210> 390			
<211> 634			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 390			
Lys Thr Tyr Thr Pro Asn Pro Trp Met Leu Phe Ile Arg Ser Phe Asp			
1	5	10	15
Gly Ile Ile Thr Val Ala Ala Leu Val Ala Ile Ala Ile His Leu Ile			
20	25	30	
Leu Trp Leu Ala Leu Asp Leu Asp Gly Leu Ala Lys Asn Trp Pro Leu			
35	40	45	
Ile Ala Ile Val Ile Val Gly Gly Ile Pro Leu Met Trp Asp Val Leu			
50	55	60	
Lys Ser Ala Ile Lys Thr Arg Gly Gly Ala Asp Thr Leu Ala Ala Val			
65	70	75	80
Ser Ile Ile Thr Ser Val Leu Leu Gly Glu Trp Leu Val Ala Ala Ile			
85	90	95	
Ile Val Leu Met Leu Ser Gly Gly Glu Ala Leu Glu Glu Ala Ala Ser			
100	105	110	
Arg Arg Ala Ser Gly Thr Leu Asp Ala Leu Ala Arg Arg Ala Pro Ser			
115	120	125	
Thr Ala His Arg Leu Leu Gly Ala Thr Ile Leu Asp Gly Thr Glu Glu			
130	135	140	
Ile Ala Val Glu Glu Ile Thr Val Gly Asp Leu Val Ala Val Leu Pro			
145	150	155	160
His Glu Leu Cys Pro Val Asp Gly Glu Ile Val Ala Gly His Gly Thr			
165	170	175	
Met Asp Glu Ser Tyr Leu Thr Gly Glu Pro Tyr Val Val Ser Lys Ser			
180	185	190	
Lys Gly Ser Gln Ala Met Ser Gly Ala Val Asn Gly Asp Thr Pro Leu			
195	200	205	

Thr Ile Val Ala Thr Lys Leu Ala His Asp Ser Arg Tyr Ala Gln Ile
 210 215 220
 Val Gly Val Leu His Glu Ala Glu Asn Asn Arg Pro Glu Met Arg Arg
 225 230 235 240
 Met Ala Asp Arg Leu Gly Ala Trp Tyr Thr Val Ile Ala Leu Ala Leu
 245 250 255
 Gly Gly Leu Gly Trp Ile Val Ser Gly Asp Pro Val Arg Phe Leu Ala
 260 265 270
 Val Val Val Val Ala Thr Pro Cys Pro Leu Leu Ile Ala Val Pro Val
 275 280 285
 Ala Ile Ile Gly Ala Ile Ser Leu Ala Ala Arg Arg Gly Ile Ile Val
 290 295 300
 Lys Asn Pro Gly Met Leu Glu Asn Ala Ser Gly Val Lys Thr Val Met
 305 310 315 320
 Phe Asp Lys Thr Gly Thr Leu Thr Tyr Gly Arg Pro Val Ile Thr Asp
 325 330 335
 Ile His Thr Ala Pro Gly Val Glu Glu Asp Thr Val Leu Ala Leu Ala
 340 345 350
 Ala Ser Val Glu Arg Tyr Ser Arg His Pro Leu Ala Asp Ala Ile Arg
 355 360 365
 Glu Gly Ala Lys Ala Arg Glu Leu His Leu Pro Asp Val Val Glu Val
 370 375 380
 Ser Glu Arg Pro Gly Gln Gly Leu Thr Gly Thr Val Gly Glu His Leu
 385 390 395 400
 Val Arg Ile Thr Asn Arg Arg Ser Thr Leu Glu Ile Asp Pro Asp Ser
 405 410 415
 Lys Asn Tyr Ile Pro Val Thr Ser Ser Gly Met Glu Ser Val Val Leu
 420 425 430
 Val Asp Asp Lys Tyr Ala Ala Leu Ile Arg Leu Arg Asp Glu Pro Arg
 435 440 445
 Ala Ser Ala Ser Glu Phe Ile Ala His Leu Pro Lys Lys His Lys Val
 450 455 460
 Asp Lys Leu Met Ile Ile Ser Gly Asp Arg Ala Ser Glu Val Arg Tyr
 465 470 475 480
 Leu Ala Asp Lys Val Gly Ile Asp Glu Val His Ala Glu Ala Ser Pro
 485 490 495
 Glu Asp Lys Leu Asn Ile Val Asn Arg His Asn Glu His Gly Ala Thr
 500 505 510
 Met Phe Leu Gly Asp Gly Ile Asn Asp Ala Pro Ala Met Ala Val Ala
 515 520 525

Thr Val Gly Val Ala Met Gly Ala Asp Ser Asp Val Thr Ser Glu Ala
530 535 540

Ala Asp Ala Val Ile Leu Asp Ser Ser Leu Glu Arg Leu Asp Asp Leu
545 550 555 560

Leu His Ile Ser Ala Arg Met Arg Arg Ile Ala Leu Gln Ser Ala Gly
565 570 575

Gly Gly Met Ala Leu Ser Val Ile Gly Met Ile Leu Ala Val Phe Gly
580 585 590

Phe Leu Thr Pro Leu Met Gly Ala Ile Phe Gln Glu Val Ile Asp Val
595 600 605

Leu Ala Ile Leu Asn Ser Ala Arg Val Ala Leu Pro Arg Gly Ala Ile
610 615 620

Ser Asp Phe Asp Thr Gln Glu Lys Val Ser
625 630

<210> 391

<211> 2001

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1978)

<223> FRXA01338

<400> 391

atccttgccct tgccaaggga agcctgtaca tgctggtcag ggacattttt atgggtgata 60

atgggggttta tgaataaaaa cttatacccc aaatccctgg atg tta ttc atc cgc 115
Met Leu Phe Ile Arg
1 5

tca ttt gat ggc atc atc act gtc gca gcc ctt gtt gcc atc gca ata 163
Ser Phe Asp Gly Ile Ile Thr Val Ala Ala Leu Val Ala Ile Ala Ile
10 15 20

cat ctc att tta tgg ctg gct cta gat cta gat ggc ctt gct aaa aac 211
His Leu Ile Leu Trp Leu Ala Leu Asp Leu Asp Gly Leu Ala Lys Asn
25 30 35

tgg cct tta ata gcc atc gtt atc gta ggt ggc att ccg ttg atg tgg 259
Trp Pro Leu Ile Ala Ile Val Ile Val Gly Gly Ile Pro Leu Met Trp
40 45 50

gat gtg ctg aaa tca gcc att aaa act cgc ggt ggc gcg gat act tta 307
Asp Val Leu Lys Ser Ala Ile Lys Thr Arg Gly Gly Ala Asp Thr Leu
55 60 65

gca gca gtc tcc atc att act tct gtg ttg tta ggg gag tgg ttg gtt 355
Ala Ala Val Ser Ile Ile Thr Ser Val Leu Leu Gly Glu Trp Leu Val
70 75 80 85

gcc gcg atc atc gtg ctc atg ctc tct ggt ggt gaa gcg cta gaa gag 403
Ala Ala Ile Ile Val Leu Met Leu Ser Gly Gly Glu Ala Leu Glu Glu

				90				95				100				
gca	gca	tca	cgg	cga	gcc	agt	ggc	acc	ttg	gac	gca	ctt	gcc	cgg	cgc	451
Ala	Ala	Ser	Arg	Arg	Ala	Ser	Gly	Thr	Leu	Asp	Ala	Leu	Ala	Arg	Arg	
105								110				115				
gca	cca	agt	aca	gct	cac	cgc	ctg	ttg	ggg	gca	acc	att	ctt	gat	gga	499
Ala	Pro	Ser	Thr	Ala	His	Arg	Leu	Leu	Gly	Ala	Thr	Ile	Leu	Asp	Gly	
120								125				130				
acc	gaa	gag	atc	gcc	gtg	gaa	gag	atc	acg	gtt	ggg	gat	tta	gtg	gcg	547
Thr	Glu	Glu	Ile	Ala	Val	Glu	Glu	Ile	Thr	Val	Gly	Asp	Leu	Val	Ala	
135								140				145				
gtg	ctc	ccg	cat	gaa	ctt	tgt	ccc	gtg	gat	ggg	gaa	atc	gtg	gca	ggc	595
Val	Leu	Pro	His	Glu	Leu	Cys	Pro	Val	Asp	Gly	Glu	Ile	Val	Ala	Gly	
150				155				160				165				
cac	ggc	acc	atg	gat	gag	tct	tat	ctc	acg	ggg	gag	ccc	tat	gtg	gtg	643
His	Gly	Thr	Met	Asp	Glu	Ser	Tyr	Leu	Thr	Gly	Glu	Pro	Tyr	Val	Val	
				170				175				180				
agt	aaa	tct	aaa	ggg	tcc	caa	gca	atg	tcc	ggg	gca	gtc	aat	ggg	gat	691
Ser	Lys	Ser	Lys	Gly	Ser	Gln	Ala	Met	Ser	Gly	Ala	Val	Asn	Gly	Asp	
185								190				195				
act	ccg	ctg	acg	att	gtt	gcc	aca	aag	ctt	gcc	cat	gat	tcc	aga	tac	739
Thr	Pro	Leu	Thr	Ile	Val	Ala	Thr	Lys	Leu	Ala	His	Asp	Ser	Arg	Tyr	
200								205				210				
gcc	caa	att	gtt	ggg	gta	ctc	cat	gaa	gca	gaa	aac	aac	cgc	cca	gaa	787
Ala	Gln	Ile	Val	Gly	Val	Leu	His	Glu	Ala	Glu	Asn	Asn	Arg	Pro	Glu	
215				220				225								
atg	cgc	agg	atg	gct	gac	cgt	ctt	ggc	gcg	tgg	tat	acg	gtg	att	gca	835
Met	Arg	Arg	Met	Ala	Asp	Arg	Leu	Gly	Ala	Trp	Tyr	Thr	Val	Ile	Ala	
230				235				240				245				
ctt	gcc	ctc	ggg	ggg	ctt	ggc	tgg	att	gtc	tcc	ggc	gac	cca	gtg	agg	883
Leu	Ala	Leu	Gly	Gly	Leu	Gly	Trp	Ile	Val	Ser	Gly	Asp	Pro	Val	Arg	
				250				255				260				
ttc	ttg	gct	gtt	gtc	gtt	gtc	gcc	acc	cca	tgt	cca	ttg	ctc	att	gca	931
Phe	Leu	Ala	Val	Val	Val	Val	Ala	Thr	Pro	Cys	Pro	Leu	Leu	Ile	Ala	
265								270				275				
gtg	cca	gtg	gcg	atc	atc	ggg	gcg	att	tct	ctt	gcg	gct	cgt	cgg	ggc	979
Val	Pro	Val	Ala	Ile	Ile	Gly	Ala	Ile	Ser	Leu	Ala	Ala	Arg	Arg	Gly	
280				285				290								
atc	atc	gtg	aag	aac	cct	gga	atg	ctg	gaa	aac	gct	tca	gga	gta	aag	1027
Ile	Ile	Val	Lys	Asn	Pro	Gly	Met	Leu	Glu	Asn	Ala	Ser	Gly	Val	Lys	
295				300				305								
aca	gtg	atg	ttc	gat	aag	act	gga	acg	ctc	acc	tat	ggc	agg	cca	gtg	1075
Thr	Val	Met	Phe	Asp	Lys											

gct ttg gct gct tca gta gag cgc tac tcc aga cac ccg ttg gct gac Ala Leu Ala Ala Ser Val Glu Arg Tyr Ser Arg His Pro Leu Ala Asp 345 350 355	1171
gcg att cgt gag ggc gca aaa gcc agg gaa ctt cat ctg cct gat gta Ala Ile Arg Glu Gly Ala Lys Ala Arg Glu Leu His Leu Pro Asp Val 360 365 370	1219
gtg gaa gta tcg gaa cgt cca gga cag gga cta acc ggc acg gtg ggc Val Glu Val Ser Glu Arg Pro Gly Gln Gly Leu Thr Gly Thr Val Gly 375 380 385	1267
gag cac ctg gtt cga ata acc aat agg cgc agc aca cta gaa att gat Glu His Leu Val Arg Ile Thr Asn Arg Arg Ser Thr Leu Glu Ile Asp 390 395 400 405	1315
cca gac agc aag aac tac att ccg gtg aca agt tcc ggc atg gaa tct Pro Asp Ser Lys Asn Tyr Ile Pro Val Thr Ser Ser Gly Met Glu Ser 410 415 420	1363
gtg gtg ctt gtt gat gat aaa tat gca gca ctc att cgc ctc cgg gat Val Val Leu Val Asp Asp Lys Tyr Ala Ala Leu Ile Arg Leu Arg Asp 425 430 435	1411
gaa cct cgt gca tct gcc agt gag ttc atc gcg cac ttg ccc aag aag Glu Pro Arg Ala Ser Ala Ser Glu Phe Ile Ala His Leu Pro Lys Lys 440 445 450	1459
cac aaa gtg gac aag ctc atg att atc tct ggt gat cgc gca tct gag His Lys Val Asp Lys Leu Met Ile Ile Ser Gly Asp Arg Ala Ser Glu 455 460 465	1507
gtt cgt tac ctt gcg gac aag gtt ggc att gat gag gta cac gca gag Val Arg Tyr Leu Ala Asp Lys Val Gly Ile Asp Glu Val His Ala Glu 470 475 480 485	1555
gcc tca ccg gaa gac aag ctg aac att gtt aat ccg cat aat gag cac Ala Ser Pro Glu Asp Lys Leu Asn Ile Val Asn Arg His Asn Glu His 490 495 500	1603
ggc gcc acc atg ttc tta ggt gat gga atc aac gat gcg cca gcc atg Gly Ala Thr Met Phe Leu Gly Asp Gly Ile Asn Asp Ala Pro Ala Met 505 510 515	1651
gcc gtt gcc acc gtt ggt gtc gcg atg gga gca gac tcc gat gtc acg Ala Val Ala Thr Val Gly Val Ala Met Gly Ala Asp Ser Asp Val Thr 520 525 530	1699
tcc gaa gca gca gat gct gtg att ttg gat tct tcc ctg gaa cgt ctc Ser Glu Ala Ala Asp Ala Val Ile Leu Asp Ser Ser Leu Glu Arg Leu 535 540 545	1747
gac gat ctg ctc cac atc agt gca cgg atg cgt cga ata gcg ttg caa Asp Asp Leu Leu His Ile Ser Ala Arg Met Arg Arg Ile Ala Leu Gln 550 555 560 565	1795
tct gcg ggc ggt ggc atg gcg ttg agt gtc ata gga atg atc ctc gcg Ser Ala Gly Gly Gly Met Ala Leu Ser Val Ile Gly Met Ile Leu Ala 570 575 580	1843

gta ttt gga ttc ttg acg cca ctg atg ggt gcg atc ttc caa gag gtc 1891
 Val Phe Gly Phe Leu Thr Pro Leu Met Gly Ala Ile Phe Gln Glu Val
 585 590 595

att gac gtg ctg gct atc ctc aat tcc gct cgg gtc gca ctg cca cgc 1939
 Ile Asp Val Leu Ala Ile Leu Asn Ser Ala Arg Val Ala Leu Pro Arg
 600 605 610

gga gcg att agt gat ttt gat acg caa gaa aaa gtt tct tagcagggtta 1988
 Gly Ala Ile Ser Asp Phe Asp Thr Gln Glu Lys Val Ser
 615 620 625

acctaaatgt cgt 2001

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<211> 626

<212> PRT

<213> Corynebacterium glutamicum

<400> 392

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Val Ala Ile Ala Ile His Leu Ile Leu Trp Leu Ala Leu Asp Leu Asp
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Gly Leu Ala Lys Asn Trp Pro Leu Ile Ala Ile Val Ile Val Gly Gly
 35 40 45

Ile Pro Leu Met Trp Asp Val Leu Lys Ser Ala Ile Lys Thr Arg Gly
 50 55 60

Gly Ala Asp Thr Leu Ala Ala Val Ser Ile Ile Thr Ser Val Leu Leu
 65 70 75 80

Gly Glu Trp Leu Val Ala Ala Ile Ile Val Leu Met Leu Ser Gly Gly
 85 90 95

Glu Ala Leu Glu Glu Ala Ala Ser Arg Arg Ala Ser Gly Thr Leu Asp
 100 105 110

Ala Leu Ala Arg Arg Ala Pro Ser Thr Ala His Arg Leu Leu Gly Ala
 115 120 125

Thr Ile Leu Asp Gly Thr Glu Glu Ile Ala Val Glu Glu Ile Thr Val
 130 135 140

Gly Asp Leu Val Ala Val Leu Pro His Glu Leu Cys Pro Val Asp Gly
 145 150 155 160

Glu Ile Val Ala Gly His Gly Thr Met Asp Glu Ser Tyr Leu Thr Gly
 165 170 175

Glu Pro Tyr Val Val Ser Lys Ser Lys Gly Ser Gln Ala Met Ser Gly
 180 185 190

Ala Val Asn Gly Asp Thr Pro Leu Thr Ile Val Ala Thr Lys Leu Ala
 195 200 205

His Asp Ser Arg Tyr Ala Gln Ile Val Gly Val Leu His Glu Ala Glu

210					215					220					
Asn	Asn	Arg	Pro	Glu	Met	Arg	Arg	Met	Ala	Asp	Arg	Leu	Gly	Ala	Trp
225					230					235					240
Tyr	Thr	Val	Ile	Ala	Leu	Ala	Leu	Gly	Gly	Leu	Gly	Trp	Ile	Val	Ser
				245					250						255
Gly	Asp	Pro	Val	Arg	Phe	Leu	Ala	Val	Val	Val	Val	Ala	Thr	Pro	Cys
			260					265					270		
Pro	Leu	Leu	Ile	Ala	Val	Pro	Val	Ala	Ile	Ile	Gly	Ala	Ile	Ser	Leu
			275				280						285		
Ala	Ala	Arg	Arg	Gly	Ile	Ile	Val	Lys	Asn	Pro	Gly	Met	Leu	Glu	Asn
							295					300			
Ala	Ser	Gly	Val	Lys	Thr	Val	Met	Phe	Asp	Lys	Thr	Gly	Thr	Leu	Thr
305							310					315			320
Tyr	Gly	Arg	Pro	Val	Ile	Thr	Asp	Ile	His	Thr	Ala	Pro	Gly	Val	Glu
				325					330						335
Glu	Asp	Thr	Val	Leu	Ala	Leu	Ala	Ala	Ser	Val	Glu	Arg	Tyr	Ser	Arg
			340					345							350
His	Pro	Leu	Ala	Asp	Ala	Ile	Arg	Glu	Gly	Ala	Lys	Ala	Arg	Glu	Leu
			355				360								365
His	Leu	Pro	Asp	Val	Val	Glu	Val	Ser	Glu	Arg	Pro	Gly	Gln	Gly	Leu
			370				375					380			
Thr	Gly	Thr	Val	Gly	Glu	His	Leu	Val	Arg	Ile	Thr	Asn	Arg	Arg	Ser
385							390					395			400
Thr	Leu	Glu	Ile	Asp	Pro	Asp	Ser	Lys	Asn	Tyr	Ile	Pro	Val	Thr	Ser
				405					410						415
Ser	Gly	Met	Glu	Ser	Val	Val	Leu	Val	Asp	Asp	Lys	Tyr	Ala	Ala	Leu
			420					425							430
Ile	Arg	Leu	Arg	Asp	Glu	Pro	Arg	Ala	Ser	Ala	Ser	Glu	Phe	Ile	Ala
			435				440								445
His	Leu	Pro	Lys	Lys	His	Lys	Val	Asp	Lys	Leu	Met	Ile	Ile	Ser	Gly
			450				455					460			
Asp	Arg	Ala	Ser	Glu	Val	Arg	Tyr	Leu	Ala	Asp	Lys	Val	Gly	Ile	Asp
465							470					475			480
Glu	Val	His	Ala	Glu	Ala	Ser	Pro	Glu	Asp	Lys	Leu	Asn	Ile	Val	Asn
				485					490						495
Arg	His	Asn	Glu	His	Gly	Ala	Thr	Met	Phe	Leu	Gly	Asp	Gly	Ile	Asn
			500					505							510
Asp	Ala	Pro	Ala	Met	Ala	Val	Ala	Thr	Val	Gly	Val	Ala	Met	Gly	Ala
			515					520							525
Asp	Ser	Asp	Val	Thr	Ser	Glu	Ala	Ala	Asp	Ala	Val	Ile	Leu	Asp	Ser
			530				535								540

Ser Leu Glu Arg Leu Asp Asp Leu Leu His Ile Ser Ala Arg Met Arg
 545 550 555 560

Arg Ile Ala Leu Gln Ser Ala Gly Gly Gly Met Ala Leu Ser Val Ile
 565 570 575

Gly Met Ile Leu Ala Val Phe Gly Phe Leu Thr Pro Leu Met Gly Ala
 580 585 590

Ile Phe Gln Glu Val Ile Asp Val Leu Ala Ile Leu Asn Ser Ala Arg
 595 600 605

Val Ala Leu Pro Arg Gly Ala Ile Ser Asp Phe Asp Thr Gln Glu Lys
 610 615 620

Val Ser
 625

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 <223> RXA01625

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tctgctgtta gaagataccc gacagaaagg ggccaataat atg gct atc aag aac 115
 Met Ala Ile Lys Asn
 1 5

tac acc gtc gaa ggc atg act tgt gga cac tgc gtc tcc tcc gta aag 163
 Tyr Thr Val Glu Gly Met Thr Cys Gly His Cys Val Ser Ser Val Lys
 10 15 20

gaa gag gtc gga gag gtt gct ggc gtc acc gct gtg gac gtc acc cta 211
 Glu Glu Val Gly Glu Val Ala Gly Val Thr Ala Val Asp Val Thr Leu
 25 30 35

gaa acc ggt gcc gtg cag gtt acc ggc gaa gac ttc acc gac gag gct 259
 Glu Thr Gly Ala Val Gln Val Thr Gly Glu Asp Phe Thr Asp Glu Ala
 40 45 50

gtc aag gct gct gtc gtt gag gct ggc tac aag gtt gtt gca 301
 Val Lys Ala Ala Val Val Glu Ala Gly Tyr Lys Val Val Ala
 55 60 65

taaaccctg aaaagtttaa agc 324

<210> 394
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<400> 394

Met Ala Ile Lys Asn Tyr Thr Val Glu Gly Met Thr Cys Gly His Cys
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Val Ser Ser Val Lys Glu Glu Val Gly Glu Val Ala Gly Val Thr Ala
 20 25 30

Val Asp Val Thr Leu Glu Thr Gly Ala Val Gln Val Thr Gly Glu Asp
 35 40 45

Phe Thr Asp Glu Ala Val Lys Ala Ala Val Val Glu Ala Gly Tyr Lys
 50 55 60

Val Val Ala
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<210> 395

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<220>

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<222> (101)..(2776)

<223> RXA02220

<400> 395

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ggcggggcac gcggccaatc atgtgaaagg tctgttttag gtg tgc tcc cct ctc 115
 Val Ser Ser Pro Leu
 1 5

ccc gct gcc gtc aca tca aaa ccc gcc cac gcg ctt tcc tct gat gag 163
 Pro Ala Ala Val Thr Ser Lys Pro Ala His Ala Leu Ser Ser Asp Glu
 10 15 20

gtg tta gaa aat ctc ggg gtc cag gac acc gga ttg acc tcc gcg gag 211
 Val Leu Glu Asn Leu Gly Val Gln Asp Thr Gly Leu Thr Ser Ala Glu
 25 30 35

gca aca cag cgt ttg gaa gca aac ggg cca aac gag ctt cct caa act 259
 Ala Thr Gln Arg Leu Glu Ala Asn Gly Pro Asn Glu Leu Pro Gln Thr
 40 45 50

cca cct gaa aca gtc tgg caa cgg cta ttc cgc cag gtc aac gat cca 307
 Pro Pro Glu Thr Val Trp Gln Arg Leu Phe Arg Gln Val Asn Asp Pro
 55 60 65

atg atc tac gtt ctc att gcc gcc gcg gta ctc acg gcg ttt ctt ggg 355
 Met Ile Tyr Val Leu Ile Ala Ala Ala Val Leu Thr Ala Phe Leu Gly
 70 75 80 85

cat tgg aca gac acc atc gtg atc ggc gcc gtt gtc atc atc aac atg 403
 His Trp Thr Asp Thr Ile Val Ile Gly Ala Val Val Ile Ile Asn Met
 90 95 100

atg gtt ggg ttc atc caa gag ggc aaa gct gcg gat gcg ttg gca tgc 451
 Met Val Gly Phe Ile Gln Glu Gly Lys Ala Ala Asp Ala Leu Ala Ser
 105 110 115

atc cgc aac atg ctc tcc ccg gaa tcc gcg gcg ttg cgc gat ggg gtc	499
Ile Arg Asn Met Leu Ser Pro Glu Ser Ala Ala Leu Arg Asp Gly Val	
120 125 130	
ttc cac aaa att gat gcg gca gag ctg gtg gtc ggt gac gtt gtg aaa	547
Phe His Lys Ile Asp Ala Ala Glu Leu Val Val Gly Asp Val Val Lys	
135 140 145	
cta tcc gcc ggc gat aaa gtg ccc gct gac ctg cgc atg ctc gcc gcc	595
Leu Ser Ala Gly Asp Lys Val Pro Ala Asp Leu Arg Met Leu Ala Ala	
150 155 160 165	
acc aat ctg cac att gag gaa tcc gcg ctc acc ggc gag gcg gaa gca	643
Thr Asn Leu His Ile Glu Glu Ser Ala Leu Thr Gly Glu Ala Glu Ala	
170 175 180	
gtg gtc aaa ggt act gat cca gtt gag gcc gac gcc gga atc ggc gac	691
Val Val Lys Gly Thr Asp Pro Val Glu Ala Asp Ala Gly Ile Gly Asp	
185 190 195	
cgc aca tcc atg gcg ttt tca gga acg ctg gtg ctc aca ggc agc ggc	739
Arg Thr Ser Met Ala Phe Ser Gly Thr Leu Val Leu Thr Gly Ser Gly	
200 205 210	
acc ggc gtg gtc acc gcc acc ggt gca ggc aca gaa atc ggg cac atc	787
Thr Gly Val Val Thr Ala Thr Gly Ala Gly Thr Glu Ile Gly His Ile	
215 220 225	
acc acc atg ctt gcc gac gtc gac tcc gtg gat acc cca ttg act cgg	835
Thr Thr Met Leu Ala Asp Val Asp Ser Val Asp Thr Pro Leu Thr Arg	
230 235 240 245	
tcg atg aaa aag ttc tca tcg gcg tta gca atc gtg tgt gta ttc cta	883
Ser Met Lys Lys Phe Ser Ser Ala Leu Ala Ile Val Cys Val Phe Leu	
250 255 260	
gcg atc ctc atg ctg gtg gtt gcc ggt cta gtc cac cac aca cct ttg	931
Ala Ile Leu Met Leu Val Val Ala Gly Leu Val His His Thr Pro Leu	
265 270 275	
gaa gag ctc att ctt tcc gcc atc ggc ttt gcg gtg gct gcc att ccg	979
Glu Glu Leu Ile Leu Ser Ala Ile Gly Phe Ala Val Ala Ala Ile Pro	
280 285 290	
gag ggt cta cct gcg gtt atc gcc atc acg ctg gca ttg ggt gtg caa	1027
Glu Gly Leu Pro Ala Val Ile Ala Ile Thr Leu Ala Leu Gly Val Gln	
295 300 305	
aag atg gca gct cga aat gcg att acg cgc cgg ttg aat tcc gtg gaa	1075
Lys Met Ala Ala Arg Asn Ala Ile Thr Arg Arg Leu Asn Ser Val Glu	
310 315 320 325	
aca ctt ggc tct gtc acc acc atc tgc acg gat aaa acc ggc aca ctc	1123
Thr Leu Gly Ser Val Thr Thr Ile Cys Thr Asp Lys Thr Gly Thr Leu	
330 335 340	
acc cgc aat gag atg aca gtc cgc gca atc gcc acc ggt acg agt ctt	1171
Thr Arg Asn Glu Met Thr Val Arg Ala Ile Ala Thr Gly Thr Ser Leu	
345 350 355	

tat gac gtc agt gga gca ggc tac gaa cct ctc ggg gaa atc cgc tta	1219
Tyr Asp Val Ser Gly Ala Gly Tyr Glu Pro Leu Gly Glu Ile Arg Leu	
360 365 370	
aaa gac ggc gag caa gta tcc aag cag gat ttc cca gat ctc tac gcc	1267
Lys Asp Gly Glu Gln Val Ser Lys Gln Asp Phe Pro Asp Leu Tyr Ala	
375 380 385	
atg gcg ttg gtc gca gcg aac gtc aac gac gcc gaa att tac caa gaa	1315
Met Ala Leu Val Ala Ala Asn Val Asn Asp Ala Glu Ile Tyr Gln Glu	
390 395 400 405	
gac ggc atg tgg agg ctt tcc ggc gaa ccc acc gac ggc ggt att cgt	1363
Asp Gly Met Trp Arg Leu Ser Gly Glu Pro Thr Asp Gly Gly Ile Arg	
410 415 420	
gcc ttt gca atg aaa acc aac gct gaa atc ttg acc cga aca gcc gaa	1411
Ala Phe Ala Met Lys Thr Asn Ala Glu Ile Leu Thr Arg Thr Ala Glu	
425 430 435	
gtc ccc ttc gat tcc gca tac aaa tac atg gcg acg ctt cac acc atc	1459
Val Pro Phe Asp Ser Ala Tyr Lys Tyr Met Ala Thr Leu His Thr Ile	
440 445 450	
gat gga gca aac acc atg ctg gtc aag ggc gct ccc gat cgt tta ttg	1507
Asp Gly Ala Asn Thr Met Leu Val Lys Gly Ala Pro Asp Arg Leu Leu	
455 460 465	
gat aga agt gca cag cag cgc aac ggt gaa cca ctt gac cgg ccg tat	1555
Asp Arg Ser Ala Gln Arg Asn Gly Glu Pro Leu Asp Arg Pro Tyr	
470 475 480 485	
tgg gaa cag ctc atc gag gac ctc gcg tcc caa ggc ctc cgc gtg ctg	1603
Trp Glu Gln Leu Ile Glu Asp Leu Ala Ser Gln Gly Leu Arg Val Leu	
490 495 500	
gct gcg gca tat aaa gag ctt ccc cac agc acg tca aca att act cca	1651
Ala Ala Ala Tyr Lys Glu Leu Pro His Ser Thr Ser Thr Ile Thr Pro	
505 510 515	
gaa gat gtt gac cag ggc gaa ctc acc ttc ctc ggg ctc tac ggc atc	1699
Glu Asp Val Asp Gln Gly Glu Leu Thr Phe Leu Gly Leu Tyr Gly Ile	
520 525 530	
atg gat ccg cca cgc gaa gaa gtc atc gaa gcc atg aaa gtg gtg caa	1747
Met Asp Pro Pro Arg Glu Glu Val Ile Glu Ala Met Lys Val Val Gln	
535 540 545	
tcg gca ggc gtt cgc gtc cgc atg atc acc ggc gat cac tcc tcc acg	1795
Ser Ala Gly Val Arg Val Arg Met Ile Thr Gly Asp His Ser Ser Thr	
550 555 560 565	
gcc cgc gca atc gcc cgc gaa gtg gga atc cgc ggc cag aac gtg ctc	1843
Ala Arg Ala Ile Ala Arg Glu Val Gly Ile Arg Gly Gln Asn Val Leu	
570 575 580	
acc ggt gcg gaa att act gcg gct act gat gag gag ctg cag gga ctc	1891
Thr Gly Ala Glu Ile Thr Ala Ala Thr Asp Glu Glu Leu Gln Gly Leu	
585 590 595	
gtc gat aat gct gat ctt ttt gtg cgc acc agc ccc gag cac aag ctg	1939

Val	Asp	Asn	Ala	Asp	Leu	Phe	Val	Arg	Thr	Ser	Pro	Glu	His	Lys	Leu	
		600					605					610				
cgc	gtc	gtg	cgc	gca	ctg	caa	gct	aac	ggc	gaa	gtc	gcg	tcc	atg	acc	1987
Arg	Val	Val	Arg	Ala	Leu	Gln	Ala	Asn	Gly	Glu	Val	Ala	Ser	Met	Thr	
	615					620					625					
ggc	gac	ggc	gtc	aac	gat	gcg	cca	gcg	cta	aaa	caa	gcc	gac	gtc	ggc	2035
Gly	Asp	Gly	Val	Asn	Asp	Ala	Pro	Ala	Leu	Lys	Gln	Ala	Asp	Val	Gly	
630					635					640					645	
gtc	gcc	atg	ggc	att	aag	ggc	acc	gaa	gcc	acc	aaa	gac	gcg	gcc	gac	2083
Val	Ala	Met	Gly	Ile	Lys	Gly	Thr	Glu	Ala	Thr	Lys	Asp	Ala	Ala	Asp	
				650						655					660	
atc	gtg	ctt	gcc	gac	gac	aat	ttc	gcc	aca	atc	gcc	ggc	gcc	gta	gaa	2131
Ile	Val	Leu	Ala	Asp	Asp	Asn	Phe	Ala	Thr	Ile	Ala	Gly	Ala	Val	Glu	
			665					670							675	
atg	ggt	cgc	acc	atc	tac	gac	aac	ctg	cgc	aaa	gcc	gtc	gtc	ttc	atg	2179
Met	Gly	Arg	Thr	Ile	Tyr	Asp	Asn	Leu	Arg	Lys	Ala	Val	Val	Phe	Met	
		680					685					690				
ctc	ccc	acc	aac	ggc	gcc	caa	ggc	ctc	gtc	att	ttc	atc	gcg	atg	ctg	2227
Leu	Pro	Thr	Asn	Gly	Ala	Gln	Gly	Leu	Val	Ile	Phe	Ile	Ala	Met	Leu	
	695					700					705					
ctc	ggc	tgg	gaa	ctg	ccc	atc	acc	gca	ctt	caa	gtg	ctg	tgg	atc	aac	2275
Leu	Gly	Trp	Glu	Leu	Pro	Ile	Thr	Ala	Leu	Gln	Val	Leu	Trp	Ile	Asn	
710						715				720					725	
ctc	atc	acc	gcc	atc	aca	ctg	tcc	ctg	gcg	ctg	tcc	ttc	gag	ccg	gcc	2323
Leu	Ile	Thr	Ala	Ile	Thr	Leu	Ser	Leu	Ala	Leu	Ser	Phe	Glu	Pro	Ala	
				730					735					740		
gag	ccc	ggc	atc	atg	aac	aga	aaa	ccc	aga	aac	ccc	aag	agc	ggg	ctt	2371
Glu	Pro	Gly	Ile	Met	Asn	Arg	Lys	Pro	Arg	Asn	Pro	Lys	Ser	Gly	Leu	
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Ile	Asp	Ala	Pro	Ser	Val	Leu	Arg	Ile	Val	Tyr	Val	Ser	Leu	Leu	Leu	
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Gly	Gly	Ala	Thr	Phe	Trp	Ala	Phe	Leu	Gly	Ala	Arg	Asp	Ala	Gly	Ile	
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Gln	Val	Phe	Tyr	Leu	Leu	Ser	Ser	Arg	Tyr	Phe	Glu	Val	Ser	Ala	Leu	
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cga	aaa	gaa	ctc	ttc	acc	acc	aac	ccg	att	tcc	tgg	ctg	tgc	atc	gca	2611
Arg	Lys	Glu	Leu	Phe	Thr	Thr	Asn	Pro	Ile	Ser	Trp	Leu	Cys	Ile	Ala	
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ctc	atg	ctg	atc	ctg	caa	ctg	gcc	ttt	gtc	tac	ctg	ccg	ttc	atg	caa	2659
Leu	Met	Leu	Ile	Leu	Gln	Leu	Ala	Phe	Val	Tyr	Leu	Pro	Phe	Met	Gln	

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 Ser Thr Phe Asp Thr Ala Ala Leu Thr Leu Arg Asp Trp Val Met Pro
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ctg gtg ttt ggt gtt gtt gtc ttt gcg gtc gtt gaa acc gag aaa ttc 2755
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Gln Val Asn Asp Pro Met Ile Tyr Val Leu Ile Ala Ala Ala Val Leu
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Thr Ala Phe Leu Gly His Trp Thr Asp Thr Ile Val Ile Gly Ala Val
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Val Ile Ile Asn Met Met Val Gly Phe Ile Gln Glu Gly Lys Ala Ala
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Asp Ala Leu Ala Ser Ile Arg Asn Met Leu Ser Pro Glu Ser Ala Ala
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Gly Asp Val Val Lys Leu Ser Ala Gly Asp Lys Val Pro Ala Asp Leu
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Arg Met Leu Ala Ala Thr Asn Leu His Ile Glu Glu Ser Ala Leu Thr
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Gly Glu Ala Glu Ala Val Val Lys Gly Thr Asp Pro Val Glu Ala Asp
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Ala Gly Ile Gly Asp Arg Thr Ser Met Ala Phe Ser Gly Thr Leu Val
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Leu Thr Gly Ser Gly Thr Gly Val Val Thr Ala Thr Gly Ala Gly Thr

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Val Cys Val Phe Leu Ala Ile Leu Met Leu Val Val Ala Gly Leu Val 260 265 270		
His His Thr Pro Leu Glu Glu Leu Ile Leu Ser Ala Ile Gly Phe Ala 275 280 285		
Val Ala Ala Ile Pro Glu Gly Leu Pro Ala Val Ile Ala Ile Thr Leu 290 295 300		
Ala Leu Gly Val Gln Lys Met Ala Ala Arg Asn Ala Ile Thr Arg Arg 305 310 315 320		
Leu Asn Ser Val Glu Thr Leu Gly Ser Val Thr Thr Ile Cys Thr Asp 325 330 335		
Lys Thr Gly Thr Leu Thr Arg Asn Glu Met Thr Val Arg Ala Ile Ala 340 345 350		
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Gly Glu Ile Arg Leu Lys Asp Gly Glu Gln Val Ser Lys Gln Asp Phe 370 375 380		
Pro Asp Leu Tyr Ala Met Ala Leu Val Ala Ala Asn Val Asn Asp Ala 385 390 395 400		
Glu Ile Tyr Gln Glu Asp Gly Met Trp Arg Leu Ser Gly Glu Pro Thr 405 410 415		
Asp Gly Gly Ile Arg Ala Phe Ala Met Lys Thr Asn Ala Glu Ile Leu 420 425 430		
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Leu Asp Arg Pro Tyr Trp Glu Gln Leu Ile Glu Asp Leu Ala Ser Gln 485 490 495		
Gly Leu Arg Val Leu Ala Ala Ala Tyr Lys Glu Leu Pro His Ser Thr 500 505 510		
Ser Thr Ile Thr Pro Glu Asp Val Asp Gln Gly Glu Leu Thr Phe Leu 515 520 525		
Gly Leu Tyr Gly Ile Met Asp Pro Pro Arg Glu Glu Val Ile Glu Ala 530 535 540		

Met Lys Val Val Gln Ser Ala Gly Val Arg Val Arg Met Ile Thr Gly
 545 550 555 560
 Asp His Ser Ser Thr Ala Arg Ala Ile Ala Arg Glu Val Gly Ile Arg
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 Gly Gln Asn Val Leu Thr Gly Ala Glu Ile Thr Ala Ala Thr Asp Glu
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 Glu Leu Gln Gly Leu Val Asp Asn Ala Asp Leu Phe Val Arg Thr Ser
 595 600 605
 Pro Glu His Lys Leu Arg Val Val Arg Ala Leu Gln Ala Asn Gly Glu
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 Ala Gly Ala Val Glu Met Gly Arg Thr Ile Tyr Asp Asn Leu Arg Lys
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 Phe Ile Ala Met Leu Leu Gly Trp Glu Leu Pro Ile Thr Ala Leu Gln
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 Val Leu Trp Ile Asn Leu Ile Thr Ala Ile Thr Leu Ser Leu Ala Leu
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 Ser Phe Glu Pro Ala Glu Pro Gly Ile Met Asn Arg Lys Pro Arg Asn
 740 745 750
 Pro Lys Ser Gly Leu Ile Asp Ala Pro Ser Val Leu Arg Ile Val Tyr
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 Val Ser Leu Leu Leu Gly Gly Ala Thr Phe Trp Ala Phe Leu Gly Ala
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 785 790 795 800
 Thr Leu Ala Val Ser Gln Val Phe Tyr Leu Leu Ser Ser Arg Tyr Phe
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 Glu Val Ser Ala Leu Arg Lys Glu Leu Phe Thr Thr Asn Pro Ile Ser
 820 825 830
 Trp Leu Cys Ile Ala Leu Met Leu Ile Leu Gln Leu Ala Phe Val Tyr
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Phe	Met	Ile	Ala	Ala	Ala	Ile	Val	Ala	Gly	Trp	Pro	Ile	Ala	Gln	Ser	20		
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His	Arg	Val	Glu	Asp	Ala	Gln	Asp	Asp	Lys	Ala	Arg	Thr	Gln	Thr	Phe	
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Ile	Val	Ala	Gly	Ile	Gly	Arg	Ala	Ala	Arg	Asp	Gly	Val	Leu	Ile	Lys	
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ggt	gga	gaa	tac	cta	gaa	acc	gcc	gcg	aaa	gtc	gac	gtc	gtt	gtc	gtg	931
Gly	Gly	Glu	Tyr	Leu	Glu	Thr	Ala	Ala	Lys	Val	Asp	Val	Val	Val	Val	
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Glu	Val	Ile	Glu	Pro	Ala	Tyr	Ser	Gln	Gly	Glu	Val	Leu	Glu	Leu	Ala	
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Ala	Arg	Ala	Glu	Thr	Ala	Ser	Glu	His	Pro	Leu	Ala	Asp	Ala	Ile	Ile	
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Arg	Gly	Ala	Gln	Asp	Arg	Gly	Leu	Ser	Thr	Thr	Leu	Val	Glu	Ala	Ala	
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Glu	Asn	Ile	Thr	Gly	Arg	Gly	Ile	Ile	Ala	Asn	Val	Asp	Gly	Gln	Ala	
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Val	Ala	Val	Gly	Ser	Ala	Glu	Leu	Leu	Asp	His	Glu	Pro	Asp	Ser	Thr	
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Arg	Ile	Leu	Glu	Leu	Asn	Ala	Glu	Gly	Lys	Thr	Ala	Met	Phe	Val	Gly	
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Ser Asp Ser Ala Ser Ala Ile Glu Ser Leu His Lys Ala Gly Ile Gln	410	415	420	
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Val Val Met Ala Thr Gly Asp Ala His Arg Val Ala Gln Asn Val Ala	425	430	435	
tcc aag ctg gga gtg gat gaa gtc tac tca gag cta ctc cct gaa cag				1459
Ser Lys Leu Gly Val Asp Glu Val Tyr Ser Glu Leu Leu Pro Glu Gln	440	445	450	
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Lys Leu Glu Leu Val Arg Asp Leu Gln Ala Ala Gly Lys Thr Val Ala	455	460	465	
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Met Val Gly Asp Gly Val Asn Asp Thr Pro Ala Leu Ala Ala Ala Asp	470	475	480	485
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Ile Gly Val Ala Met Gly Val Ala Gly Ser Pro Ala Ala Ile Glu Thr	490	495	500	
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Ala Asp Ile Ala Leu Met Ala Asp Arg Leu Pro Arg Leu Ala His Ala	505	510	515	
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Val Thr Leu Ala Lys Arg Thr Val Arg Thr Met Arg Ile Asn Ile Leu	520	525	530	
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Ile Ala Leu Ala Thr Val Met Val Leu Leu Ala Gly Val Leu Phe Gly	535	540	545	
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Gly Val Thr Met Ser Val Gly Met Leu Val His Glu Ala Ser Val Leu	550	555	560	565
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Leu Val Ile Ser Ile Ala Met Leu Leu Leu Arg Pro Thr Leu Lys Glu	570	575	580	
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 Ser Thr Glu Val Val Glu Leu Trp Glu Leu Glu Pro Gly Asp Ile Val
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 Ala Glu Lys Gly Gln Gly Ser Asp Val Tyr Ala Gly Thr Trp Leu Arg
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 Ser Gly Val Leu Arg Val Glu Ala Thr Gly Ile Gly Ser Asp Ser Thr
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 Leu Ala Lys Ile Ile His Arg Val Glu Asp Ala Gln Asp Asp Lys Ala
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 Arg Thr Gln Thr Phe Leu Glu Lys Phe Ser Lys Trp Tyr Thr Pro Gly
 195 200 205
 Val Met Ile Ala Ala Ala Val Val Gly Leu Ile Thr Trp Asp Val Glu
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 Ser Ile Pro Val Ser Ile Val Ala Gly Ile Gly Arg Ala Ala Arg Asp
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 Gly Val Leu Ile Lys Gly Gly Glu Tyr Leu Glu Thr Ala Ala Lys Val
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 Asp Val Val Val Val Asp Lys Thr Gly Thr Leu Thr Thr Gly Arg Pro
 275 280 285
 Glu Leu Thr Asp Val Glu Val Ile Glu Pro Ala Tyr Ser Gln Gly Glu
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 Val Leu Glu Leu Ala Ala Arg Ala Glu Thr Ala Ser Glu His Pro Leu
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 Ala Asp Ala Ile Ile Arg Gly Ala Gln Asp Arg Gly Leu Ser Thr Thr

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<223> FRXA00980

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 135 140 145

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 Ala Leu Ala Thr Val Met Val Leu Leu Ala Gly Val Leu Phe Gly Gly
 150 155 160 165

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 Val Thr Met Ser Val Gly Met Leu Val His Glu Ala Ser Val Leu Leu
 170 175 180

gtt atc agc atc gcc atg ctg ttg ctg cgt cca aca ctt aaa gaa gat 691
 Val Ile Ser Ile Ala Met Leu Leu Leu Arg Pro Thr Leu Lys Glu Asp
 185 190 195

gct gcg caa gca agt gat att aaa cgc tcg gaa ata caa cag atc gca 739
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<213> Corynebacterium glutamicum

<400> 400

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20 25 30

Ala Gly Ile Gln Val Val Met Ala Thr Gly Asp Ala His Arg Val Ala
35 40 45

Gln Asn Val Ala Ser Lys Leu Gly Val Asp Glu Val Tyr Ser Glu Leu
50 55 60

Leu Pro Glu Gln Lys Leu Glu Leu Val Arg Asp Leu Gln Ala Ala Gly
65 70 75 80

Lys Thr Val Ala Met Val Gly Asp Gly Val Asn Asp Thr Pro Ala Leu
85 90 95

Ala Ala Ala Asp Ile Gly Val Ala Met Gly Val Ala Gly Ser Pro Ala
100 105 110

Ala Ile Glu Thr Ala Asp Ile Ala Leu Met Ala Asp Arg Leu Pro Arg
115 120 125

Leu Ala His Ala Val Thr Leu Ala Lys Arg Thr Val Arg Thr Met Arg
130 135 140

Ile Asn Ile Leu Ile Ala Leu Ala Thr Val Met Val Leu Leu Ala Gly
145 150 155 160

Val Leu Phe Gly Gly Val Thr Met Ser Val Gly Met Leu Val His Glu
165 170 175

Ala Ser Val Leu Leu Val Ile Ser Ile Ala Met Leu Leu Leu Arg Pro
180 185 190

Thr Leu Lys Glu Asp Ala Ala Gln Ala Ser Asp Ile Lys Arg Ser Glu
195 200 205

Ile Gln Gln Ile Ala
210

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<211> 2007

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<222> (101)..(1984)

<223> RXN02348

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                                   Met Leu Asn Arg Met
                                   1 5

aaa agt gcg cgg cca aaa tca gtc gct cca aaa tcc gga caa gct tta 163
Lys Ser Ala Arg Pro Lys Ser Val Ala Pro Lys Ser Gly Gln Ala Leu
                                   10 15 20

ctc act ctc ggt gcc cta ggt gtt gtg ttc ggc gac atc ggc acc agc 211
Leu Thr Leu Gly Ala Leu Gly Val Val Phe Gly Asp Ile Gly Thr Ser
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ccc ctg tac tca ctt cac act gca ttc agc atg cag cac aac aaa gtc 259
Pro Leu Tyr Ser Leu His Thr Ala Phe Ser Met Gln His Asn Lys Val
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gaa gtc act cag gaa aat gtg tac ggc atc atc tcc atg gtg ttg tgg 307
Glu Val Thr Gln Glu Asn Val Tyr Gly Ile Ile Ser Met Val Leu Trp
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acc atc act ttg atc gtc acc gtc aaa tac gtc atg ctg gtc acc cga 355
Thr Ile Thr Leu Ile Val Thr Val Lys Tyr Val Met Leu Val Thr Arg
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gct gac aac caa gga caa ggt ggc atc ctg gcg ctc gtt gct ttg ctg 403
Ala Asp Asn Gln Gly Gln Gly Gly Ile Leu Ala Leu Val Ala Leu Leu
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aaa aac cgt ggg cac tgg gga aaa ttc gtg gca gta gcc ggc atg ttg 451
Lys Asn Arg Gly His Trp Gly Lys Phe Val Ala Val Ala Gly Met Leu
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ggc gcc gca ttg ttt tat ggc gat gtg gtg atc acc ccg gcg atc tct 499
Gly Ala Ala Leu Phe Tyr Gly Asp Val Val Ile Thr Pro Ala Ile Ser
                                   120 125 130

gtt ctc agc gca aca gaa ggc ttg acg gtt atc tcc cca agc ttt gag 547
Val Leu Ser Ala Thr Glu Gly Leu Thr Val Ile Ser Pro Ser Phe Glu
                                   135 140 145

cgc ttc att ctg ccc gta tct ctc gca gtt ctg atc gct att ttt gca 595
Arg Phe Ile Leu Pro Val Ser Leu Ala Val Leu Ile Ala Ile Phe Ala
                                   150 155 160 165

atc caa ccg ctc ggt aca gaa aaa gtc ggc aaa gcc ttc ggc ccc atc 643
Ile Gln Pro Leu Gly Thr Glu Lys Val Gly Lys Ala Phe Gly Pro Ile
                                   170 175 180

atg ttg ctg tgg ttt gtc acc ctt gca gga ttg gga att ccg caa atc 691
Met Leu Leu Trp Phe Val Thr Leu Ala Gly Leu Gly Ile Pro Gln Ile
                                   185 190 195

atc ggg cac cca gaa atc ttg cag agc ttg tct cca cat tgg gcc ctg 739
Ile Gly His Pro Glu Ile Leu Gln Ser Leu Ser Pro His Trp Ala Leu
                                   200 205 210

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cgc ttg att gtg gct gag cct ttc caa gca ttt gtg ctg ctt ggt gcc	787
Arg Leu Ile Val Ala Glu Pro Phe Gln Ala Phe Val Leu Leu Gly Ala	
215 220 225	
ggt gtc ctg aca gta acg ggt gcg gaa gcg ctc tac gct gat atg ggc	835
Val Val Leu Thr Val Thr Gly Ala Glu Ala Leu Tyr Ala Asp Met Gly	
230 235 240 245	
cat ttt ggg gcg agg cca atc aga gtg gcg tgg ttt tgc gtc gtc atg	883
His Phe Gly Ala Arg Pro Ile Arg Val Ala Trp Phe Cys Val Val Met	
250 255 260	
cct gct tta atc ttg acg tat ttg ggg cag ggc gcc ttg gtg atc aac	931
Pro Ala Leu Ile Leu Thr Tyr Leu Gly Gln Gly Ala Leu Val Ile Asn	
265 270 275	
cag cct gaa gcg gtg cgc aac ccc atg ttt tat ctc gcg ccg gaa ggt	979
Gln Pro Glu Ala Val Arg Asn Pro Met Phe Tyr Leu Ala Pro Glu Gly	
280 285 290	
ctg cgg att ccg ttg gtt att ttg gcg acc atc gct acg gtg atc gca	1027
Leu Arg Ile Pro Leu Val Ile Leu Ala Thr Ile Ala Thr Val Ile Ala	
295 300 305	
tcg cag gcc gtg att tct ggt gcg tat tca ttg acc aag cag gcc gtg	1075
Ser Gln Ala Val Ile Ser Gly Ala Tyr Ser Leu Thr Lys Gln Ala Val	
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Asn Leu Lys Leu Leu Pro Arg Met Val Ile Arg His Thr Ser Arg Lys	
330 335 340	
gag gaa ggc cag atc tat atg cca ctg gtt aat gga ttg ctg ttt gta	1171
Glu Glu Gly Gln Ile Tyr Met Pro Leu Val Asn Gly Leu Leu Phe Val	
345 350 355	
tcc gtg atg gtt gtg gtg ctg gta ttc cga tcc tct gaa agc ctc gcc	1219
Ser Val Met Val Val Val Leu Val Phe Arg Ser Ser Glu Ser Leu Ala	
360 365 370	
agc gcg tac gga ctt gca gtg acc gga acc ttg gtg ctg gtc agc gtc	1267
Ser Ala Tyr Gly Leu Ala Val Thr Gly Thr Leu Val Leu Val Ser Val	
375 380 385	
ctg tat ctg atc tat gtt cac acc aca tgg tgg aaa aca gcg ctg ttc	1315
Leu Tyr Leu Ile Tyr Val His Thr Thr Trp Trp Lys Thr Ala Leu Phe	
390 395 400 405	
att gtg ctc atc ggt att cca gaa gta ctt cta ttc gcc tcg aac acc	1363
Ile Val Leu Ile Gly Ile Pro Glu Val Leu Leu Phe Ala Ser Asn Thr	
410 415 420	
acg aaa att cac gac ggt ggc tgg ctt cca cta ctt att gcg gcc gtg	1411
Thr Lys Ile His Asp Gly Gly Trp Leu Pro Leu Leu Ile Ala Ala Val	
425 430 435	
ctc atc gtg gtg atg cgg acc tgg gag tgg gga agt gac cgc gtc aat	1459
Leu Ile Val Val Met Arg Thr Trp Glu Trp Gly Ser Asp Arg Val Asn	
440 445 450	
cag gaa cgc gca gag ctg gaa ctt ccc atg gat aag ttc ttg gag aaa	1507

Gln Glu Arg Ala Glu Leu Glu Leu Pro Met Asp Lys Phe Leu Glu Lys
 455 460 465

ctc gat cag cca cac aat att ggt ctg cgt aaa gtt gcc gaa gtg gca 1555
 Leu Asp Gln Pro His Asn Ile Gly Leu Arg Lys Val Ala Glu Val Ala
 470 475 480 485

gta ttt cca cat ggc acc agc gat act gtc ccg ttg tca ttg gtt cgc 1603
 Val Phe Pro His Gly Thr Ser Asp Thr Val Pro Leu Ser Leu Val Arg
 490 495 500

tgc gtg aaa gac ctc aag ctt tta tac cga gag atc gtg atc gtt cga 1651
 Cys Val Lys Asp Leu Lys Leu Leu Tyr Arg Glu Ile Val Ile Val Arg
 505 510 515

atc gtc caa gaa cac gtt ccg cac gtg cca cca gag gaa cgc gcg gaa 1699
 Ile Val Gln Glu His Val Pro His Val Pro Pro Glu Glu Arg Ala Glu
 520 525 530

atg gaa gtg ctc cat cac gcc ccg atc aga gtc gtg cga gtt gat ctg 1747
 Met Glu Val Leu His His Ala Pro Ile Arg Val Val Arg Val Asp Leu
 535 540 545

cac ctt ggt tat ttt gat gag cag aac ctg cct gag cat ctc cat gcc 1795
 His Leu Gly Tyr Phe Asp Glu Gln Asn Leu Pro Glu His Leu His Ala
 550 555 560 565

att gac cca aca tgg gat aac gcc acc tac ttc ctg tct gcc ctg act 1843
 Ile Asp Pro Thr Trp Asp Asn Ala Thr Tyr Phe Leu Ser Ala Leu Thr
 570 575 580

ctt cgg agc agg ttg cct gga aag att gct ggc tgg cgt gat cgt ttg 1891
 Leu Arg Ser Arg Leu Pro Gly Lys Ile Ala Gly Trp Arg Asp Arg Leu
 585 590 595

tat ctt tcg atg gaa cgt aat cag gca tct cga act gag tct ttc aaa 1939
 Tyr Leu Ser Met Glu Arg Asn Gln Ala Ser Arg Thr Glu Ser Phe Lys
 600 605 610

ttg caa cca agc aaa acc atc acg gtt gga aca gag ctg cac ctt 1984
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<211> 628

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<213> Corynebacterium glutamicum

<400> 402

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 20 25 30

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 35 40 45

Gln His Asn Lys Val Glu Val Thr Gln Glu Asn Val Tyr Gly Ile Ile
 50 55 60
 Ser Met Val Leu Trp Thr Ile Thr Leu Ile Val Thr Val Lys Tyr Val
 65 70 75 80
 Met Leu Val Thr Arg Ala Asp Asn Gln Gly Gln Gly Gly Ile Leu Ala
 85 90 95
 Leu Val Ala Leu Leu Lys Asn Arg Gly His Trp Gly Lys Phe Val Ala
 100 105 110
 Val Ala Gly Met Leu Gly Ala Ala Leu Phe Tyr Gly Asp Val Val Ile
 115 120 125
 Thr Pro Ala Ile Ser Val Leu Ser Ala Thr Glu Gly Leu Thr Val Ile
 130 135 140
 Ser Pro Ser Phe Glu Arg Phe Ile Leu Pro Val Ser Leu Ala Val Leu
 145 150 155 160
 Ile Ala Ile Phe Ala Ile Gln Pro Leu Gly Thr Glu Lys Val Gly Lys
 165 170 175
 Ala Phe Gly Pro Ile Met Leu Leu Trp Phe Val Thr Leu Ala Gly Leu
 180 185 190
 Gly Ile Pro Gln Ile Ile Gly His Pro Glu Ile Leu Gln Ser Leu Ser
 195 200 205
 Pro His Trp Ala Leu Arg Leu Ile Val Ala Glu Pro Phe Gln Ala Phe
 210 215 220
 Val Leu Leu Gly Ala Val Val Leu Thr Val Thr Gly Ala Glu Ala Leu
 225 230 235 240
 Tyr Ala Asp Met Gly His Phe Gly Ala Arg Pro Ile Arg Val Ala Trp
 245 250 255
 Phe Cys Val Val Met Pro Ala Leu Ile Leu Thr Tyr Leu Gly Gln Gly
 260 265 270
 Ala Leu Val Ile Asn Gln Pro Glu Ala Val Arg Asn Pro Met Phe Tyr
 275 280 285
 Leu Ala Pro Glu Gly Leu Arg Ile Pro Leu Val Ile Leu Ala Thr Ile
 290 295 300
 Ala Thr Val Ile Ala Ser Gln Ala Val Ile Ser Gly Ala Tyr Ser Leu
 305 310 315 320
 Thr Lys Gln Ala Val Asn Leu Lys Leu Leu Pro Arg Met Val Ile Arg
 325 330 335
 His Thr Ser Arg Lys Glu Glu Gly Gln Ile Tyr Met Pro Leu Val Asn
 340 345 350
 Gly Leu Leu Phe Val Ser Val Met Val Val Val Leu Val Phe Arg Ser
 355 360 365
 Ser Glu Ser Leu Ala Ser Ala Tyr Gly Leu Ala Val Thr Gly Thr Leu

370	375	380
Val Leu Val Ser Val Leu Tyr Leu Ile Tyr Val His Thr Thr Trp Trp 385 390 395 400		
Lys Thr Ala Leu Phe Ile Val Leu Ile Gly Ile Pro Glu Val Leu Leu 405 410 415		
Phe Ala Ser Asn Thr Thr Lys Ile His Asp Gly Gly Trp Leu Pro Leu 420 425 430		
Leu Ile Ala Ala Val Leu Ile Val Val Met Arg Thr Trp Glu Trp Gly 435 440 445		
Ser Asp Arg Val Asn Gln Glu Arg Ala Glu Leu Glu Leu Pro Met Asp 450 455 460		
Lys Phe Leu Glu Lys Leu Asp Gln Pro His Asn Ile Gly Leu Arg Lys 465 470 475 480		
Val Ala Glu Val Ala Val Phe Pro His Gly Thr Ser Asp Thr Val Pro 485 490 495		
Leu Ser Leu Val Arg Cys Val Lys Asp Leu Lys Leu Leu Tyr Arg Glu 500 505 510		
Ile Val Ile Val Arg Ile Val Gln Glu His Val Pro His Val Pro Pro 515 520 525		
Glu Glu Arg Ala Glu Met Glu Val Leu His His Ala Pro Ile Arg Val 530 535 540		
Val Arg Val Asp Leu His Leu Gly Tyr Phe Asp Glu Gln Asn Leu Pro 545 550 555 560		
Glu His Leu His Ala Ile Asp Pro Thr Trp Asp Asn Ala Thr Tyr Phe 565 570 575		
Leu Ser Ala Leu Thr Leu Arg Ser Arg Leu Pro Gly Lys Ile Ala Gly 580 585 590		
Trp Arg Asp Arg Leu Tyr Leu Ser Met Glu Arg Asn Gln Ala Ser Arg 595 600 605		
Thr Glu Ser Phe Lys Leu Gln Pro Ser Lys Thr Ile Thr Val Gly Thr 610 615 620		
Glu Leu His Leu 625		

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<211> 1157

<212> DNA

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<222> (1)..(1134)

<223> FRXA02348

<400> 403

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acg tat ttg ggg cag ggc gcc ttg gtg atc aac cag cct gaa gcg gtg	96
Thr Tyr Leu Gly Gln Gly Ala Leu Val Ile Asn Gln Pro Glu Ala Val	
20 25 30	
cgc aac ccc atg ttt tat ctc gcg ccg gaa ggt ctg cgg att ccg ttg	144
Arg Asn Pro Met Phe Tyr Leu Ala Pro Glu Gly Leu Arg Ile Pro Leu	
35 40 45	
gtt att ttg gcg acc atc gct acg gtg atc gca tgc cag gcc gtg att	192
Val Ile Leu Ala Thr Ile Ala Thr Val Ile Ala Ser Gln Ala Val Ile	
50 55 60	
tct ggt gcg tat tca ttg acc aag cag gcc gtg aat ttg aaa ctg ctg	240
Ser Gly Ala Tyr Ser Leu Thr Lys Gln Ala Val Asn Leu Lys Leu Leu	
65 70 75 80	
cca cgc atg gtg atc cgg cat acc tcc cgc aaa gag gaa ggc cag atc	288
Pro Arg Met Val Ile Arg His Thr Ser Arg Lys Glu Glu Gly Gln Ile	
85 90 95	
tat atg cca ctg gtt aat gga ttg ctg ttt gta tcc gtg atg gtt gtg	336
Tyr Met Pro Leu Val Asn Gly Leu Leu Phe Val Ser Val Met Val Val	
100 105 110	
gtg ctg gta ttc cga tcc tct gaa agc ctc gcc agc gcg tac gga ctt	384
Val Leu Val Phe Arg Ser Ser Glu Ser Leu Ala Ser Ala Tyr Gly Leu	
115 120 125	
gca gtg acc gga acc ttg gtg ctg gtc agc gtc ctg tat ctg atc tat	432
Ala Val Thr Gly Thr Leu Val Leu Val Ser Val Leu Tyr Leu Ile Tyr	
130 135 140	
gtt cac acc aca tgg tgg aaa aca gcg ctg ttc att gtg ctc atc ggt	480
Val His Thr Thr Trp Trp Lys Thr Ala Leu Phe Ile Val Leu Ile Gly	
145 150 155 160	
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Ile Pro Glu Val Leu Leu Phe Ala Ser Asn Thr Thr Lys Ile His Asp	
165 170 175	
ggt ggc tgg ctt cca cta ctt att gcg gcc gtg ctc atc gtg gtg atg	576
Gly Gly Trp Leu Pro Leu Leu Ile Ala Ala Val Leu Ile Val Val Met	
180 185 190	
cgg acc tgg gag tgg gga agt gac cgc gtc aat cag gaa cgc gca gag	624
Arg Thr Trp Glu Trp Gly Ser Asp Arg Val Asn Gln Glu Arg Ala Glu	
195 200 205	
ctg gaa ctt ccc atg gat aag ttc ttg gag aaa ctc gat cag cca cac	672
Leu Glu Leu Pro Met Asp Lys Phe Leu Glu Lys Leu Asp Gln Pro His	
210 215 220	
aat att ggt ctg cgt aaa gtt gcc gaa gtg gca gta ttt cca cat ggc	720
Asn Ile Gly Leu Arg Lys Val Ala Glu Val Ala Val Phe Pro His Gly	
225 230 235 240	

acc agc gat act gtc ccg ttg tca ttg gtt cgc tgc gtg aaa gac ctc 768
 Thr Ser Asp Thr Val Pro Leu Ser Leu Val Arg Cys Val Lys Asp Leu
 245 250 255

aag ctt tta tac cga gag atc gtg atc gtt cga atc gtc caa gaa cac 816
 Lys Leu Leu Tyr Arg Glu Ile Val Ile Val Arg Ile Val Gln Glu His
 260 265 270

gtt ccg cac gtg cca cca gag gaa cgc gcg gaa atg gaa gtg ctc cat 864
 Val Pro His Val Pro Pro Glu Glu Arg Ala Glu Met Glu Val Leu His
 275 280 285

cac gcc ccg atc aga gtc gtg cga gtt gat ctg cac ctt ggt tat ttt 912
 His Ala Pro Ile Arg Val Val Arg Val Asp Leu His Leu Gly Tyr Phe
 290 295 300

gat gag cag aac ctg cct gag cat ctc cat gcc att gac cca aca tgg 960
 Asp Glu Gln Asn Leu Pro Glu His Leu His Ala Ile Asp Pro Thr Trp
 305 310 315 320

gat aac gcc acc tac ttc ctg tct gcc ctg act ctt cgg agc agg ttg 1008
 Asp Asn Ala Thr Tyr Phe Leu Ser Ala Leu Thr Leu Arg Ser Arg Leu
 325 330 335

cct gga aag att gct ggc tgg cgt gat cgt ttg tat ctt tgc atg gaa 1056
 Pro Gly Lys Ile Ala Gly Trp Arg Asp Arg Leu Tyr Leu Ser Met Glu
 340 345 350

cgt aat cag gca tct cga act gag tct ttc aaa ttg caa cca agc aaa 1104
 Arg Asn Gln Ala Ser Arg Thr Glu Ser Phe Lys Leu Gln Pro Ser Lys
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acc atc acg gtt gga aca gag ctg cac ctt taatcaggca gttgctggcc 1154
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 370 375

aac 1157

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 35 40 45
 Val Ile Leu Ala Thr Ile Ala Thr Val Ile Ala Ser Gln Ala Val Ile
 50 55 60
 Ser Gly Ala Tyr Ser Leu Thr Lys Gln Ala Val Asn Leu Lys Leu Leu
 65 70 75 80
 Pro Arg Met Val Ile Arg His Thr Ser Arg Lys Glu Glu Gly Gln Ile

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<223> FRXA02344

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 Met Leu Asn Arg Met
 1 5

aaa agt gcg cgg cca aaa tca gtc gct cca aaa tcc gga caa gct tta 163
 Lys Ser Ala Arg Pro Lys Ser Val Ala Pro Lys Ser Gly Gln Ala Leu
 10 15 20

ctc act ctc ggt gcc cta ggt gtt gtg ttc ggc gac atc ggc acc agc 211
 Leu Thr Leu Gly Ala Leu Gly Val Val Phe Gly Asp Ile Gly Thr Ser
 25 30 35

ccc ctg tac tca ctt cac act gca ttc agc atg cag cac aac aaa gtc 259
 Pro Leu Tyr Ser Leu His Thr Ala Phe Ser Met Gln His Asn Lys Val
 40 45 50

gaa gtc act cag gaa aat gtg tac ggc atc atc tcc atg gtg ttg tgg 307
 Glu Val Thr Gln Glu Asn Val Tyr Gly Ile Ile Ser Met Val Leu Trp
 55 60 65

acc atc act ttg atc gtc acc gtc aaa tac gtc atg ctg gtc acc cga 355
 Thr Ile Thr Leu Ile Val Thr Val Lys Tyr Val Met Leu Val Thr Arg
 70 75 80 85

gct gac aac caa gga caa ggt ggc atc ctg gcg ctc gtt gct ttg ctg 403
 Ala Asp Asn Gln Gly Gln Gly Gly Ile Leu Ala Leu Val Ala Leu Leu
 90 95 100

aaa aac cgt ggg cac tgg gga aaa ttc gtg gca gta gcc ggc atg ttg 451
 Lys Asn Arg Gly His Trp Gly Lys Phe Val Ala Val Ala Gly Met Leu
 105 110 115

ggc gcc gca ttg ttt tat ggc gat gtg gtg atc acc ccg gcg atc tct 499
 Gly Ala Ala Leu Phe Tyr Gly Asp Val Val Ile Thr Pro Ala Ile Ser
 120 125 130

gtt ctc agc gca aca gaa ggc ttg acg gtt atc tcc cca agc ttt gag 547
 Val Leu Ser Ala Thr Glu Gly Leu Thr Val Ile Ser Pro Ser Phe Glu
 135 140 145

gcg ttc att ctg ccc gta tct ctc gca gtt ctg atc gct att ttt gca 595
 Arg Phe Ile Leu Pro Val Ser Leu Ala Val Leu Ile Ala Ile Phe Ala
 150 155 160 165

atc caa ccg ctc ggt aca gaa aaa gtc ggc aaa gcc ttc ggc ccc atc 643
 Ile Gln Pro Leu Gly Thr Glu Lys Val Gly Lys Ala Phe Gly Pro Ile
 170 175 180

atg ttg ctg tgg ttt gtc acc ctt gca gga ttg gga att ccg caa atc 691
 Met Leu Leu Trp Phe Val Thr Leu Ala Gly Leu Gly Ile Pro Gln Ile
 185 190 195

cgc ttg att gtg gct gag cct ttc caa gca ttt gtg ctg 778
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 <222> (1)..(1035)
 <223> RXN00960

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 Gly Leu Ile Ala Tyr Gly Ala Ser Gln Ala Leu Tyr Pro Trp Leu Leu
 20 25 30
 aaa gac cac caa agc gtc acc gaa atc gac ctt gat gca ggt gcc ctc 144
 Lys Asp His Gln Ser Val Thr Glu Ile Asp Leu Asp Ala Gly Ala Leu
 35 40 45
 cag ccc tac ttc aac atc gag atg cca cca cca ttt gaa gtg atg acc 192
 Gln Pro Tyr Phe Asn Ile Glu Met Pro Pro Pro Phe Glu Val Met Thr
 50 55 60
 gca ctg ctg ctg gca ttc tgc ctc ggc ctg ggc atg gct gta att aaa 240
 Ala Leu Leu Leu Ala Phe Cys Leu Gly Leu Gly Met Ala Val Ile Lys
 65 70 75 80
 tca gac acc ctg ttc aag gta acc cgc gaa ctc gag cgc gta gtc atg 288
 Ser Asp Thr Leu Phe Lys Val Thr Arg Glu Leu Glu Arg Val Val Met
 85 90 95
 aag acc atc acc gcc ttt gtc atc cca ctg ctg cca ctc ttc atc ttc 336
 Lys Thr Ile Thr Ala Phe Val Ile Pro Leu Leu Pro Leu Phe Ile Phe
 100 105 110
 ggc atc ttc ctc ggc atg ggc atg aac ggt ggc ctc ctg gag atc atg 384
 Gly Ile Phe Leu Gly Met Gly Met Asn Gly Gly Leu Leu Glu Ile Met
 115 120 125
 tcc gcc ttt ggc aag gta ctg att ctc gcc gtc gtg gga acc ctg ctc 432
 Ser Ala Phe Gly Lys Val Leu Ile Leu Ala Val Val Gly Thr Leu Leu
 130 135 140
 ttc cta gcc atc cag ttc att atc gct ggt gca gta tcc aag aag aac 480
 Phe Leu Ala Ile Gln Phe Ile Ile Ala Gly Ala Val Ser Lys Lys Asn
 145 150 155 160
 cca tgg aaa ctg ttc aaa aac atg ctc cct gca tac ttc act gca ctg 528
 Pro Trp Lys Leu Phe Lys Asn Met Leu Pro Ala Tyr Phe Thr Ala Leu
 165 170 175
 ggc act tcc tct tca gcg gca acc atc cca gtg acc tac cag cag acc 576
 Gly Thr Ser Ser Ser Ala Ala Thr Ile Pro Val Thr Tyr Gln Gln Thr
 180 185 190
 ctg aaa aac gat gtt gat gtc aac gtc gca ggc ttt gtt gtc cca ctg 624
 Leu Lys Asn Asp Val Asp Val Asn Val Ala Gly Phe Val Val Pro Leu

195	200	205	
tgc gcc acc atc cac cta gct gga tcg atg atg aag atc ggc ctc ttc			672
Cys Ala Thr Ile His Leu Ala Gly Ser Met Met Lys Ile Gly Leu Phe			
210	215	220	
acc ttc gct gtt gtc ttc atg tac gac atg gaa gta ggc gtc ggc ctc			720
Thr Phe Ala Val Val Phe Met Tyr Asp Met Glu Val Gly Val Gly Leu			
225	230	235	240
tcc atc gga ttc ctc ctc atg ctg ggc atc acc atg atc gcc gca cca			768
Ser Ile Gly Phe Leu Leu Met Leu Gly Ile Thr Met Ile Ala Ala Pro			
	245	250	255
ggc gtt ccc ggc gga gcc atc atg gca gca acc ggc atg ctg gcc tcc			816
Gly Val Pro Gly Gly Ala Ile Met Ala Ala Thr Gly Met Leu Ala Ser			
	260	265	270
atg ctc gga ttc aac acc gaa caa gtc gcc ctc atg atc gcc gct tac			864
Met Leu Gly Phe Asn Thr Glu Gln Val Ala Leu Met Ile Ala Ala Tyr			
	275	280	285
atc gcg att gac tcc ttc ggc acc gca gca aac gtc acc ggc gac ggc			912
Ile Ala Ile Asp Ser Phe Gly Thr Ala Ala Asn Val Thr Gly Asp Gly			
	290	295	300
gca atc gca gtc atc gtg aac aaa ttc gcc aag ggc cag ctg cac acc			960
Ala Ile Ala Val Ile Val Asn Lys Phe Ala Lys Gly Gln Leu His Thr			
305	310	315	320
act tcc cca gat gaa atc gaa gaa gac gac cgc gtt gcc ttc gac atc			1008
Thr Ser Pro Asp Glu Ile Glu Glu Asp Asp Arg Val Ala Phe Asp Ile			
	325	330	335
act cca tcg gat gtg gaa cat cac aag tagaaacccg cattttctgt agt			1058
Thr Pro Ser Asp Val Glu His His Lys			
	340	345	

<210> 408

<211> 345

<212> PRT

<213> Corynebacterium glutamicum

<400> 408

Met	Ala	Arg	His	Cys	Cys	Ser	Asn	Arg	Tyr	Ala	Ser	Thr	Val	Phe	Ser
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Gly	Leu	Ile	Ala	Tyr	Gly	Ala	Ser	Gln	Ala	Leu	Tyr	Pro	Trp	Leu	Leu
		20						25					30		

Lys	Asp	His	Gln	Ser	Val	Thr	Glu	Ile	Asp	Leu	Asp	Ala	Gly	Ala	Leu
		35					40					45			

Gln	Pro	Tyr	Phe	Asn	Ile	Glu	Met	Pro	Pro	Pro	Phe	Glu	Val	Met	Thr
	50					55					60				

Ala	Leu	Leu	Leu	Ala	Phe	Cys	Leu	Gly	Leu	Gly	Met	Ala	Val	Ile	Lys
65					70					75					80

Ser	Asp	Thr	Leu	Phe	Lys	Val	Thr	Arg	Glu	Leu	Glu	Arg	Val	Val	Met
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

85					90					95					
Lys	Thr	Ile	Thr	Ala	Phe	Val	Ile	Pro	Leu	Leu	Pro	Leu	Phe	Ile	Phe
			100					105					110		
Gly	Ile	Phe	Leu	Gly	Met	Gly	Met	Asn	Gly	Gly	Leu	Leu	Glu	Ile	Met
		115					120					125			
Ser	Ala	Phe	Gly	Lys	Val	Leu	Ile	Leu	Ala	Val	Val	Gly	Thr	Leu	Leu
	130					135					140				
Phe	Leu	Ala	Ile	Gln	Phe	Ile	Ile	Ala	Gly	Ala	Val	Ser	Lys	Lys	Asn
145				150					155						160
Pro	Trp	Lys	Leu	Phe	Lys	Asn	Met	Leu	Pro	Ala	Tyr	Phe	Thr	Ala	Leu
			165						170					175	
Gly	Thr	Ser	Ser	Ser	Ala	Ala	Thr	Ile	Pro	Val	Thr	Tyr	Gln	Gln	Thr
		180						185					190		
Leu	Lys	Asn	Asp	Val	Asp	Val	Asn	Val	Ala	Gly	Phe	Val	Val	Pro	Leu
	195						200					205			
Cys	Ala	Thr	Ile	His	Leu	Ala	Gly	Ser	Met	Met	Lys	Ile	Gly	Leu	Phe
	210					215					220				
Thr	Phe	Ala	Val	Val	Phe	Met	Tyr	Asp	Met	Glu	Val	Gly	Val	Gly	Leu
225					230					235					240
Ser	Ile	Gly	Phe	Leu	Leu	Met	Leu	Gly	Ile	Thr	Met	Ile	Ala	Ala	Pro
			245						250					255	
Gly	Val	Pro	Gly	Gly	Ala	Ile	Met	Ala	Ala	Thr	Gly	Met	Leu	Ala	Ser
			260					265					270		
Met	Leu	Gly	Phe	Asn	Thr	Glu	Gln	Val	Ala	Leu	Met	Ile	Ala	Ala	Tyr
	275						280					285			
Ile	Ala	Ile	Asp	Ser	Phe	Gly	Thr	Ala	Ala	Asn	Val	Thr	Gly	Asp	Gly
	290					295					300				
Ala	Ile	Ala	Val	Ile	Val	Asn	Lys	Phe	Ala	Lys	Gly	Gln	Leu	His	Thr
305					310					315					320
Thr	Ser	Pro	Asp	Glu	Ile	Glu	Glu	Asp	Asp	Arg	Val	Ala	Phe	Asp	Ile
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Thr	Pro	Ser	Asp	Val	Glu	His	His	Lys							
			340					345							

<210> 409

<211> 482

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(459)

<223> FRXA00960

<400> 409

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1				5					10					15		
tgc	gcc	acc	atc	cac	cta	gct	gga	tcg	atg	atg	aag	atc	ggc	ctc	ttc	96
Cys	Ala	Thr	Ile	His	Leu	Ala	Gly	Ser	Met	Met	Lys	Ile	Gly	Leu	Phe	
			20					25					30			
acc	ttc	gct	gtt	gtc	ttc	atg	tac	gac	atg	gaa	gta	ggc	gtc	ggc	ctc	144
Thr	Phe	Ala	Val	Val	Phe	Met	Tyr	Asp	Met	Glu	Val	Gly	Val	Gly	Leu	
		35					40					45				
tcc	atc	gga	ttc	ctc	ctc	atg	ctg	ggc	atc	acc	atg	atc	gcc	gca	cca	192
Ser	Ile	Gly	Phe	Leu	Leu	Met	Leu	Gly	Ile	Thr	Met	Ile	Ala	Ala	Pro	
	50					55					60					
ggc	gtt	ccc	ggc	gga	gcc	atc	atg	gca	gca	acc	ggc	atg	ctg	gcc	tcc	240
Gly	Val	Pro	Gly	Gly	Ala	Ile	Met	Ala	Ala	Thr	Gly	Met	Leu	Ala	Ser	
65					70				75					80		
atg	ctc	gga	ttc	aac	acc	gaa	caa	gtc	gcc	ctc	atg	atc	gcc	gct	tac	288
Met	Leu	Gly	Phe	Asn	Thr	Glu	Gln	Val	Ala	Leu	Met	Ile	Ala	Ala	Tyr	
				85				90					95			
atc	gcg	att	gac	tcc	ttc	ggc	acc	gca	gca	aac	gtc	acc	ggc	gac	ggc	336
Ile	Ala	Ile	Asp	Ser	Phe	Gly	Thr	Ala	Ala	Asn	Val	Thr	Gly	Asp	Gly	
			100					105					110			
gca	atc	gca	gtc	atc	gtg	aac	aaa	ttc	gcc	aag	ggc	cag	ctg	cac	acc	384
Ala	Ile	Ala	Val	Ile	Val	Asn	Lys	Phe	Ala	Lys	Gly	Gln	Leu	His	Thr	
		115				120						125				
act	tcc	cca	gat	gaa	atc	gaa	gaa	gac	gac	cgc	gtt	gcc	ttc	gac	atc	432
Thr	Ser	Pro	Asp	Glu	Ile	Glu	Glu	Asp	Asp	Arg	Val	Ala	Phe	Asp	Ile	
	130					135					140					
act	cca	tcg	gat	gtg	gaa	cat	cac	aag	tagaaa	cccg	catttt	ctgt				479
Thr	Pro	Ser	Asp	Val	Glu	His	His	Lys								
145					150											
agt																482

<210> 410

<211> 153

<212> PRT

<213> Corynebacterium glutamicum

<400> 410

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Cys	Ala	Thr	Ile	His	Leu	Ala	Gly	Ser	Met	Met	Lys	Ile	Gly	Leu	Phe	
			20					25					30			
Thr	Phe	Ala	Val	Val	Phe	Met	Tyr	Asp	Met	Glu	Val	Gly	Val	Gly	Leu	
		35					40					45				
Ser	Ile	Gly	Phe	Leu	Leu	Met	Leu	Gly	Ile	Thr	Met	Ile	Ala	Ala	Pro	
	50					55					60					

Gly Val Pro Gly Gly Ala Ile Met Ala Ala Thr Gly Met Leu Ala Ser
 65 70 75 80
 Met Leu Gly Phe Asn Thr Glu Gln Val Ala Leu Met Ile Ala Ala Tyr
 85 90 95
 Ile Ala Ile Asp Ser Phe Gly Thr Ala Ala Asn Val Thr Gly Asp Gly
 100 105 110
 Ala Ile Ala Val Ile Val Asn Lys Phe Ala Lys Gly Gln Leu His Thr
 115 120 125
 Thr Ser Pro Asp Glu Ile Glu Glu Asp Asp Arg Val Ala Phe Asp Ile
 130 135 140
 Thr Pro Ser Asp Val Glu His His Lys
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<210> 411

<211> 1509

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1486)

<223> RXA01070

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 Met Ala Asn Ala Thr
 1 5
 gca cag aag ggc cgt ttc ggc ctt ccc ggc tgg atg act ggc ttt ggt 163
 Ala Gln Lys Gly Arg Phe Gly Leu Pro Gly Trp Met Thr Gly Phe Gly
 10 15 20
 gcc cag gtt atc gcc ggc ctc att ctt ggt ctt att ctc ggc ctt gtc 211
 Ala Gln Val Ile Ala Gly Leu Ile Leu Gly Leu Ile Leu Gly Leu Val
 25 30 35
 gcc cga ggc atg gac agc ggc gct gca gac ggt gaa gca agc tgg ctt 259
 Ala Arg Gly Met Asp Ser Gly Ala Ala Asp Gly Glu Ala Ser Trp Leu
 40 45 50
 acc ggt ctt ctt agc ggc gtc ggt tct gct tat gtt tct cta ctt aaa 307
 Thr Gly Leu Leu Ser Gly Val Gly Ser Ala Tyr Val Ser Leu Leu Lys
 55 60 65
 gtt atg gtt cca cca ctg gtg ttc gct gca gtg gtt acc agt gtg gca 355
 Val Met Val Pro Pro Leu Val Phe Ala Ala Val Val Thr Ser Val Ala
 70 75 80 85
 aag ttg cgc gag gta gct aac gct gct cgc ctg gct gtt tcc acc ttg 403
 Lys Leu Arg Glu Val Ala Asn Ala Ala Arg Leu Ala Val Ser Thr Leu
 90 95 100

gtg tgg ttc gcc att act gca ttc ttc tct gtg ctc gcg ggt atc gcc	451
Val Trp Phe Ala Ile Thr Ala Phe Phe Ser Val Leu Ala Gly Ile Ala	
105 110 115	
gta gcg ctg att atg cag cct ggt gtt gga tcc act gtc gac gca tct	499
Val Ala Leu Ile Met Gln Pro Gly Val Gly Ser Thr Val Asp Ala Ser	
120 125 130	
aat gct gct gat cct tct cgc gtg ggc agc tgg ctg ggc ttt atc cag	547
Asn Ala Ala Asp Pro Ser Arg Val Gly Ser Trp Leu Gly Phe Ile Gln	
135 140 145	
tcc gtt att cca tca aac att ctg gga ctt tcc ggt tct tac agt gag	595
Ser Val Ile Pro Ser Asn Ile Leu Gly Leu Ser Gly Ser Tyr Ser Glu	
150 155 160 165	
aac tct ggt gtg aac ctg tcc ttc aac gtg ctg cag atc ctg gtt atc	643
Asn Ser Gly Val Asn Leu Ser Phe Asn Val Leu Gln Ile Leu Val Ile	
170 175 180	
tcc att gcg att ggt gtt gca gct ctg aag gct ggc aag tcc gcc gag	691
Ser Ile Ala Ile Gly Val Ala Ala Leu Lys Ala Gly Lys Ser Ala Glu	
185 190 195	
cct ttc ttg aag ttc acc gag tcc ttc ctc aag atc atc cag atc gtg	739
Pro Phe Leu Lys Phe Thr Glu Ser Phe Leu Lys Ile Ile Gln Ile Val	
200 205 210	
ttg tgg tgg att att cgc ctg gct cca att ggt tcc gct gcg ctg atc	787
Leu Trp Trp Ile Ile Arg Leu Ala Pro Ile Gly Ser Ala Ala Leu Ile	
215 220 225	
ggt aat gct gtt gct acc tac ggt tgg tct gca ctt gga tcc ctg ggc	835
Gly Asn Ala Val Ala Thr Tyr Gly Trp Ser Ala Leu Gly Ser Leu Gly	
230 235 240 245	
aag ttt gtt ctt gcg atc tac gtt ggt ctg gca atc gtc atg ttc gtt	883
Lys Phe Val Leu Ala Ile Tyr Val Gly Leu Ala Ile Val Met Phe Val	
250 255 260	
atc tac cca gtc gtg ctg aag ctc aat gga att cct gtt ctt gga ttc	931
Ile Tyr Pro Val Val Leu Lys Leu Asn Gly Ile Pro Val Leu Gly Phe	
265 270 275	
ttc aag cgc gtt tgg cct gtc aca agc ctt ggc ttt gtt acc cgt tcc	979
Phe Lys Arg Val Trp Pro Val Thr Ser Leu Gly Phe Val Thr Arg Ser	
280 285 290	
tcc atg ggc gtt atg cca gtt acc cag cgc gtt act gag cag tcc ttg	1027
Ser Met Gly Val Met Pro Val Thr Gln Arg Val Thr Glu Gln Ser Leu	
295 300 305	
ggt gtt cca tct gcg tac gct tcc ttt gct atc cca ctg ggt gcg acc	1075
Gly Val Pro Ser Ala Tyr Ala Ser Phe Ala Ile Pro Leu Gly Ala Thr	
310 315 320 325	
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Ser Lys Met Asp Gly Cys Ala Ala Val Tyr Pro Ala Val Ala Ala Ile	
330 335 340	
ttc gtg gca cag ttc tac ggc att gac ttg agc atc atg gat tac gta	1171

Phe Val Ala Gln Phe Tyr Gly Ile Asp Leu Ser Ile Met Asp Tyr Val
 345 350 355
 ctg atc atg atc gtc tct gtc ctg ggc tct gct gca act gca ggc acc 1219
 Leu Ile Met Ile Val Ser Val Leu Gly Ser Ala Ala Thr Ala Gly Thr
 360 365 370
 act ggc gca acc gtc atg ctg acc ctg acc cta tcc acc ttg ggt ctg 1267
 Thr Gly Ala Thr Val Met Leu Thr Leu Thr Leu Ser Thr Leu Gly Leu
 375 380 385
 cca ctt gct ggt gtt ggt ctg ctg ctg gct atc gag cca atc atc gac 1315
 Pro Leu Ala Gly Val Gly Leu Leu Leu Ala Ile Glu Pro Ile Ile Asp
 390 395 400 405
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 Met Gly Arg Thr Ala Thr Asn Val Thr Gly Gln Ala Leu Val Pro Ala
 410 415 420
 atc gtt gct aag cgc gag ggc att ctg gat cag gat gtg tgg gat gct 1411
 Ile Val Ala Lys Arg Glu Gly Ile Leu Asp Gln Asp Val Trp Asp Ala
 425 430 435
 gct gaaaag ggt ggc gct gct att gaa atg gca acc gtc tct gag aaa 1459
 Ala Glu Lys Gly Gly Ala Ala Ile Glu Met Ala Thr Val Ser Glu Lys
 440 445 450
 gaa act gag cct gca gag gtt cgc tcc taagctctct tgagtacctg aga 1509
 Glu Thr Glu Pro Ala Glu Val Arg Ser
 455 460
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 <212> PRT
 <213> *Corynebacterium glutamicum*
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 20 25 30
 Ile Leu Gly Leu Val Ala Arg Gly Met Asp Ser Gly Ala Ala Asp Gly
 35 40 45
 Glu Ala Ser Trp Leu Thr Gly Leu Leu Ser Gly Val Gly Ser Ala Tyr
 50 55 60
 Val Ser Leu Leu Lys Val Met Val Pro Pro Leu Val Phe Ala Ala Val
 65 70 75 80
 Val Thr Ser Val Ala Lys Leu Arg Glu Val Ala Asn Ala Ala Arg Leu
 85 90 95
 Ala Val Ser Thr Leu Val Trp Phe Ala Ile Thr Ala Phe Phe Ser Val
 100 105 110
 Leu Ala Gly Ile Ala Val Ala Leu Ile Met Gln Pro Gly Val Gly Ser
 115 120 125

Thr	Val	Asp	Ala	Ser	Asn	Ala	Ala	Asp	Pro	Ser	Arg	Val	Gly	Ser	Trp	130	135	140	
Leu	Gly	Phe	Ile	Gln	Ser	Val	Ile	Pro	Ser	Asn	Ile	Leu	Gly	Leu	Ser	145	150	155	160
Gly	Ser	Tyr	Ser	Glu	Asn	Ser	Gly	Val	Asn	Leu	Ser	Phe	Asn	Val	Leu	165	170	175	
Gln	Ile	Leu	Val	Ile	Ser	Ile	Ala	Ile	Gly	Val	Ala	Ala	Leu	Lys	Ala	180	185	190	
Gly	Lys	Ser	Ala	Glu	Pro	Phe	Leu	Lys	Phe	Thr	Glu	Ser	Phe	Leu	Lys	195	200	205	
Ile	Ile	Gln	Ile	Val	Leu	Trp	Trp	Ile	Ile	Arg	Leu	Ala	Pro	Ile	Gly	210	215	220	
Ser	Ala	Ala	Leu	Ile	Gly	Asn	Ala	Val	Ala	Thr	Tyr	Gly	Trp	Ser	Ala	225	230	235	240
Leu	Gly	Ser	Leu	Gly	Lys	Phe	Val	Leu	Ala	Ile	Tyr	Val	Gly	Leu	Ala	245	250	255	
Ile	Val	Met	Phe	Val	Ile	Tyr	Pro	Val	Val	Leu	Lys	Leu	Asn	Gly	Ile	260	265	270	
Pro	Val	Leu	Gly	Phe	Phe	Lys	Arg	Val	Trp	Pro	Val	Thr	Ser	Leu	Gly	275	280	285	
Phe	Val	Thr	Arg	Ser	Ser	Met	Gly	Val	Met	Pro	Val	Thr	Gln	Arg	Val	290	295	300	
Thr	Glu	Gln	Ser	Leu	Gly	Val	Pro	Ser	Ala	Tyr	Ala	Ser	Phe	Ala	Ile	305	310	315	320
Pro	Leu	Gly	Ala	Thr	Ser	Lys	Met	Asp	Gly	Cys	Ala	Ala	Val	Tyr	Pro	325	330	335	
Ala	Val	Ala	Ala	Ile	Phe	Val	Ala	Gln	Phe	Tyr	Gly	Ile	Asp	Leu	Ser	340	345	350	
Ile	Met	Asp	Tyr	Val	Leu	Ile	Met	Ile	Val	Ser	Val	Leu	Gly	Ser	Ala	355	360	365	
Ala	Thr	Ala	Gly	Thr	Thr	Gly	Ala	Thr	Val	Met	Leu	Thr	Leu	Thr	Leu	370	375	380	
Ser	Thr	Leu	Gly	Leu	Pro	Leu	Ala	Gly	Val	Gly	Leu	Leu	Leu	Ala	Ile	385	390	395	400
Glu	Pro	Ile	Ile	Asp	Met	Gly	Arg	Thr	Ala	Thr	Asn	Val	Thr	Gly	Gln	405	410	415	
Ala	Leu	Val	Pro	Ala	Ile	Val	Ala	Lys	Arg	Glu	Gly	Ile	Leu	Asp	Gln	420	425	430	
Asp	Val	Trp	Asp	Ala	Ala	Glu	Lys	Gly	Gly	Ala	Ala	Ile	Glu	Met	Ala	435	440	445	

Thr Val Ser Glu Lys Glu Thr Glu Pro Ala Glu Val Arg Ser
 450 455 460

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(405)
 <223> RXA02628

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 ctc gca gtt gcc gtg gtc atc ggt act gcc ttc acc gct atc gtg aca 96
 Leu Ala Val Ala Val Val Ile Gly Thr Ala Phe Thr Ala Ile Val Thr
 20 25 30
 gca ttc tcc gag agc atc atc aac cca ttg atc gct tcc atc ggc agc 144
 Ala Phe Ser Glu Ser Ile Ile Asn Pro Leu Ile Ala Ser Ile Gly Ser
 35 40 45
 aca gag gtt gaa ggc ctc ggc ttc cac atc cgc gcc ggc aat gcc gca 192
 Thr Glu Val Glu Gly Leu Gly Phe His Ile Arg Ala Gly Asn Ala Ala
 50 55 60
 aca ttc gtg gat ttt ggt gct gtc atc acc gca gcg atc aac ttc ctc 240
 Thr Phe Val Asp Phe Gly Ala Val Ile Thr Ala Ala Ile Asn Phe Leu
 65 70 75 80
 atc atc gca gca att gtc tac ttc gtt ctc gtt gct cca atg aac aag 288
 Ile Ile Ala Ala Ile Val Tyr Phe Val Leu Val Ala Pro Met Asn Lys
 85 90 95
 ctc agc gaa acc ctc gca aag cgc aag ggt gtt gaa gaa gac gag acc 336
 Leu Ser Glu Thr Leu Ala Lys Arg Lys Gly Val Glu Glu Asp Glu Thr
 100 105 110
 cca gct tcc atc gaa gca gaa ctc ctc acc gag atc cgc gat ctc ctg 384
 Pro Ala Ser Ile Glu Ala Glu Leu Leu Thr Glu Ile Arg Asp Leu Leu
 115 120 125
 cag gag caa aag cgc ctt cag tagttaaag gccctaaaag cac 428
 Gln Glu Gln Lys Arg Leu Gln
 130 135

<210> 414
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 1 5 10 15

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															atg atc tac cgc agg	115		
															Met Ile Tyr Arg Arg			
															1	5		
gtg gga aat tct ggg ctg aag ctt ccg gca att tcg ctt ggg ctg tgg															163			
Val Gly Asn Ser Gly Leu Lys Leu Pro Ala Ile Ser Leu Gly Leu Trp																		
															10	20		
cac aac ttc ggt gat gac aag ccg ctt tca acg cag cgc agc att att															211			
His Asn Phe Gly Asp Asp Lys Pro Leu Ser Thr Gln Arg Ser Ile Ile																		
															25	30	35	
cac cgc gcg ttt gat agg gga gtc act cac ttc gat ttg gct aat aac															259			
His Arg Ala Phe Asp Arg Gly Val Thr His Phe Asp Leu Ala Asn Asn																		
															40	45	50	
tat gga cct cca gca ggt tcc gca gag acc aac ttt ggc agg att ttg															307			
Tyr Gly Pro Pro Ala Gly Ser Ala Glu Thr Asn Phe Gly Arg Ile Leu																		
															55	60	65	
cgt gag gat ctc aaa agc cac cgc gat gag ttg atc att tct tcc aag															355			
Arg Glu Asp Leu Lys Ser His Arg Asp Glu Leu Ile Ile Ser Ser Lys																		
															70	75	80	85

gcg ggt tgg gat atg tgg cct gga cct tat ggt ttt ggt ggt tcc cga 403
 Ala Gly Trp Asp Met Trp Pro Gly Pro Tyr Gly Phe Gly Gly Ser Arg
 90 95 100

aag tat cta gtg agt tcc ctt gat cag tcc ctg act cgc ctc ggc ttg 451
 Lys Tyr Leu Val Ser Ser Leu Asp Gln Ser Leu Thr Arg Leu Gly Leu
 105 110 115

gat tac gtg gat att ttc tat cat cac cgc ccg gat cca gat act cct 499
 Asp Tyr Val Asp Ile Phe Tyr His His Arg Pro Asp Pro Asp Thr Pro
 120 125 130

ttg gaa gaa acc atg tac gca ttg cgt gac att gtt gcg tct gga aag 547
 Leu Glu Glu Thr Met Tyr Ala Leu Arg Asp Ile Val Ala Ser Gly Lys
 135 140 145

gct ctt tac gtg ggt att tct tcc tac ggt cca gag ctc aca gcg gag 595
 Ala Leu Tyr Val Gly Ile Ser Ser Tyr Gly Pro Glu Leu Thr Ala Glu
 150 155 160 165

gcg gct gag ttc atg gcg gag gag ggc tgc ccg ctt ctg att cat cag 643
 Ala Ala Glu Phe Met Ala Glu Glu Gly Cys Pro Leu Leu Ile His Gln
 170 175 180

cca agc tat tcc atc att aat cgt tgg gtg gag gaa ccg ggc gat gac 691
 Pro Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu Glu Pro Gly Asp Asp
 185 190 195

ggt gag aac ttg ttg cag tca gct gcc aac aat ggt ctt ggc gtc att 739
 Gly Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn Gly Leu Gly Val Ile
 200 205 210

gct ttc tca cca ctt gcg cag ggc ctg ctc acg gac aaa tat ctc gat 787
 Ala Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr Asp Lys Tyr Leu Asp
 215 220 225

gga att cca gag ggt tcc cgc gcc agc cag ggt aag tcc ctg tct gag 835
 Gly Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly Lys Ser Leu Ser Glu
 230 235 240 245

ggc atg ttg aac gtg aac aat att gat atg gtc cgc aag ctc aat gac 883
 Gly Met Leu Asn Val Asn Asn Ile Asp Met Val Arg Lys Leu Asn Asp
 250 255 260

atc gcc cag gaa cgc ggg cag tca ctt gcg cag atg gcg ctt gca tgg 931
 Ile Ala Gln Glu Arg Gly Gln Ser Leu Ala Gln Met Ala Leu Ala Trp
 265 270 275

gtg ctg cgc gag caa aga gag tac ggc gcc gga tta ccg tgaccagtgc 980
 Val Leu Arg Glu Gln Arg Glu Tyr Gly Ala Gly Leu Pro
 280 285 290

attgattggt gct 993

<210> 416

<211> 290

<212> PRT

<213> Corynebacterium glutamicum

<400> 416

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 20 25 30
 Gln Arg Ser Ile Ile His Arg Ala Phe Asp Arg Gly Val Thr His Phe
 35 40 45
 Asp Leu Ala Asn Asn Tyr Gly Pro Pro Ala Gly Ser Ala Glu Thr Asn
 50 55 60
 Phe Gly Arg Ile Leu Arg Glu Asp Leu Lys Ser His Arg Asp Glu Leu
 65 70 75 80
 Ile Ile Ser Ser Lys Ala Gly Trp Asp Met Trp Pro Gly Pro Tyr Gly
 85 90 95
 Phe Gly Gly Ser Arg Lys Tyr Leu Val Ser Ser Leu Asp Gln Ser Leu
 100 105 110
 Thr Arg Leu Gly Leu Asp Tyr Val Asp Ile Phe Tyr His His Arg Pro
 115 120 125
 Asp Pro Asp Thr Pro Leu Glu Glu Thr Met Tyr Ala Leu Arg Asp Ile
 130 135 140
 Val Ala Ser Gly Lys Ala Leu Tyr Val Gly Ile Ser Ser Tyr Gly Pro
 145 150 155 160
 Glu Leu Thr Ala Glu Ala Ala Glu Phe Met Ala Glu Glu Gly Cys Pro
 165 170 175
 Leu Leu Ile His Gln Pro Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu
 180 185 190
 Glu Pro Gly Asp Asp Gly Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn
 195 200 205
 Gly Leu Gly Val Ile Ala Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr
 210 215 220
 Asp Lys Tyr Leu Asp Gly Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly
 225 230 235 240
 Lys Ser Leu Ser Glu Gly Met Leu Asn Val Asn Asn Ile Asp Met Val
 245 250 255
 Arg Lys Leu Asn Asp Ile Ala Gln Glu Arg Gly Gln Ser Leu Ala Gln
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 Met Ala Leu Ala Trp Val Leu Arg Glu Gln Arg Glu Tyr Gly Ala Gly
 275 280 285
 Leu Pro
 290

<210> 417

<211> 1209

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1186)

<223> FRXA01395

<220>

<223> All occurrences of n = any nucleotide

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<223> All occurrences of Xaa = any amino acid

<400> 417

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                                         Met Ala Val Met Ala
                                         1 5

tat caa cca gca gac aat cgc tat gac gac atg atc tac cgc agg gtg 163
Tyr Gln Pro Ala Asp Asn Arg Tyr Asp Asp Met Ile Tyr Arg Arg Val
      10 15 20

gga aat tct ggg ctg aag ctt ccg gca att tcg ctt ggg ctg tgg cac 211
Gly Asn Ser Gly Leu Lys Leu Pro Ala Ile Ser Leu Gly Leu Trp His
      25 30 35

aac ttc ggt gat gac aag ccg ctt tca acg cag cgc agc att att cac 259
Asn Phe Gly Asp Asp Lys Pro Leu Ser Thr Gln Arg Ser Ile Ile His
      40 45 50

cgc gcg ttt gat agg gga gtc act cac ttc gat ttg gct aat aac tat 307
Arg Ala Phe Asp Arg Gly Val Thr His Phe Asp Leu Ala Asn Asn Tyr
      55 60 65

gga cct cca gca ggt tcc gca gag acc aac ttt ggc agg att ttg cgt 355
Gly Pro Pro Ala Gly Ser Ala Glu Thr Asn Phe Gly Arg Ile Leu Arg
      70 75 80 85

gag gat ctc aaa agc cac cgc gat gag ttg atc att tct tcc aag gcg 403
Glu Asp Leu Lys Ser His Arg Asp Glu Leu Ile Ile Ser Ser Lys Ala
      90 95 100

ggt tgg gat atg tgg cct gga cct tat ggt ttt ggt ggt tcc cga aag 451
Gly Trp Asp Met Trp Pro Gly Pro Tyr Gly Phe Gly Gly Ser Arg Lys
      105 110 115

tat cta gtg agt tcc ctt gat cag tcc ctg act cgc ctc ggc ttg gat 499
Tyr Leu Val Ser Ser Leu Asp Gln Ser Leu Thr Arg Leu Gly Leu Asp
      120 125 130

tac gtg gat att ttc tat cat cac cgc ccg gat cca gat act cct ttg 547
Tyr Val Asp Ile Phe Tyr His His Arg Pro Asp Pro Asp Thr Pro Leu
      135 140 145

gaa gaa acc atg tac gca ttg cgt gac att gtt gcg tct gga aag gct 595
Glu Glu Thr Met Tyr Ala Leu Arg Asp Ile Val Ala Ser Gly Lys Ala
      150 155 160 165

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ctt tac gtg ggt att tct tcc tac ggt cca gag ctc aca gcg gag gcg 643
 Leu Tyr Val Gly Ile Ser Ser Tyr Gly Pro Glu Leu Thr Ala Glu Ala
 170 175 180

gct gag ttc atg gcg gag gag ggc tgc ccg ctt ctg att cat cag cca 691
 Ala Glu Phe Met Ala Glu Glu Gly Cys Pro Leu Leu Ile His Gln Pro
 185 190 195

agc tat tcc atc att aat cgt tgg gtg gag gaa ccg ggc gat gac ggt 739
 Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu Glu Pro Gly Asp Asp Gly
 200 205 210

gag aac ttg ttg cag tca gct gcc aac aat ggt ctt ggc gtc att gct 787
 Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn Gly Leu Gly Val Ile Ala
 215 220 225

ttc tca cca ctt gcg cag ggc ctg ctc acg gac aaa tat ctc gat gga 835
 Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr Asp Lys Tyr Leu Asp Gly
 230 235 240 245

att cca gag ggt tcc cgc gcc agc cag ggt aag tcc ctk tst kac ggs 883
 Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly Lys Ser Xaa Xaa Xaa Xaa
 250 255 260

wtg ttg aac gtg aac aat att gat wtg gtc ccm ars ytn awk rsa wtt 931
 Xaa Leu Asn Val Asn Asn Ile Asp Xaa Val Xaa Xaa Xaa Xaa Xaa Xaa
 265 270 275

tcc mar ram acc ggg cag tcc ttt nnc cna aag gnc ttt tgt tgg gtt 979
 Ser Xaa Xaa Thr Gly Gln Ser Phe Xaa Xaa Lys Xaa Phe Cys Trp Val
 280 285 290

gtt gcc caa cca agg aaa gta cgg cgc cgg att acc gtg acc agt gca 1027
 Val Ala Gln Pro Arg Lys Val Arg Arg Arg Ile Thr Val Thr Ser Ala
 295 300 305

ttg att ggt gct tcg tca gtt gag cag ctg gac aac agc ctt gat tca 1075
 Leu Ile Gly Ala Ser Ser Val Glu Gln Leu Asp Asn Ser Leu Asp Ser
 310 315 320 325

ctc aac aac ttg gag ttt tct gac gcc gag ttg gag gcg atc gat gag 1123
 Leu Asn Asn Leu Glu Phe Ser Asp Ala Glu Leu Glu Ala Ile Asp Glu
 330 335 340

att tcc cac gac gcc ggc atc aac att tgg gcg aag gcc acc gat tcc 1171
 Ile Ser His Asp Ala Gly Ile Asn Ile Trp Ala Lys Ala Thr Asp Ser
 345 350 355

aaa acc cgc gaa aac taacccatca acatcagttt gat 1209
 Lys Thr Arg Glu Asn
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<210> 418

<211> 362

<212> PRT

<213> Corynebacterium glutamicum

<220>

<223> All occurrences of Xaa = any amino acid

<400> 418

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 20 25 30
 Leu Gly Leu Trp His Asn Phe Gly Asp Asp Lys Pro Leu Ser Thr Gln
 35 40 45
 Arg Ser Ile Ile His Arg Ala Phe Asp Arg Gly Val Thr His Phe Asp
 50 55 60
 Leu Ala Asn Asn Tyr Gly Pro Pro Ala Gly Ser Ala Glu Thr Asn Phe
 65 70 75 80
 Gly Arg Ile Leu Arg Glu Asp Leu Lys Ser His Arg Asp Glu Leu Ile
 85 90 95
 Ile Ser Ser Lys Ala Gly Trp Asp Met Trp Pro Gly Pro Tyr Gly Phe
 100 105 110
 Gly Gly Ser Arg Lys Tyr Leu Val Ser Ser Leu Asp Gln Ser Leu Thr
 115 120 125
 Arg Leu Gly Leu Asp Tyr Val Asp Ile Phe Tyr His His Arg Pro Asp
 130 135 140
 Pro Asp Thr Pro Leu Glu Glu Thr Met Tyr Ala Leu Arg Asp Ile Val
 145 150 155 160
 Ala Ser Gly Lys Ala Leu Tyr Val Gly Ile Ser Ser Tyr Gly Pro Glu
 165 170 175
 Leu Thr Ala Glu Ala Ala Glu Phe Met Ala Glu Glu Gly Cys Pro Leu
 180 185 190
 Leu Ile His Gln Pro Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu Glu
 195 200 205
 Pro Gly Asp Asp Gly Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn Gly
 210 215 220
 Leu Gly Val Ile Ala Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr Asp
 225 230 235 240
 Lys Tyr Leu Asp Gly Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly Lys
 245 250 255
 Ser Xaa Xaa Xaa Xaa Xaa Leu Asn Val Asn Asn Ile Asp Xaa Val Xaa
 260 265 270
 Xaa Xaa Xaa Xaa Xaa Ser Xaa Xaa Thr Gly Gln Ser Phe Xaa Xaa Lys
 275 280 285
 Xaa Phe Cys Trp Val Val Ala Gln Pro Arg Lys Val Arg Arg Arg Ile
 290 295 300
 Thr Val Thr Ser Ala Leu Ile Gly Ala Ser Ser Val Glu Gln Leu Asp
 305 310 315 320

Asn Ser Leu Asp Ser Leu Asn Asn Leu Glu Phe Ser Asp Ala Glu Leu
 325 330 335

Glu Ala Ile Asp Glu Ile Ser His Asp Ala Gly Ile Asn Ile Trp Ala
 340 345 350

Lys Ala Thr Asp Ser Lys Thr Arg Glu Asn
 355 360

<210> 419

<211> 1911

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1888)

<223> RXA02597

<400> 419

ataccacactt tgcaagaatt acaaacgggg gcacccctcaa tgacttgaaa cactttatag 60

agtagaaagt gagtcacgac acttttttaaa ggaggatgct ttg ccc gaa caa gac 115
 Leu Pro Glu Gln Asp
 1 5

tta acc acc ttg gcc aat gat tgg ctc caa gct ttt gaa aag gcc act 163
 Leu Thr Thr Leu Ala Asn Asp Trp Leu Gln Ala Phe Glu Lys Ala Thr
 10 15 20

gct agt tcc agc cct gat gaa gct gcc act gca gtc gtg caa ctt ttt 211
 Ala Ser Ser Ser Pro Asp Glu Ala Ala Thr Ala Val Val Gln Leu Phe
 25 30 35

gag gat gaa gga tac tgg cga gac ctt ctt gca ttc acg tgg aac ctc 259
 Glu Asp Glu Gly Tyr Trp Arg Asp Leu Leu Ala Phe Thr Trp Asn Leu
 40 45 50

acc acc gct gaa ggt gca gat gaa atc gcc gag atg att cgc aat acg 307
 Thr Thr Ala Glu Gly Ala Asp Glu Ile Ala Glu Met Ile Arg Asn Thr
 55 60 65

tgg cca tca agc atc ttc cga aac gtt gag cta aag ggc gaa cca gct 355
 Trp Pro Ser Ser Ile Phe Arg Asn Val Glu Leu Lys Gly Glu Pro Ala
 70 75 80 85

gat gaa gga gat ggt gtc act cgc gta cat ttc tcc tgc gaa tcc gca 403
 Asp Glu Gly Asp Gly Val Thr Arg Val His Phe Ser Cys Glu Ser Ala
 90 95 100

gac ttc aag tgc acg ggc att gtc cgc ctt cgt aat ggc aag gcg tgg 451
 Asp Phe Lys Cys Thr Gly Ile Val Arg Leu Arg Asn Gly Lys Ala Trp
 105 110 115

acg cta ctc acc tca gct cgt gag ctc ctg gag cac cca gag ccc aag 499
 Thr Leu Leu Thr Ser Ala Arg Glu Leu Leu Glu His Pro Glu Pro Lys
 120 125 130

ggg cgc aac cgt gag atg ggc gtc gtc cat gga caa aat gag gac acc 547
 Gly Arg Asn Arg Glu Met Gly Val Val His Gly Gln Asn Glu Asp Thr

135	140	145	
cga aat tgg act gac cgc aag aat gat cga caa gca gcg ttg ggt gtc			595
Arg Asn Trp Thr Asp Arg Lys Asn Asp Arg Gln Ala Ala Leu Gly Val			
150	155	160	165
acc gag cag cca tac acc ctc atc atc ggt ggt gga cag ggt ggc att			643
Thr Glu Gln Pro Tyr Thr Leu Ile Ile Gly Gly Gly Gln Gly Gly Ile			
	170	175	180
gcc ttg ggc gca cga ctc aag cga ctt ggt gta ccc gct cta atc att			691
Ala Leu Gly Ala Arg Leu Lys Arg Leu Gly Val Pro Ala Leu Ile Ile			
	185	190	195
gat aaa gca tct cgc ccg ggc gac cag tgg cgt agc cgt tac cat tct			739
Asp Lys Ala Ser Arg Pro Gly Asp Gln Trp Arg Ser Arg Tyr His Ser			
	200	205	210
ctc tgc ctg cac gat cca gtt tgg tac gac cac ctg cct tac att cca			787
Leu Cys Leu His Asp Pro Val Trp Tyr Asp His Leu Pro Tyr Ile Pro			
	215	220	225
ttc cca gat cat tgg cca gta ttt act cca aag gac aag atg ggt gac			835
Phe Pro Asp His Trp Pro Val Phe Thr Pro Lys Asp Lys Met Gly Asp			
	230	235	240
tgg ctc gag cac tat gtc ggc atc atg gat ttg gac tat tgg acc aac			883
Trp Leu Glu His Tyr Val Gly Ile Met Asp Leu Asp Tyr Trp Thr Asn			
	250	255	260
acc gag tgc ctg cgc gcc tca tac aat gag gac acc aag cag tgg gat			931
Thr Glu Cys Leu Arg Ala Ser Tyr Asn Glu Asp Thr Lys Gln Trp Asp			
	265	270	275
gtg acg gtc aat cgt gat ggc gcg gag tcc acg ctc cac ccc acc caa			979
Val Thr Val Asn Arg Asp Gly Ala Glu Ser Thr Leu His Pro Thr Gln			
	280	285	290
cta gtc atg gct act gga atg tcg ggc agc ccg aac aaa cca act ttg			1027
Leu Val Met Ala Thr Gly Met Ser Gly Ser Pro Asn Lys Pro Thr Leu			
	295	300	305
cct ggc cag gat aag ttc cag ggt gaa att cgg cac tct tca gag cac			1075
Pro Gly Gln Asp Lys Phe Gln Gly Glu Ile Arg His Ser Ser Glu His			
	310	315	320
ccc ggc ggc gat gtc gat cgc gat aag aac gtt gta gtt ctg ggc gct			1123
Pro Gly Gly Asp Val Asp Arg Asp Lys Asn Val Val Val Leu Gly Ala			
	330	335	340
aac aac tca gcc cac gac atc tgc gcg gat ctt tat tcc aat ggt gca			1171
Asn Asn Ser Ala His Asp Ile Cys Ala Asp Leu Tyr Ser Asn Gly Ala			
	345	350	355
aag ccc gtg atg att cag cgc tcg tct aca cac atc gtg cgt tct gat			1219
Lys Pro Val Met Ile Gln Arg Ser Ser Thr His Ile Val Arg Ser Asp			
	360	365	370
tcg ctg atg cgc gaa gtc ttc ggg cct ctc tat tct gag gat gcc gtt			1267
Ser Leu Met Arg Glu Val Phe Gly Pro Leu Tyr Ser Glu Asp Ala Val			
	375	380	385

gaa gcc gga att gat acc gat act gcc gat ctc ctg ttt gcg tcg tgg 1315
 Glu Ala Gly Ile Asp Thr Asp Thr Ala Asp Leu Leu Phe Ala Ser Trp
 390 395 400 405

 cca tat aag gtg ctg cca ggt gtg cag aag cag gct ttc gac aag atc 1363
 Pro Tyr Lys Val Leu Pro Gly Val Gln Lys Gln Ala Phe Asp Lys Ile
 410 415 420

 cgt gag gac gac aag gag ttc tac gac aag ctt gaa aat gct gga ttc 1411
 Arg Glu Asp Asp Lys Glu Phe Tyr Asp Lys Leu Glu Asn Ala Gly Phe
 425 430 435

 ttg ctt gat ttc ggc gat gac gat tcg ggg ctt ttc tta aag tac ctt 1459
 Leu Leu Asp Phe Gly Asp Asp Ser Gly Leu Phe Leu Lys Tyr Leu
 440 445 450

 cgc cgt ggc tct ggc tac tac atc gat gtc ggc gcc tct gaa ctg gtg 1507
 Arg Arg Gly Ser Gly Tyr Tyr Ile Asp Val Gly Ala Ser Glu Leu Val
 455 460 465

 gct gat gga aag att ccg gtg cgc tcc aat gtc agc att gaa gac gtc 1555
 Ala Asp Gly Lys Ile Pro Val Arg Ser Asn Val Ser Ile Glu Asp Val
 470 475 480 485

 aag gaa aac tct gtg gtg ctc aca gat ggt act gag ctc cca gct gac 1603
 Lys Glu Asn Ser Val Val Leu Thr Asp Gly Thr Glu Leu Pro Ala Asp
 490 495 500

 gtg att gtt cta gcg acc ggc tat gga aac atg aac aac tgg gtt gct 1651
 Val Ile Val Leu Ala Thr Gly Tyr Gly Asn Met Asn Asn Trp Val Ala
 505 510 515

 cag ctg gtt gat cag gaa acc gct gac aag gtc ggc cca tgc tgg ggt 1699
 Gln Leu Val Asp Gln Glu Thr Ala Asp Lys Val Gly Pro Cys Trp Gly
 520 525 530

 ctg ggc tct gaa acc acc aag gat cca ggc cca tgg gaa ggc gag ttg 1747
 Leu Gly Ser Glu Thr Thr Lys Asp Pro Gly Pro Trp Glu Gly Glu Leu
 535 540 545

 cgc aat atg tgg aag ccc aca aac gtg gat tcg ctg tgg ttc cat ggt 1795
 Arg Asn Met Trp Lys Pro Thr Asn Val Asp Ser Leu Trp Phe His Gly
 550 555 560 565

 ggc aac ctt cac cag tca cgc cat tac tca cgg tat ttg tcc atg cag 1843
 Gly Asn Leu His Gln Ser Arg His Tyr Ser Arg Tyr Leu Ser Met Gln
 570 575 580

 ttg aag gcg cgc tac gaa ggt atg aac act ccg gtg tac agc aag 1888
 Leu Lys Ala Arg Tyr Glu Gly Met Asn Thr Pro Val Tyr Ser Lys
 585 590 595

 tagatacaaaa gaaaaggcca tct 1911

<210> 420

<211> 596

<212> PRT

<213> Corynebacterium glutamicum

<400> 420

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 20 25 30
 Val Val Gln Leu Phe Glu Asp Glu Gly Tyr Trp Arg Asp Leu Leu Ala
 35 40 45
 Phe Thr Trp Asn Leu Thr Thr Ala Glu Gly Ala Asp Glu Ile Ala Glu
 50 55 60
 Met Ile Arg Asn Thr Trp Pro Ser Ser Ile Phe Arg Asn Val Glu Leu
 65 70 75 80
 Lys Gly Glu Pro Ala Asp Glu Gly Asp Gly Val Thr Arg Val His Phe
 85 90 95
 Ser Cys Glu Ser Ala Asp Phe Lys Cys Thr Gly Ile Val Arg Leu Arg
 100 105 110
 Asn Gly Lys Ala Trp Thr Leu Leu Thr Ser Ala Arg Glu Leu Leu Glu
 115 120 125
 His Pro Glu Pro Lys Gly Arg Asn Arg Glu Met Gly Val Val His Gly
 130 135 140
 Gln Asn Glu Asp Thr Arg Asn Trp Thr Asp Arg Lys Asn Asp Arg Gln
 145 150 155 160
 Ala Ala Leu Gly Val Thr Glu Gln Pro Tyr Thr Leu Ile Ile Gly Gly
 165 170 175
 Gly Gln Gly Gly Ile Ala Leu Gly Ala Arg Leu Lys Arg Leu Gly Val
 180 185 190
 Pro Ala Leu Ile Ile Asp Lys Ala Ser Arg Pro Gly Asp Gln Trp Arg
 195 200 205
 Ser Arg Tyr His Ser Leu Cys Leu His Asp Pro Val Trp Tyr Asp His
 210 215 220
 Leu Pro Tyr Ile Pro Phe Pro Asp His Trp Pro Val Phe Thr Pro Lys
 225 230 235 240
 Asp Lys Met Gly Asp Trp Leu Glu His Tyr Val Gly Ile Met Asp Leu
 245 250 255
 Asp Tyr Trp Thr Asn Thr Glu Cys Leu Arg Ala Ser Tyr Asn Glu Asp
 260 265 270
 Thr Lys Gln Trp Asp Val Thr Val Asn Arg Asp Gly Ala Glu Ser Thr
 275 280 285
 Leu His Pro Thr Gln Leu Val Met Ala Thr Gly Met Ser Gly Ser Pro
 290 295 300
 Asn Lys Pro Thr Leu Pro Gly Gln Asp Lys Phe Gln Gly Glu Ile Arg
 305 310 315 320

His Ser Ser Glu His Pro Gly Gly Asp Val Asp Arg Asp Lys Asn Val
 325 330 335
 Val Val Leu Gly Ala Asn Asn Ser Ala His Asp Ile Cys Ala Asp Leu
 340 345 350
 Tyr Ser Asn Gly Ala Lys Pro Val Met Ile Gln Arg Ser Ser Thr His
 355 360 365
 Ile Val Arg Ser Asp Ser Leu Met Arg Glu Val Phe Gly Pro Leu Tyr
 370 375 380
 Ser Glu Asp Ala Val Glu Ala Gly Ile Asp Thr Asp Thr Ala Asp Leu
 385 390 395 400
 Leu Phe Ala Ser Trp Pro Tyr Lys Val Leu Pro Gly Val Gln Lys Gln
 405 410 415
 Ala Phe Asp Lys Ile Arg Glu Asp Asp Lys Glu Phe Tyr Asp Lys Leu
 420 425 430
 Glu Asn Ala Gly Phe Leu Leu Asp Phe Gly Asp Asp Asp Ser Gly Leu
 435 440 445
 Phe Leu Lys Tyr Leu Arg Arg Gly Ser Gly Tyr Tyr Ile Asp Val Gly
 450 455 460
 Ala Ser Glu Leu Val Ala Asp Gly Lys Ile Pro Val Arg Ser Asn Val
 465 470 475 480
 Ser Ile Glu Asp Val Lys Glu Asn Ser Val Val Leu Thr Asp Gly Thr
 485 490 495
 Glu Leu Pro Ala Asp Val Ile Val Leu Ala Thr Gly Tyr Gly Asn Met
 500 505 510
 Asn Asn Trp Val Ala Gln Leu Val Asp Gln Glu Thr Ala Asp Lys Val
 515 520 525
 Gly Pro Cys Trp Gly Leu Gly Ser Glu Thr Thr Lys Asp Pro Gly Pro
 530 535 540
 Trp Glu Gly Glu Leu Arg Asn Met Trp Lys Pro Thr Asn Val Asp Ser
 545 550 555 560
 Leu Trp Phe His Gly Gly Asn Leu His Gln Ser Arg His Tyr Ser Arg
 565 570 575
 Tyr Leu Ser Met Gln Leu Lys Ala Arg Tyr Glu Gly Met Asn Thr Pro
 580 585 590
 Val Tyr Ser Lys
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<210> 421

<211> 367

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS
 <222> (101)..(367)
 <223> RXA01454

<400> 421

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                                         Met Met Leu Ile Val
                                         1 5

gct ttc ctg atc gca ctc gtt ggc cat tac ctc atg ggt ggc att cgc 163
Ala Phe Leu Ile Ala Leu Val Gly His Tyr Leu Met Gly Gly Ile Arg
                10                15                20

gct gga aac cag atg acg ggc cag aag tcc ttt gta tcc cgt ggt gcg 211
Ala Gly Asn Gln Met Thr Gly Gln Lys Ser Phe Val Ser Arg Gly Ala
                25                30                35

cgc act cag ctt gcg gta act gct ggt ctg tgg atg ctt gtt aag gtc 259
Arg Thr Gln Leu Ala Val Thr Ala Gly Leu Trp Met Leu Val Lys Val
                40                45                50

gct ggc tac tgg ctg gat cgc tat gac ctg ctg act aag gaa aac tca 307
Ala Gly Tyr Trp Leu Asp Arg Tyr Asp Leu Leu Thr Lys Glu Asn Ser
                55                60                65

acc ttc aca ggt gca agc tac acc gac atc aat gca cag ctg cca gcg 355
Thr Phe Thr Gly Ala Ser Tyr Thr Asp Ile Asn Ala Gln Leu Pro Ala
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aag atc atc ctg 367
Lys Ile Ile Leu

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<210> 422
 <211> 89
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 422

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Met Gly Gly Ile Arg Ala Gly Asn Gln Met Thr Gly Gln Lys Ser Phe
  20 25 30

Val Ser Arg Gly Ala Arg Thr Gln Leu Ala Val Thr Ala Gly Leu Trp
  35 40 45

Met Leu Val Lys Val Ala Gly Tyr Trp Leu Asp Arg Tyr Asp Leu Leu
  50 55 60

Thr Lys Glu Asn Ser Thr Phe Thr Gly Ala Ser Tyr Thr Asp Ile Asn
  65 70 75 80

Ala Gln Leu Pro Ala Lys Ile Ile Leu
  85

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<210>	424
<211>	154
<212>	PRT

<213> Corynebacterium glutamicum

<400> 424

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 1              5              10              15

Met Ser Val Gly Phe Tyr Thr Asp Trp Leu Trp Phe Gly Glu Val Asp
      20              25              30

Phe Arg Gly Val Phe Ser Lys Val Ile Val Thr Arg Ile Val Leu Phe
      35              40              45

Val Ile Phe Ala Leu Ile Ala Gly Phe Val Thr Trp Leu Ala Gly Tyr
      50              55              60

Phe Val Thr Lys Leu Arg Pro Asp Glu Met Ser Ala Phe Asp Thr Gln
      65              70              75              80

Ser Pro Val Tyr Gln Tyr Arg Gln Met Ile Glu Asn Ser Leu Arg Arg
      85              90              95

Val Met Val Ile Ile Pro Ile Phe Val Ala Leu Leu Ala Gly Leu Ile
      100              105              110

Gly Gln Arg Ser Trp Arg Thr Val Gln Met Trp Leu Asn Gly Gln Asp
      115              120              125

Phe Gly Val Ser Asp Gln Gln Phe Gly Leu Asp Tyr Gly Phe Tyr Ala
      130              135              140

Phe Asp Leu Pro Met Leu Arg Leu Ile Ala
      145              150

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<210> 425

<211> 987

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(964)

<223> RXA02684

<400> 425

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                               Val Leu Ala Val Gly
                               1              5

ttg gtg ctt gtg ttt gtg gtg acg ctg tgg gcg gat tcg aag ctg aat 163
Leu Val Leu Val Phe Val Val Thr Leu Trp Ala Asp Ser Lys Leu Asn
      10              15              20

cgc gtg gat gcc acg cct gcg acg cag gtg gcg aac act gcc gga acg 211
Arg Val Asp Ala Thr Pro Ala Thr Gln Val Ala Asn Thr Ala Gly Thr
      25              30              35

aac tgg ctg ctg gta ggt tcg gat tcg cgg cag ggt tta agt gat gag 259
Asn Trp Leu Leu Val Gly Ser Asp Ser Arg Gln Gly Leu Ser Asp Glu

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40	45	50	
gat att gag cgg cta ggt acc ggc ggc gat atc ggt gtg ggc cgt acg Asp Ile Glu Arg Leu Gly Thr Gly Gly Asp Ile Gly Val Gly Arg Thr 55 60 65			307
gac acg atc atg gtg ttg cat atg ccg cgt act ggc gag ccg acg ctg Asp Thr Ile Met Val Leu His Met Pro Arg Thr Gly Glu Pro Thr Leu 70 75 80 85			355
ttg tcg att ccg cgt gat tct tat gtc aat gtc cct ggc tgg ggc atg Leu Ser Ile Pro Arg Asp Ser Tyr Val Asn Val Pro Gly Trp Gly Met 90 95 100			403
gat aag gca aac gcc gca ttt acc gtg ggt ggc ccg gaa ctg ctg acg Asp Lys Ala Asn Ala Ala Phe Thr Val Gly Gly Pro Glu Leu Leu Thr 105 110 115			451
caa acc gtg gag gag gca act ggc ctg cga att gat cac tat gca gaa Gln Thr Val Glu Glu Ala Thr Gly Leu Arg Ile Asp His Tyr Ala Glu 120 125 130			499
atc ggc atg ggt ggt ttg gcg aac atg gtt gat gcc gtg ggc ggc gtg Ile Gly Met Gly Gly Leu Ala Asn Met Val Asp Ala Val Gly Gly Val 135 140 145			547
gaa atg tgt cct gct gag ccg atg tat gat ccg ctc gcg aac ctg gat Glu Met Cys Pro Ala Glu Pro Met Tyr Asp Pro Leu Ala Asn Leu Asp 150 155 160 165			595
att cag gct ggt tgc cag gaa ttt gat ggg gca gcc gcg ctg ggt tat Ile Gln Ala Gly Cys Gln Glu Phe Asp Gly Ala Ala Ala Leu Gly Tyr 170 175 180			643
gtg cgc act cgt gcc aca gcc ctg ggt gat ctg gac ccg gtg gtg cgt Val Arg Thr Arg Ala Thr Ala Leu Gly Asp Leu Asp Arg Val Val Arg 185 190 195			691
cag ccg gaa ttc ttc tcc gct ctg ctg agt aca gct acg tcc ccg ggc Gln Arg Glu Phe Phe Ser Ala Leu Leu Ser Thr Ala Thr Ser Pro Gly 200 205 210			739
acg ttg ctg aat ccg ttc cgc acc ttc ccg atg atc tcc aac gcg gtg Thr Leu Leu Asn Pro Phe Arg Thr Phe Pro Met Ile Ser Asn Ala Val 215 220 225			787
gga aca ttc acc gtc ggc gag ggc gat cac gtg tgg cac ctg gcc cga Gly Thr Phe Thr Val Gly Glu Gly Asp His Val Trp His Leu Ala Arg 230 235 240 245			835
ttg gcg ctg gcg atg cgc gga gga atc gtg acg gag acc gtg ccg att Leu Ala Leu Ala Met Arg Gly Gly Ile Val Thr Glu Thr Val Pro Ile 250 255 260			883
gcc tca ttc gca gat tac gat gtg gga aat gtt gcg att tgg gac gaa Ala Ser Phe Ala Asp Tyr Asp Val Gly Asn Val Ala Ile Trp Asp Glu 265 270 275			931
gct gga gcc gaa gca cta ttt agc tcc atg cgc taaaacccca ggtaatcggt Ala Gly Ala Glu Ala Leu Phe Ser Ser Met Arg 280 285			984

cac

987

<210> 426

<211> 288

<212> PRT

<213> Corynebacterium glutamicum

<400> 426

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 20 25 30

Asn Thr Ala Gly Thr Asn Trp Leu Leu Val Gly Ser Asp Ser Arg Gln
 35 40 45

Gly Leu Ser Asp Glu Asp Ile Glu Arg Leu Gly Thr Gly Gly Asp Ile
 50 55 60

Gly Val Gly Arg Thr Asp Thr Ile Met Val Leu His Met Pro Arg Thr
 65 70 75 80

Gly Glu Pro Thr Leu Leu Ser Ile Pro Arg Asp Ser Tyr Val Asn Val
 85 90 95

Pro Gly Trp Gly Met Asp Lys Ala Asn Ala Ala Phe Thr Val Gly Gly
 100 105 110

Pro Glu Leu Leu Thr Gln Thr Val Glu Glu Ala Thr Gly Leu Arg Ile
 115 120 125

Asp His Tyr Ala Glu Ile Gly Met Gly Gly Leu Ala Asn Met Val Asp
 130 135 140

Ala Val Gly Gly Val Glu Met Cys Pro Ala Glu Pro Met Tyr Asp Pro
 145 150 155 160

Leu Ala Asn Leu Asp Ile Gln Ala Gly Cys Gln Glu Phe Asp Gly Ala
 165 170 175

Ala Ala Leu Gly Tyr Val Arg Thr Arg Ala Thr Ala Leu Gly Asp Leu
 180 185 190

Asp Arg Val Val Arg Gln Arg Glu Phe Phe Ser Ala Leu Leu Ser Thr
 195 200 205

Ala Thr Ser Pro Gly Thr Leu Leu Asn Pro Phe Arg Thr Phe Pro Met
 210 215 220

Ile Ser Asn Ala Val Gly Thr Phe Thr Val Gly Glu Gly Asp His Val
 225 230 235 240

Trp His Leu Ala Arg Leu Ala Leu Ala Met Arg Gly Gly Ile Val Thr
 245 250 255

Glu Thr Val Pro Ile Ala Ser Phe Ala Asp Tyr Asp Val Gly Asn Val
 260 265 270

Ala Ile Trp Asp Glu Ala Gly Ala Glu Ala Leu Phe Ser Ser Met Arg
 275 280 285

<210> 427

<211> 522

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(499)

<223> RXN02391

<400> 427

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 aggcggtaac gctgaacggc ggcgggtaag atatttgagc atg aca caa tca gat 115
 Met Thr Gln Ser Asp
 1 5
 tta ccc gat gat gtt cag gaa ttg gtc act aag atc ttt gga ctg gca 163
 Leu Pro Asp Asp Val Gln Glu Leu Val Thr Lys Ile Phe Gly Leu Ala
 10 15 20
 cgt gat ggg gga gca gaa tcc gca gca acc ctc ggt gca tat gtc gac 211
 Arg Asp Gly Gly Ala Glu Ser Ala Ala Thr Leu Gly Ala Tyr Val Asp
 25 30 35
 aac ggc gtt gac gtt aac ctg tcc aac caa gat ggc aac act ttg ctc 259
 Asn Gly Val Asp Val Asn Leu Ser Asn Gln Asp Gly Asn Thr Leu Leu
 40 45 50
 atg ctc gca gca tat gca gga cat gct gat gtc gtg cag gcg ttg att 307
 Met Leu Ala Ala Tyr Ala Gly His Ala Asp Val Val Gln Ala Leu Ile
 55 60 65
 gag cgt ggc gcc gat gtg gat cgc gtg aac aac cgc aat cag acg ccg 355
 Glu Arg Gly Ala Asp Val Asp Arg Val Asn Asn Arg Asn Gln Thr Pro
 70 75 80 85
 ctg gcg ggc gcg atc ttt aag aag gaa gaa gcc gtc att gag gca ctg 403
 Leu Ala Gly Ala Ile Phe Lys Lys Glu Glu Ala Val Ile Glu Ala Leu
 90 95 100
 ctt gct ggt ggt gct gac cca tac gct gga act cca act gct gtt gat 451
 Leu Ala Gly Gly Ala Asp Pro Tyr Ala Gly Thr Pro Thr Ala Val Asp
 105 110 115
 acc gcc aag atg ttt ggc cgc gag gat ctc gta gct cgc ttc gag tca 499
 Thr Ala Lys Met Phe Gly Arg Glu Asp Leu Val Ala Arg Phe Glu Ser
 120 125 130
 taggccggtg gagtggaccg ctt 522

<210> 428

<211> 133

<212> PRT

<213> Corynebacterium glutamicum

<400> 428

Met Thr Gln Ser Asp Leu Pro Asp Asp Val Gln Glu Leu Val Thr Lys
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Ile Phe Gly Leu Ala Arg Asp Gly Gly Ala Glu Ser Ala Ala Thr Leu
 20 25 30

Gly Ala Tyr Val Asp Asn Gly Val Asp Val Asn Leu Ser Asn Gln Asp
 35 40 45

Gly Asn Thr Leu Leu Met Leu Ala Ala Tyr Ala Gly His Ala Asp Val
 50 55 60

Val Gln Ala Leu Ile Glu Arg Gly Ala Asp Val Asp Arg Val Asn Asn
 65 70 75 80

Arg Asn Gln Thr Pro Leu Ala Gly Ala Ile Phe Lys Lys Glu Glu Ala
 85 90 95

Val Ile Glu Ala Leu Leu Ala Gly Gly Ala Asp Pro Tyr Ala Gly Thr
 100 105 110

Pro Thr Ala Val Asp Thr Ala Lys Met Phe Gly Arg Glu Asp Leu Val
 115 120 125

Ala Arg Phe Glu Ser
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<210> 429

<211> 2826

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2803)

<223> RXN02549

<400> 429

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gccgtaactg cagacgatgc cctgctcggt ggccctgagt atg gtt cac gcg aag 115
 Met Val His Ala Lys
 1 5

cag act aag aag cca ctt ccc cgt ttt ctt cac tcg gcg cat ttc tat 163
 Gln Thr Lys Lys Pro Leu Pro Arg Phe Leu His Ser Ala His Phe Tyr
 10 15 20

gtc tgg att gtg ctg ggt ttt gtg gtg ttt gcg caa cct tat ggt cag 211
 Val Trp Ile Val Leu Gly Phe Val Val Phe Ala Gln Pro Tyr Gly Gln
 25 30 35

gtt gct gcc gat act aaa cta gat ttg ctg ctc aac ccc gca gga ttt 259
 Val Ala Ala Asp Thr Lys Leu Asp Leu Leu Leu Asn Pro Ala Gly Phe
 40 45 50

tta acc ggt gcg ctt cat gcg tgg act gac acg ttc acc ttg ggt cag 307
 Leu Thr Gly Ala Leu His Ala Trp Thr Asp Thr Phe Thr Leu Gly Gln
 55 60 65

ttg	caa	aac	caa	gct	tat	ggc	tat	ctg	ttt	ccc	caa	ggg	ttt	ttc	ttc	355
Leu	Gln	Asn	Gln	Ala	Tyr	Gly	Tyr	Leu	Phe	Pro	Gln	Gly	Phe	Phe	Phe	
70					75					80					85	
ctc	ata	act	gat	ttc	ctc	cct	gac	tgg	att	gcg	cag	cga	ctg	tgg	tgg	403
Leu	Ile	Thr	Asp	Phe	Leu	Pro	Asp	Trp	Ile	Ala	Gln	Arg	Leu	Trp	Trp	
				90					95					100		
tgg	ctt	gtt	ctt	ggc	ctg	gga	ttt	tct	gga	ttc	tac	gca	ctg	gta	gcc	451
Trp	Leu	Val	Leu	Gly	Leu	Gly	Phe	Ser	Gly	Phe	Tyr	Ala	Leu	Val	Ala	
			105					110					115			
cgg	ctg	ggg	att	ggc	aat	cct	gca	ttc	agg	gtg	atc	gcc	gcg	ctg	ctg	499
Arg	Leu	Gly	Ile	Gly	Asn	Pro	Ala	Phe	Arg	Val	Ile	Ala	Ala	Leu	Leu	
			120				125					130				
ttt	gct	ctg	tcc	ccg	cgc	acg	ctc	acc	acc	ctc	act	gca	atc	tcc	tcc	547
Phe	Ala	Leu	Ser	Pro	Arg	Thr	Leu	Thr	Thr	Leu	Thr	Ala	Ile	Ser	Ser	
	135					140					145					
gaa	act	tgg	cct	atc	atg	ctc	gcg	cca	tgg	gta	tgt	ctg	cct	ctg	ctt	595
Glu	Thr	Trp	Pro	Ile	Met	Leu	Ala	Pro	Trp	Val	Cys	Leu	Pro	Leu	Leu	
150					155				160						165	
tcg	cga	aat	gtg	gat	gca	cgg	gcc	atc	gcg	ttg	tcc	tta	ctt	ccc	gcg	643
Ser	Arg	Asn	Val	Asp	Ala	Arg	Ala	Ile	Ala	Leu	Ser	Leu	Leu	Pro	Ala	
				170				175						180		
gca	tgc	atg	ggt	gca	gtt	aat	gcc	acc	gcc	acg	atg	gca	gca	ctc	atc	691
Ala	Cys	Met	Gly	Ala	Val	Asn	Ala	Thr	Ala	Thr	Met	Ala	Ala	Leu	Ile	
			185				190						195			
ccg	gca	gcg	ctg	atc	ttg	ctg	tat	aga	ggg	ctc	ttc	tta	agg	ctg	ctt	739
Pro	Ala	Ala	Leu	Ile	Leu	Leu	Tyr	Arg	Gly	Leu	Phe	Leu	Arg	Leu	Leu	
		200					205					210				
ctg	tgg	gga	atg	ggc	gtt	ctc	gct	gtt	aat	tca	tgg	tgg	atc	gga	cct	787
Leu	Trp	Gly	Met	Gly	Val	Leu	Ala	Val	Asn	Ser	Trp	Trp	Ile	Gly	Pro	
	215					220					225					
ttg	ttg	gtg	ctt	ggc	aaa	tac	gcc	ccg	ccc	ttc	acc	gaa	ttc	atc	gaa	835
Leu	Leu	Val	Leu	Gly	Lys	Tyr	Ala	Pro	Pro	Phe	Thr	Glu	Phe	Ile	Glu	
230					235					240					245	
agt	tcc	tcc	gtc	acc	act	tcc	tgg	ctc	aac	cca	gta	gaa	ata	ctc	cgc	883
Ser	Ser	Ser	Val	Thr	Thr	Ser	Trp	Leu	Asn	Pro	Val	Glu	Ile	Leu	Arg	
				250					255					260		
gga	acc	acc	agt	tgg	aca	ccc	ttc	gta	gac	act	gaa	cga	caa	gcc	gga	931
Gly	Thr	Thr	Ser	Trp	Thr	Pro	Phe	Val	Asp	Thr	Glu	Arg	Gln	Ala	Gly	
			265				270						275			
tat	ctc	ctg	gtc	aac	gat	gct	ctc	ttt	gtc	acc	ctc	agc	gtt	ctc	gtc	979
Tyr	Leu	Leu	Val	Asn	Asp	Ala	Leu	Phe	Val	Thr	Leu	Ser	Val	Leu	Val	
			280				285					290				
gca	gcc	ctc	ggc	ttg	atc	ggc	ctc	acc	ttg	atg	aaa	cac	cgt	gga	ctg	1027
Ala	Ala	Leu	Gly	Leu	Ile	Gly	Leu	Thr	Leu	Met	Lys	His	Arg	Gly	Leu	
	295					300					305					

tgg gca ttc atg ctg gcc atc gga ctc ctc atc ctc ggc agc gcc cac	1075
Trp Ala Phe Met Leu Ala Ile Gly Leu Leu Ile Leu Gly Ser Ala His	
310 315 320 325	
cta acg gct gtt caa gaa ttc ctc gac ggc cca ggc gca gca ctt cga	1123
Leu Thr Ala Val Gln Glu Phe Leu Asp Gly Pro Gly Ala Ala Leu Arg	
330 335 340	
aac atc cac aaa ttt gat cta tta gtc cgc atg ccg ttg atg gtg ggc	1171
Asn Ile His Lys Phe Asp Leu Leu Val Arg Met Pro Leu Met Val Gly	
345 350 355	
gtt gcc gca ttg ggg tcg cat atc agt ctg ccc ttg ctt ggg acg act	1219
Val Ala Ala Leu Gly Ser His Ile Ser Leu Pro Leu Leu Gly Thr Thr	
360 365 370	
gca ttg acc agc gga caa ggc aaa cac cac acc atc ccg ctg cct ctc	1267
Ala Leu Thr Ser Gly Gln Gly Lys His His Thr Ile Pro Leu Pro Leu	
375 380 385	
caa aaa cgc caa gcc gca gga ctc ctc gtg gtg atc atc gct gtc ggt	1315
Gln Lys Arg Gln Ala Ala Gly Leu Leu Val Val Ile Ile Ala Val Gly	
390 395 400 405	
gct ctt gct ccc gca tgg tcg gca cgg ctg cta cct cag gga acg tgg	1363
Ala Leu Ala Pro Ala Trp Ser Ala Arg Leu Leu Pro Gln Gly Thr Trp	
410 415 420	
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Asp Glu Val Pro Asp Tyr Trp Tyr Glu Ala Thr Glu Phe Leu Asn Gln	
425 430 435	
aac gcc aca ggc acc cgc acg ttg att tgg cct agc tcg ccg ttt gcc	1459
Asn Ala Thr Gly Thr Arg Thr Leu Ile Trp Pro Ser Ser Pro Phe Ala	
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cgc cag gac tgg gga tgg act cgg gat gaa cca gct caa cca ctt ctt	1507
Arg Gln Asp Trp Gly Trp Thr Arg Asp Glu Pro Ala Gln Pro Leu Leu	
455 460 465	
gat gtt ccg tgg gct gtc cgc gat gcc att cct ttg gtt ccc ccg gag	1555
Asp Val Pro Trp Ala Val Arg Asp Ala Ile Pro Leu Val Pro Pro Glu	
470 475 480 485	
gcg att cgc gga tta gat ggt ctc gac gac cta ggc act cta ggc acc	1603
Ala Ile Arg Gly Leu Asp Gly Leu Asp Asp Leu Gly Thr Leu Gly Thr	
490 495 500	
ggt cta aac gac gag gct tta aaa cgt cta ggc atc ggc gca gta ctg	1651
Gly Leu Asn Asp Glu Ala Leu Lys Arg Leu Gly Ile Gly Ala Val Leu	
505 510 515	
gtg agg cat gat ctg gaa gcc gac cca gat att gag gtg gat ctg cct	1699
Val Arg His Asp Leu Glu Ala Asp Pro Asp Ile Glu Val Asp Leu Pro	
520 525 530	
ggg gaa aag cac act ttt ggc tcc caa ggc caa gta gac gtc tac ctc	1747
Gly Glu Lys His Thr Phe Gly Ser Gln Gly Gln Val Asp Val Tyr Leu	
535 540 545	
acc gac ccc gac cgc aat atg tgg atc act tcc ggc aca tcc aag cag	1795

Thr Asp Pro Asp Arg Asn Met Trp Ile Thr Ser Gly Thr Ser Lys Gln 550 555 560 565	
ctg ccc acc gtc gct ggc ggc ggc gaa atc ctc tcg ctc cta gac acc Leu Pro Thr Val Ala Gly Gly Gly Glu Ile Leu Ser Leu Leu Asp Thr 570 575 580	1843
atc aac ggc tat tcc ccg agg act ttg gtg agt gag aat gcc cag atc Ile Asn Gly Tyr Ser Pro Arg Thr Leu Val Ser Glu Asn Ala Gln Ile 585 590 595	1891
gtc acc gat acc cct cag cta gtc ggc aca aat tac ggc gat ggc acc Val Thr Asp Thr Pro Gln Leu Val Gly Thr Asn Tyr Gly Asp Gly Thr 600 605 610	1939
agt tcc gca gca ttg gcc agc ctt gat gag act gag gtg aaa aac cgc Ser Ser Ala Ala Leu Ala Ser Leu Asp Glu Thr Glu Val Lys Asn Arg 615 620 625	1987
atc gtg gat tat cct tcc gcg ggg cca atg acg cag gtg gtg cag gaa Ile Val Asp Tyr Pro Ser Ala Gly Pro Met Thr Gln Val Val Gln Glu 630 635 640 645	2035
ggt tcc atc acg gcg tct tcg tct ggt tcc gat gcc act tct ttc ggc Gly Ser Ile Thr Ala Ser Ser Ser Gly Ser Asp Ala Thr Ser Phe Gly 650 655 660	2083
ggc gcg gat cct gat cgt tcc ctt aat tca ctt ctt gat cat cgt tac Gly Ala Asp Pro Asp Arg Ser Leu Asn Ser Leu Leu Asp His Arg Tyr 665 670 675	2131
aac acc gcc tgg tac ccg aca cct ggc gat acg tct ccg tgg ctc gaa Asn Thr Ala Trp Tyr Pro Thr Pro Gly Asp Thr Ser Pro Trp Leu Glu 680 685 690	2179
gtc tcc ggt acc ggc acc aca tta tcg atc tcc ccc cgc agc acc gtc Val Ser Gly Thr Gly Thr Thr Leu Ser Ile Ser Pro Arg Ser Thr Val 695 700 705	2227
acc gcc acc atc acc tcc ggc gat tcc gtg atg gtc cgc gag ttc gaa Thr Ala Thr Ile Thr Ser Gly Asp Ser Val Met Val Arg Glu Phe Glu 710 715 720 725	2275
aaa ggc cgc acc acc aca gtt acg ttg gcg gag cct gaa gct cgc att Lys Gly Arg Thr Thr Thr Val Thr Leu Ala Glu Pro Glu Ala Arg Ile 730 735 740	2323
gaa ttc gat ggt ttc gta gga att tcc gag ctg tcc cta gag ggt ctc Glu Phe Asp Gly Phe Val Gly Ile Ser Glu Leu Ser Leu Glu Gly Leu 745 750 755	2371
agc cgc acc atc act gtg ccg gag acc tct cct gac gtg cag caa ttc Ser Arg Thr Ile Thr Val Pro Glu Thr Ser Pro Asp Val Gln Gln Phe 760 765 770	2419
gtt ttc caa cgc ctc aca gtg ccc acc tcg ttc ctc gac cgc act ttc Val Phe Gln Arg Leu Thr Val Pro Thr Ser Phe Leu Asp Arg Thr Phe 775 780 785	2467
aca gtc ccc cgc cac atg tcc gtc acc gtg gag gcc caa tcc tgc gtc Thr Val Pro Arg His Met Ser Val Thr Val Glu Ala Gln Ser Cys Val	2515

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<210> 430
<211> 901
<212> PRT
<213> Corynebacterium glutamicum
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Gln Pro Tyr Gly Gln Val Ala Ala Asp Thr Lys Leu Asp Leu Leu Leu
      35              40              45

Asn Pro Ala Gly Phe Leu Thr Gly Ala Leu His Ala Trp Thr Asp Thr
      50              55              60

Phe Thr Leu Gly Gln Leu Gln Asn Gln Ala Tyr Gly Tyr Leu Phe Pro
      65              70              75              80

Gln Gly Phe Phe Phe Leu Ile Thr Asp Phe Leu Pro Asp Trp Ile Ala
      85              90              95

Gln Arg Leu Trp Trp Trp Leu Val Leu Gly Leu Gly Phe Ser Gly Phe
      100              105              110

Tyr Ala Leu Val Ala Arg Leu Gly Ile Gly Asn Pro Ala Phe Arg Val
      115              120              125

Ile Ala Ala Leu Leu Phe Ala Leu Ser Pro Arg Thr Leu Thr Thr Leu
      130              135              140

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Thr Ala Ile Ser Ser Glu Thr Trp Pro Ile Met Leu Ala Pro Trp Val
 145 150 155 160
 Cys Leu Pro Leu Leu Ser Arg Asn Val Asp Ala Arg Ala Ile Ala Leu
 165 170 175
 Ser Leu Leu Pro Ala Ala Cys Met Gly Ala Val Asn Ala Thr Ala Thr
 180 185 190
 Met Ala Ala Leu Ile Pro Ala Ala Leu Ile Leu Leu Tyr Arg Gly Leu
 195 200 205
 Phe Leu Arg Leu Leu Leu Trp Gly Met Gly Val Leu Ala Val Asn Ser
 210 215 220
 Trp Trp Ile Gly Pro Leu Leu Val Leu Gly Lys Tyr Ala Pro Pro Phe
 225 230 235 240
 Thr Glu Phe Ile Glu Ser Ser Ser Val Thr Thr Ser Trp Leu Asn Pro
 245 250 255
 Val Glu Ile Leu Arg Gly Thr Thr Ser Trp Thr Pro Phe Val Asp Thr
 260 265 270
 Glu Arg Gln Ala Gly Tyr Leu Leu Val Asn Asp Ala Leu Phe Val Thr
 275 280 285
 Leu Ser Val Leu Val Ala Ala Leu Gly Leu Ile Gly Leu Thr Leu Met
 290 295 300
 Lys His Arg Gly Leu Trp Ala Phe Met Leu Ala Ile Gly Leu Leu Ile
 305 310 315 320
 Leu Gly Ser Ala His Leu Thr Ala Val Gln Glu Phe Leu Asp Gly Pro
 325 330 335
 Gly Ala Ala Leu Arg Asn Ile His Lys Phe Asp Leu Leu Val Arg Met
 340 345 350
 Pro Leu Met Val Gly Val Ala Ala Leu Gly Ser His Ile Ser Leu Pro
 355 360 365
 Leu Leu Gly Thr Thr Ala Leu Thr Ser Gly Gln Gly Lys His His Thr
 370 375 380
 Ile Pro Leu Pro Leu Gln Lys Arg Gln Ala Ala Gly Leu Leu Val Val
 385 390 395 400
 Ile Ile Ala Val Gly Ala Leu Ala Pro Ala Trp Ser Ala Arg Leu Leu
 405 410 415
 Pro Gln Gly Thr Trp Asp Glu Val Pro Asp Tyr Trp Tyr Glu Ala Thr
 420 425 430
 Glu Phe Leu Asn Gln Asn Ala Thr Gly Thr Arg Thr Leu Ile Trp Pro
 435 440 445
 Ser Ser Pro Phe Ala Arg Gln Asp Trp Gly Trp Thr Arg Asp Glu Pro
 450 455 460

Ala Gln Pro Leu Leu Asp Val Pro Trp Ala Val Arg Asp Ala Ile Pro
 465 470 475 480
 Leu Val Pro Pro Glu Ala Ile Arg Gly Leu Asp Gly Leu Asp Asp Leu
 485 490 495
 Gly Thr Leu Gly Thr Gly Leu Asn Asp Glu Ala Leu Lys Arg Leu Gly
 500 505 510
 Ile Gly Ala Val Leu Val Arg His Asp Leu Glu Ala Asp Pro Asp Ile
 515 520 525
 Glu Val Asp Leu Pro Gly Glu Lys His Thr Phe Gly Ser Gln Gly Gln
 530 535 540
 Val Asp Val Tyr Leu Thr Asp Pro Asp Arg Asn Met Trp Ile Thr Ser
 545 550 555 560
 Gly Thr Ser Lys Gln Leu Pro Thr Val Ala Gly Gly Gly Glu Ile Leu
 565 570 575
 Ser Leu Leu Asp Thr Ile Asn Gly Tyr Ser Pro Arg Thr Leu Val Ser
 580 585 590
 Glu Asn Ala Gln Ile Val Thr Asp Thr Pro Gln Leu Val Gly Thr Asn
 595 600 605
 Tyr Gly Asp Gly Thr Ser Ser Ala Ala Leu Ala Ser Leu Asp Glu Thr
 610 615 620
 Glu Val Lys Asn Arg Ile Val Asp Tyr Pro Ser Ala Gly Pro Met Thr
 625 630 635 640
 Gln Val Val Gln Glu Gly Ser Ile Thr Ala Ser Ser Ser Gly Ser Asp
 645 650 655
 Ala Thr Ser Phe Gly Gly Ala Asp Pro Asp Arg Ser Leu Asn Ser Leu
 660 665 670
 Leu Asp His Arg Tyr Asn Thr Ala Trp Tyr Pro Thr Pro Gly Asp Thr
 675 680 685
 Ser Pro Trp Leu Glu Val Ser Gly Thr Gly Thr Thr Leu Ser Ile Ser
 690 695 700
 Pro Arg Ser Thr Val Thr Ala Thr Ile Thr Ser Gly Asp Ser Val Met
 705 710 715 720
 Val Arg Glu Phe Glu Lys Gly Arg Thr Thr Thr Val Thr Leu Ala Glu
 725 730 735
 Pro Glu Ala Arg Ile Glu Phe Asp Gly Phe Val Gly Ile Ser Glu Leu
 740 745 750
 Ser Leu Glu Gly Leu Ser Arg Thr Ile Thr Val Pro Glu Thr Ser Pro
 755 760 765
 Asp Val Gln Gln Phe Val Phe Gln Arg Leu Thr Val Pro Thr Ser Phe
 770 775 780
 Leu Asp Arg Thr Phe Thr Val Pro Arg His Met Ser Val Thr Val Glu

785	790	795	800
Ala Gln Ser Cys Val Thr Leu Glu Leu Asp Gly Asp Arg Ile Asp Cys	805	810	815
Gly Pro Ser Asn Ser Pro Pro Glu Pro Thr Arg Cys Ala Pro Asn Arg	820	825	830
Asn Gly Ser Pro Ser Pro Asn Pro Leu Arg Ser Pro Leu Phe Ser Gln	835	840	845
Gln Gln Thr Ser Arg Gln His Pro Pro Thr Ala Cys Ser Ser Pro Arg	850	855	860
Ala Leu Ser Ile Gln Val Pro Ala Arg Leu Ser Thr Pro Pro Pro Phe	865	870	875
Pro Gln Ser Asn Ser Thr Pro Pro Pro Lys Val Ser Ser Ser Pro Arg	885	890	895
Thr Pro Pro Ala Ser	900		

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 <223> RXN00808

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 Val Leu Gly Thr Asn
 1 5

gtg ttt ggt gcg ctc gca gta atg ctg ttt gtg cgc ttc ctc att ccg 163
 Val Phe Gly Ala Leu Ala Val Met Leu Phe Val Arg Phe Leu Ile Pro
 10 15 20

cag cca gat gct tca aat ttc aac gct gag atc tcg tat ctg cca gct 211
 Gln Pro Asp Ala Ser Asn Phe Asn Ala Glu Ile Ser Tyr Leu Pro Ala
 25 30 35

gtt ggt ttc gca tac ctg gcg ttc gcc att gtc gcg ggc atg ctg gtg 259
 Val Gly Phe Ala Tyr Leu Ala Phe Ala Ile Val Ala Gly Met Leu Val
 40 45 50

aca ttt ttg atg ttc cgc ccg gtg ctt gat tgg cag cga agc cct gaa 307
 Thr Phe Leu Met Phe Arg Pro Val Leu Asp Trp Gln Arg Ser Pro Glu
 55 60 65

gat cat gac cga aat atg gtg cgc aac ttg gtt atg cgc atc ccc atc 355
 Asp His Asp Arg Asn Met Val Arg Asn Leu Val Met Arg Ile Pro Ile
 70 75 80 85

tac cag gca att ctg tgc gca gtg gtg tgg tta atc ggc att gca att	403
Tyr Gln Ala Ile Leu Cys Ala Val Val Trp Leu Ile Gly Ile Ala Ile	
90 95 100	
gca acg ttg att tcg gcc agt gtg tct acc agt ttg gcg ctg gtc gtg	451
Ala Thr Leu Ile Ser Ala Ser Val Ser Thr Ser Leu Ala Leu Val Val	
105 110 115	
gcg ttt tcc acg ttg atg gct gcc gca atc gtc gtg ctg ctc acc tac	499
Ala Phe Ser Thr Leu Met Ala Ala Ile Val Val Leu Leu Thr Tyr	
120 125 130	
ctt gag gct gag cgt ttg gtg cgt ccg gtt gct gcg tct gcc ctg gcg	547
Leu Glu Ala Glu Arg Leu Val Arg Pro Val Ala Ala Ser Ala Leu Ala	
135 140 145	
cgt cga ttt gag gat tcc acg ctg gaa cca cct gtg agc cag cgc ttg	595
Arg Arg Phe Glu Asp Ser Thr Leu Glu Pro Pro Val Ser Gln Arg Leu	
150 155 160 165	
cgt atg acg tgg ttg ctg acg ttg ggc att cca gtg atg gga att ctg	643
Arg Met Thr Trp Leu Leu Thr Leu Gly Ile Pro Val Met Gly Ile Leu	
170 175 180	
ctg ctt att tgg ggc tac tcg cag ggc att ttc ggc tct gat gcc tcc	691
Leu Leu Ile Trp Gly Tyr Ser Gln Gly Ile Phe Gly Ser Asp Ala Ser	
185 190 195	
gga att atg cct gcc atc gca gcg ctc gcg ttt gca tcg ttg gtc acg	739
Gly Ile Met Pro Ala Ile Ala Ala Leu Ala Phe Ala Ser Leu Val Thr	
200 205 210	
ggt tac ctg ggc aac cgg ctt gtg gtg tcc tct gtg gtg gat ccg att	787
Gly Tyr Leu Gly Asn Arg Leu Val Val Ser Ser Val Val Asp Pro Ile	
215 220 225	
cgg gaa ctt cag gag gcc atc aac agg gtt cgt cgt ggt gaa aac gat	835
Arg Glu Leu Gln Glu Ala Ile Asn Arg Val Arg Arg Gly Glu Asn Asp	
230 235 240 245	
gtg cag gtt gat att tat gat ggc tct gag atc ggt gtg ctt cag gct	883
Val Gln Val Asp Ile Tyr Asp Gly Ser Glu Ile Gly Val Leu Gln Ala	
250 255 260	
ggc ttc aat gag atg atg cgt ggc ctg cgt gaa cgt cag cgc gtc cgt	931
Gly Phe Asn Glu Met Met Arg Gly Leu Arg Glu Arg Gln Arg Val Arg	
265 270 275	
gac ctt ttc ggt cgc tac gtg ggc gct gaa gtg gcc aag cgt gcg ctg	979
Asp Leu Phe Gly Arg Tyr Val Gly Ala Glu Val Ala Lys Arg Ala Leu	
280 285 290	
gag gaa cgc ccc act ctg ggt ggc gag gac cgt aag gtt gcc gtg ttg	1027
Glu Glu Arg Pro Thr Leu Gly Gly Glu Asp Arg Lys Val Ala Val Leu	
295 300 305	
ttt gtc gat gtc atc ggc tcc act acc ttt gcc gtc aac cac act cct	1075
Phe Val Asp Val Ile Gly Ser Thr Thr Phe Ala Val Asn His Thr Pro	
310 315 320 325	
gaa gag gtt gtg gag gcg ctc aat gag ttc ttc gag cac gtc gtg gag	1123

Glu Glu Val Val Glu Ala Leu Asn Glu Phe Phe Glu His Val Val Glu
 330 335 340
 gtt gtg cac cgc aac aag ggt gtt atc aac aag ttc cag ggt gac gcg 1171
 Val Val His Arg Asn Lys Gly Val Ile Asn Lys Phe Gln Gly Asp Ala
 345 350 355
 gcg ttg gcg att ttc ggc gct ccc ctg ccc ctg tct gat gcc acc ggt 1219
 Ala Leu Ala Ile Phe Gly Ala Pro Leu Pro Leu Ser Asp Ala Thr Gly
 360 365 370
 cat gcg ctt gcg gct gcc cgt gag ctc cgc gca gag ctg aaa gat ctc 1267
 His Ala Leu Ala Ala Ala Arg Glu Leu Arg Ala Glu Leu Lys Asp Leu
 375 380 385
 cag ctc aag gcc gga att ggt gtg gct gct ggc cat gtc gtt gct ggt 1315
 Gln Leu Lys Ala Gly Ile Gly Val Ala Ala Gly His Val Val Ala Gly
 390 395 400 405
 cat atc ggc ggt cac gcg agg ttt gag tac act gtg atc ggc gac gcg 1363
 His Ile Gly Gly His Ala Arg Phe Glu Tyr Thr Val Ile Gly Asp Ala
 410 415 420
 gtg aac cag gct gcg cgc ctg acg gag atc gcg aaa acg acc cca ggc 1411
 Val Asn Gln Ala Ala Arg Leu Thr Glu Ile Ala Lys Thr Thr Pro Gly
 425 430 435
 cgc acc gtc acc aac gct tcc acg ctg cgt gag gcc aac gag gcg gag 1459
 Arg Thr Val Thr Asn Ala Ser Thr Leu Arg Glu Ala Asn Glu Ala Glu
 440 445 450
 cag gct cgc tgg acg ctc atg aag tcc gtg gag ctg cgc gga cgt agc 1507
 Gln Ala Arg Trp Thr Leu Met Lys Ser Val Glu Leu Arg Gly Arg Ser
 455 460 465
 cag atg acg cag att gcg cgg cct att cgg ccg acg ttg gcg gat agg 1555
 Gln Met Thr Gln Ile Ala Arg Pro Ile Arg Pro Thr Leu Ala Asp Arg
 470 475 480 485
 tcc taatagcgtt ttgcagcga aaa 1581
 Ser

<210> 432

<211> 486

<212> PRT

<213> Corynebacterium glutamicum

<400> 432

Val Leu Gly Thr Asn Val Phe Gly Ala Leu Ala Val Met Leu Phe Val
 1 5 10 15
 Arg Phe Leu Ile Pro Gln Pro Asp Ala Ser Asn Phe Asn Ala Glu Ile
 20 25 30
 Ser Tyr Leu Pro Ala Val Gly Phe Ala Tyr Leu Ala Phe Ala Ile Val
 35 40 45
 Ala Gly Met Leu Val Thr Phe Leu Met Phe Arg Pro Val Leu Asp Trp
 50 55 60

Gln	Arg	Ser	Pro	Glu	Asp	His	Asp	Arg	Asn	Met	Val	Arg	Asn	Leu	Val	65	70	75	80
Met	Arg	Ile	Pro	Ile	Tyr	Gln	Ala	Ile	Leu	Cys	Ala	Val	Val	Trp	Leu	85	90		95
Ile	Gly	Ile	Ala	Ile	Ala	Thr	Leu	Ile	Ser	Ala	Ser	Val	Ser	Thr	Ser	100	105		110
Leu	Ala	Leu	Val	Val	Ala	Phe	Ser	Thr	Leu	Met	Ala	Ala	Ala	Ile	Val	115	120		125
Val	Leu	Leu	Thr	Tyr	Leu	Glu	Ala	Glu	Arg	Leu	Val	Arg	Pro	Val	Ala	130	135		140
Ala	Ser	Ala	Leu	Ala	Arg	Arg	Phe	Glu	Asp	Ser	Thr	Leu	Glu	Pro	Pro	145	150		155
Val	Ser	Gln	Arg	Leu	Arg	Met	Thr	Trp	Leu	Leu	Thr	Leu	Gly	Ile	Pro	165	170		175
Val	Met	Gly	Ile	Leu	Leu	Leu	Ile	Trp	Gly	Tyr	Ser	Gln	Gly	Ile	Phe	180	185		190
Gly	Ser	Asp	Ala	Ser	Gly	Ile	Met	Pro	Ala	Ile	Ala	Ala	Leu	Ala	Phe	195	200		205
Ala	Ser	Leu	Val	Thr	Gly	Tyr	Leu	Gly	Asn	Arg	Leu	Val	Val	Ser	Ser	210	215		220
Val	Val	Asp	Pro	Ile	Arg	Glu	Leu	Gln	Glu	Ala	Ile	Asn	Arg	Val	Arg	225	230		235
Arg	Gly	Glu	Asn	Asp	Val	Gln	Val	Asp	Ile	Tyr	Asp	Gly	Ser	Glu	Ile	245	250		255
Gly	Val	Leu	Gln	Ala	Gly	Phe	Asn	Glu	Met	Met	Arg	Gly	Leu	Arg	Glu	260	265		270
Arg	Gln	Arg	Val	Arg	Asp	Leu	Phe	Gly	Arg	Tyr	Val	Gly	Ala	Glu	Val	275	280		285
Ala	Lys	Arg	Ala	Leu	Glu	Glu	Arg	Pro	Thr	Leu	Gly	Gly	Glu	Asp	Arg	290	295		300
Lys	Val	Ala	Val	Leu	Phe	Val	Asp	Val	Ile	Gly	Ser	Thr	Thr	Phe	Ala	305	310		315
Val	Asn	His	Thr	Pro	Glu	Glu	Val	Val	Glu	Ala	Leu	Asn	Glu	Phe	Phe	325	330		335
Glu	His	Val	Val	Glu	Val	Val	His	Arg	Asn	Lys	Gly	Val	Ile	Asn	Lys	340	345		350
Phe	Gln	Gly	Asp	Ala	Ala	Leu	Ala	Ile	Phe	Gly	Ala	Pro	Leu	Pro	Leu	355	360		365
Ser	Asp	Ala	Thr	Gly	His	Ala	Leu	Ala	Ala	Ala	Arg	Glu	Leu	Arg	Ala	370	375		380

Glu Leu Lys Asp Leu Gln Leu Lys Ala Gly Ile Gly Val Ala Ala Gly
 385 390 395 400
 His Val Val Ala Gly His Ile Gly Gly His Ala Arg Phe Glu Tyr Thr
 405 410 415
 Val Ile Gly Asp Ala Val Asn Gln Ala Ala Arg Leu Thr Glu Ile Ala
 420 425 430
 Lys Thr Thr Pro Gly Arg Thr Val Thr Asn Ala Ser Thr Leu Arg Glu
 435 440 445
 Ala Asn Glu Ala Glu Gln Ala Arg Trp Thr Leu Met Lys Ser Val Glu
 450 455 460
 Leu Arg Gly Arg Ser Gln Met Thr Gln Ile Ala Arg Pro Ile Arg Pro
 465 470 475 480
 Thr Leu Ala Asp Arg Ser
 485

<210> 433
 <211> 1008
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(985)
 <223> RXS01425

<400> 433
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 Val Leu Ser Pro Asp
 1 5
 tcc gga att acc tgg gcc ttg tcg atc atg ttc ttg acc ttc acc gtg 163
 Ser Gly Ile Thr Trp Ala Leu Ser Ile Met Phe Leu Thr Phe Thr Val
 10 15 20
 cgt atg gtt ctg gtc aag ccg atg gtc aac acc atg cgt tca cag cgc 211
 Arg Met Val Leu Val Lys Pro Met Val Asn Thr Met Arg Ser Gln Arg
 25 30 35
 aag atg caa gac atg gct cca aag atg cag gcc atc cgc gag aag tac 259
 Lys Met Gln Asp Met Ala Pro Lys Met Gln Ala Ile Arg Glu Lys Tyr
 40 45 50
 aaa aat gac cag cag aag atg atg gag gag acc cgc aaa ctt caa aaa 307
 Lys Asn Asp Gln Gln Lys Met Met Glu Glu Thr Arg Lys Leu Gln Lys
 55 60 65
 gaa gtg ggc gtt aac ccc atc gca ggc tgt ttg cca atg ttg gtg cag 355
 Glu Val Gly Val Asn Pro Ile Ala Gly Cys Leu Pro Met Leu Val Gln
 70 75 80 85
 atc cca gtg ttc ctg ggt ctg ttc cac gtg ctg cgc tcc ttc aac cgc 403
 Ile Pro Val Phe Leu Gly Leu Phe His Val Leu Arg Ser Phe Asn Arg

90										95										100										
acc	ggt	tct	ggc	gtt	ggc	cag	ctg	gaa	atg	acc	gtt	gag	caa	aac	gcg	451														
Thr	Gly	Ser	Gly	Val	Gly	Gln	Leu	Glu	Met	Thr	Val	Glu	Gln	Asn	Ala															
			105					110					115																	
aac	acc	ccg	aac	tac	atc	ttc	ggt	gtc	gac	gag	gtt	cag	tcc	ttc	ctg	499														
Asn	Thr	Pro	Asn	Tyr	Ile	Phe	Gly	Val	Asp	Glu	Val	Gln	Ser	Phe	Leu															
		120					125					130																		
cgt	gca	gac	ctg	ttc	ggt	gcg	cca	ctg	tcg	tcc	tac	atc	acc	atg	cct	547														
Arg	Ala	Asp	Leu	Phe	Gly	Ala	Pro	Leu	Ser	Ser	Tyr	Ile	Thr	Met	Pro															
	135					140					145																			
gct	gac	gcg	ttc	gac	gcg	ttc	ctt	ggc	ctg	gat	gtc	tcc	cgc	ctc	aac	595														
Ala	Asp	Ala	Phe	Asp	Ala	Phe	Leu	Gly	Leu	Asp	Val	Ser	Arg	Leu	Asn															
150					155				160						165															
atc	gcg	ctg	gtt	gca	gct	cca	atg	att	ttg	atc	att	gtc	gtg	gca	act	643														
Ile	Ala	Leu	Val	Ala	Ala	Pro	Met	Ile	Leu	Ile	Ile	Val	Val	Ala	Thr															
				170				175							180															
cac	atg	aac	gcg	cgt	ctg	tcc	gtc	aac	cgc	cag	gaa	gct	cgc	aag	gca	691														
His	Met	Asn	Ala	Arg	Leu	Ser	Val	Asn	Arg	Gln	Glu	Ala	Arg	Lys	Ala															
		185						190					195																	
gcc	ggc	aag	cag	cag	gcc	gct	tcc	agc	gat	cag	atg	gcc	atg	cag	atg	739														
Ala	Gly	Lys	Gln	Gln	Ala	Ala	Ser	Ser	Asp	Gln	Met	Ala	Met	Gln	Met															
		200					205					210																		
caa	atg	atg	aac	aag	atg	atg	ctc	tgg	ttc	atg	cca	gcc	acc	att	ttg	787														
Gln	Met	Met	Asn	Lys	Met	Met	Leu	Trp	Phe	Met	Pro	Ala	Thr	Ile	Leu															
	215						220				225																			
ttc	acc	ggc	ttc	atc	tgg	acc	atc	ggt	ctt	ctt	gtc	tac	atg	atg	tcc	835														
Phe	Thr	Gly	Phe	Ile	Trp	Thr	Ile	Gly	Leu	Leu	Val	Tyr	Met	Met	Ser															
230					235				240						245															
aac	aac	gtg	tgg	acc	ttc	ttc	cag	cag	cgc	tac	atc	ttc	gcc	aag	atg	883														
Asn	Asn	Val	Trp	Thr	Phe	Phe	Gln	Gln	Arg	Tyr	Ile	Phe	Ala	Lys	Met															
			250						255					260																
gac	gct	gag	gaa	gca	gct	gag	gag	gag	gaa	aag	cgc	gca	gca	aag	cgc	931														
Asp	Ala	Glu	Glu	Ala	Ala	Glu	Glu	Glu	Glu	Lys	Arg	Ala	Ala	Lys	Arg															
			265				270						275																	
act	acc	gct	cca	aag	cct	ggc	gtg	aag	cca	gaa	aac	ccc	aag	aag	cgt	979														
Thr	Thr	Ala	Pro	Lys	Pro	Gly	Val	Lys	Pro	Glu	Asn	Pro	Lys	Lys	Arg															
		280					285					290																		
aag	aag	taaaacttca	ctaaaaaccg	cca												1008														
Lys	Lys																													
	295																													

<210> 434

<211> 295

<212> PRT

<213> Corynebacterium glutamicum

<400> 434

Val Leu Ser Pro Asp Ser Gly Ile Thr Trp Ala Leu Ser Ile Met Phe
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 Leu Thr Phe Thr Val Arg Met Val Leu Val Lys Pro Met Val Asn Thr
 20 25 30
 Met Arg Ser Gln Arg Lys Met Gln Asp Met Ala Pro Lys Met Gln Ala
 35 40 45
 Ile Arg Glu Lys Tyr Lys Asn Asp Gln Gln Lys Met Met Glu Glu Thr
 50 55 60
 Arg Lys Leu Gln Lys Glu Val Gly Val Asn Pro Ile Ala Gly Cys Leu
 65 70 75 80
 Pro Met Leu Val Gln Ile Pro Val Phe Leu Gly Leu Phe His Val Leu
 85 90 95
 Arg Ser Phe Asn Arg Thr Gly Ser Gly Val Gly Gln Leu Glu Met Thr
 100 105 110
 Val Glu Gln Asn Ala Asn Thr Pro Asn Tyr Ile Phe Gly Val Asp Glu
 115 120 125
 Val Gln Ser Phe Leu Arg Ala Asp Leu Phe Gly Ala Pro Leu Ser Ser
 130 135 140
 Tyr Ile Thr Met Pro Ala Asp Ala Phe Asp Ala Phe Leu Gly Leu Asp
 145 150 155 160
 Val Ser Arg Leu Asn Ile Ala Leu Val Ala Ala Pro Met Ile Leu Ile
 165 170 175
 Ile Val Val Ala Thr His Met Asn Ala Arg Leu Ser Val Asn Arg Gln
 180 185 190
 Glu Ala Arg Lys Ala Ala Gly Lys Gln Gln Ala Ala Ser Ser Asp Gln
 195 200 205
 Met Ala Met Gln Met Gln Met Met Asn Lys Met Met Leu Trp Phe Met
 210 215 220
 Pro Ala Thr Ile Leu Phe Thr Gly Phe Ile Trp Thr Ile Gly Leu Leu
 225 230 235 240
 Val Tyr Met Met Ser Asn Asn Val Trp Thr Phe Phe Gln Gln Arg Tyr
 245 250 255
 Ile Phe Ala Lys Met Asp Ala Glu Glu Ala Ala Glu Glu Glu Glu Lys
 260 265 270
 Arg Ala Ala Lys Arg Thr Thr Ala Pro Lys Pro Gly Val Lys Pro Glu
 275 280 285
 Asn Pro Lys Lys Arg Lys Lys
 290 295

<210> 435

<211> 1856

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1833)

<223> RXS01658

<400> 435

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Asp Pro Gln Ile Leu Ser Pro Thr Phe Thr Gln Gln Gln Gln Leu Arg	
1 5 10 15	
aac ttc tac ggt ttc cca gac cag ctg gcg atg gac cgc ttt gaa gta	96
Asn Phe Tyr Gly Phe Pro Asp Gln Leu Ala Met Asp Arg Phe Glu Val	
20 25 30	
gat ggc aaa ctc cgc gac ttt gtt gtg gca gca cgt gag ctc gat cca	144
Asp Gly Lys Leu Arg Asp Phe Val Val Ala Ala Arg Glu Leu Asp Pro	
35 40 45	
aac gcc ctg cag caa aac cag cag gac tgg att aac cgt cac act gtt	192
Asn Ala Leu Gln Gln Asn Gln Gln Asp Trp Ile Asn Arg His Thr Val	
50 55 60	
tat acc cac ggc aac ggc ttc att gca gct caa gca aac cag gtg gat	240
Tyr Thr His Gly Asn Gly Phe Ile Ala Ala Gln Ala Asn Gln Val Asp	
65 70 75 80	
gag gtc gcc cgc gac gtc gga tcc act cgt ggt ggt tac cct gtc tac	288
Glu Val Ala Arg Asp Val Gly Ser Thr Arg Gly Gly Tyr Pro Val Tyr	
85 90 95	
acc gtc tct gat ttg cag tcg aat gct cgt gct gca gaa agc gaa gat	336
Thr Val Ser Asp Leu Gln Ser Asn Ala Arg Ala Ala Glu Ser Glu Asp	
100 105 110	
gct gag gag ctt ggc atc aag gtt gat gag cct cgt gtg tac tac gga	384
Ala Glu Glu Leu Gly Ile Lys Val Asp Glu Pro Arg Val Tyr Tyr Gly	
115 120 125	
cca ctg att gct tct gcg act gat ggt gct gac tac gca att gtc ggt	432
Pro Leu Ile Ala Ser Ala Thr Asp Gly Ala Asp Tyr Ala Ile Val Gly	
130 135 140	
gac acc ggc gat ggc cca gtc gag tac gac act gac acc tcc agc tac	480
Asp Thr Gly Asp Gly Pro Val Glu Tyr Asp Thr Asp Thr Ser Ser Tyr	
145 150 155 160	
acc tac gaa ggt gct ggc ggc gtg gac att gga aac atg gtc aac cgt	528
Thr Tyr Glu Gly Ala Gly Gly Val Asp Ile Gly Asn Met Val Asn Arg	
165 170 175	
gcg atg ttt gca ttg cgc tac cag gaa atg aac atg ctc ctg tct gat	576
Ala Met Phe Ala Leu Arg Tyr Gln Glu Met Asn Met Leu Leu Ser Asp	
180 185 190	
cgt gtt ggt tcc gaa tcc aag atc cta ttt gag cgc gat cct cgt tcc	624
Arg Val Gly Ser Glu Ser Lys Ile Leu Phe Glu Arg Asp Pro Arg Ser	
195 200 205	
cgt gtg gaa aag gtt gca cct tgg ttg acc act gac tcc aag acc tac	672

Arg	Val	Glu	Lys	Val	Ala	Pro	Trp	Leu	Thr	Thr	Asp	Ser	Lys	Thr	Tyr	
210						215					220					
cca	act	gtg	att	gat	ggg	cgc	atc	aag	tgg	atc	gtc	gat	ggc	tac	acc	720
Pro	Thr	Val	Ile	Asp	Gly	Arg	Ile	Lys	Trp	Ile	Val	Asp	Gly	Tyr	Thr	
225					230					235					240	
acc	ttg	gat	agt	ctt	ccg	tac	tcc	acg	cgc	acc	tca	ctg	acg	gaa	gcg	768
Thr	Leu	Asp	Ser	Leu	Pro	Tyr	Ser	Thr	Arg	Thr	Ser	Leu	Thr	Glu	Ala	
				245					250					255		
act	cag	gat	got	gtc	atg	cct	gac	ggc	acc	cca	cag	cca	ctg	atc	aca	816
Thr	Gln	Asp	Ala	Val	Met	Pro	Asp	Gly	Thr	Pro	Gln	Pro	Leu	Ile	Thr	
			260					265					270			
gat	agg	gtc	ggg	tac	atc	cgc	aac	tcc	gtg	aag	gct	gtt	gtt	gat	gcg	864
Asp	Arg	Val	Gly	Tyr	Ile	Arg	Asn	Ser	Val	Lys	Ala	Val	Val	Asp	Ala	
	275						280					285				
tac	gac	gga	act	gtt	gaa	ctc	tac	gaa	ttc	gac	acc	gaa	gat	cct	gtt	912
Tyr	Asp	Gly	Thr	Val	Glu	Leu	Tyr	Glu	Phe	Asp	Thr	Glu	Asp	Pro	Val	
	290					295					300					
ctg	aag	gca	tgg	cgt	ggc	gtg	ttc	cca	gac	acc	gtg	aag	gac	ggg	tcg	960
Leu	Lys	Ala	Trp	Arg	Gly	Val	Phe	Pro	Asp	Thr	Val	Lys	Asp	Gly	Ser	
305					310					315					320	
gag	att	tcc	gat	gag	ctt	cgc	gca	cac	ctg	cgt	tac	cca	gaa	gat	ttg	1008
Glu	Ile	Ser	Asp	Glu	Leu	Arg	Ala	His	Leu	Arg	Tyr	Pro	Glu	Asp	Leu	
				325					330					335		
ttc	aag	gtc	cag	cgt	gac	atg	ctg	gcc	aag	tac	aac	gtt	gat	gat	tct	1056
Phe	Lys	Val	Gln	Arg	Asp	Met	Leu	Ala	Lys	Tyr	Asn	Val	Asp	Asp	Ser	
			340					345					350			
gga	aca	ttc	ttc	acc	aac	gat	gcg	ttc	tgg	tct	gtc	cca	ggg	gac	cca	1104
Gly	Thr	Phe	Phe	Thr	Asn	Asp	Ala	Phe	Trp	Ser	Val	Pro	Gly	Asp	Pro	
		355					360					365				
act	gca	gcg	gag	ggc	cgc	cag	gaa	ctt	aag	cag	cct	cct	tac	tac	gtg	1152
Thr	Ala	Ala	Glu	Gly	Arg	Gln	Glu	Leu	Lys	Gln	Pro	Pro	Tyr	Tyr	Val	
	370					375					380					
gtg	gca	gca	gac	cca	gag	acc	ggg	gag	tcc	agc	ttc	cag	ctg	atc	acc	1200
Val	Ala	Ala	Asp	Pro	Glu	Thr	Gly	Glu	Ser	Ser	Phe	Gln	Leu	Ile	Thr	
385					390					395					400	
ccg	ttc	cgt	gga	ctt	cag	cgc	gag	tac	ctc	tct	gca	cac	atg	tct	gcg	1248
Pro	Phe	Arg	Gly	Leu	Gln	Arg	Glu	Tyr	Leu	Ser	Ala	His	Met	Ser	Ala	
				405					410					415		
tcg	tct	gat	cca	gtt	acc	tac	ggg	gaa	atc	act	gtt	cgt	gtg	ctg	cct	1296
Ser	Ser	Asp	Pro	Val	Thr	Tyr	Gly	Glu	Ile	Thr	Val	Arg	Val	Leu	Pro	
			420					425					430			
acc	gat	tct	gtg	acc	cag	ggg	cca	aag	cag	gcc	cag	gat	gcg	atg	atg	1344
Thr	Asp	Ser	Val	Thr	Gln	Gly	Pro	Lys	Gln	Ala	Gln	Asp	Ala	Met	Met	
		435					440					445				
tca	tct	gac	cag	gtt	gct	cag	gac	caa	aca	ctg	tgg	cgt	gga	tcg	aac	1392
Ser	Ser	Asp	Gln	Val	Ala	Gln	Asp	Gln	Thr	Leu	Trp	Arg	Gly	Ser	Asn	

450 455 460
 gat ctg cac aac gga aac ctg ttg acc ttg cca gtt ggt ggc gga gag 1440
 Asp Leu His Asn Gly Asn Leu Leu Thr Leu Pro Val Gly Gly Gly Glu
 465 470 475 480
 atc ctc tac gtt gag ccg att tac tcg cag cgc aag gat cag gca tcg 1488
 Ile Leu Tyr Val Glu Pro Ile Tyr Ser Gln Arg Lys Asp Gln Ala Ser
 485 490 495
 gcc ttc ccg aag ctt ctg cgc gtg ctg gtc ttc tac aag ggt cag gtt 1536
 Ala Phe Pro Lys Leu Leu Arg Val Leu Val Phe Tyr Lys Gly Gln Val
 500 505 510
 ggt tac gca cca acg atc gct gaa gcc cta tcg cag gtc ggc att gat 1584
 Gly Tyr Ala Pro Thr Ile Ala Glu Ala Leu Ser Gln Val Gly Ile Asp
 515 520 525
 ccg aag gaa gcg cag gac atc gaa gag gta gat ggc acc gct acg acg 1632
 Pro Lys Glu Ala Gln Asp Ile Glu Glu Val Asp Gly Thr Ala Thr Thr
 530 535 540
 cca tcg act gat gag act gac act gac act gat cag cct gca acc gaa 1680
 Pro Ser Thr Asp Glu Thr Asp Thr Asp Thr Asp Gln Pro Ala Thr Glu
 545 550 555 560
 acc cca act gca cca gtg agt gag gcg gaa gga atc gcg gcc atc aac 1728
 Thr Pro Thr Ala Pro Val Ser Glu Ala Glu Gly Ile Ala Ala Ile Asn
 565 570 575
 gat gcg ttg agc aac ctt gaa gct gct cgc gat agc tct ttc gaa gag 1776
 Asp Ala Leu Ser Asn Leu Glu Ala Ala Arg Asp Ser Ser Phe Glu Glu
 580 585 590
 tat ggt cgt gca ctc gat gcg ctt gat cgt gcc gtc gat agc tac cag 1824
 Tyr Gly Arg Ala Leu Asp Ala Leu Asp Arg Ala Val Asp Ser Tyr Gln
 595 600 605
 tcc gca cag tagcggttga gtaaacagcc cga 1856
 Ser Ala Gln
 610

<210> 436

<211> 611

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 436

Asp Pro Gln Ile Leu Ser Pro Thr Phe Thr Gln Gln Gln Gln Leu Arg
 1 5 10 15
 Asn Phe Tyr Gly Phe Pro Asp Gln Leu Ala Met Asp Arg Phe Glu Val
 20 25 30
 Asp Gly Lys Leu Arg Asp Phe Val Val Ala Ala Arg Glu Leu Asp Pro
 35 40 45
 Asn Ala Leu Gln Gln Asn Gln Gln Asp Trp Ile Asn Arg His Thr Val
 50 55 60

Tyr Thr His Gly Asn Gly Phe Ile Ala Ala Gln Ala Asn Gln Val Asp
 65 70 75 80
 Glu Val Ala Arg Asp Val Gly Ser Thr Arg Gly Gly Tyr Pro Val Tyr
 85 90 95
 Thr Val Ser Asp Leu Gln Ser Asn Ala Arg Ala Ala Glu Ser Glu Asp
 100 105 110
 Ala Glu Glu Leu Gly Ile Lys Val Asp Glu Pro Arg Val Tyr Tyr Gly
 115 120 125
 Pro Leu Ile Ala Ser Ala Thr Asp Gly Ala Asp Tyr Ala Ile Val Gly
 130 135 140
 Asp Thr Gly Asp Gly Pro Val Glu Tyr Asp Thr Asp Thr Ser Ser Tyr
 145 150 155 160
 Thr Tyr Glu Gly Ala Gly Gly Val Asp Ile Gly Asn Met Val Asn Arg
 165 170 175
 Ala Met Phe Ala Leu Arg Tyr Gln Glu Met Asn Met Leu Leu Ser Asp
 180 185 190
 Arg Val Gly Ser Glu Ser Lys Ile Leu Phe Glu Arg Asp Pro Arg Ser
 195 200 205
 Arg Val Glu Lys Val Ala Pro Trp Leu Thr Thr Asp Ser Lys Thr Tyr
 210 215 220
 Pro Thr Val Ile Asp Gly Arg Ile Lys Trp Ile Val Asp Gly Tyr Thr
 225 230 235 240
 Thr Leu Asp Ser Leu Pro Tyr Ser Thr Arg Thr Ser Leu Thr Glu Ala
 245 250 255
 Thr Gln Asp Ala Val Met Pro Asp Gly Thr Pro Gln Pro Leu Ile Thr
 260 265 270
 Asp Arg Val Gly Tyr Ile Arg Asn Ser Val Lys Ala Val Val Asp Ala
 275 280 285
 Tyr Asp Gly Thr Val Glu Leu Tyr Glu Phe Asp Thr Glu Asp Pro Val
 290 295 300
 Leu Lys Ala Trp Arg Gly Val Phe Pro Asp Thr Val Lys Asp Gly Ser
 305 310 315 320
 Glu Ile Ser Asp Glu Leu Arg Ala His Leu Arg Tyr Pro Glu Asp Leu
 325 330 335
 Phe Lys Val Gln Arg Asp Met Leu Ala Lys Tyr Asn Val Asp Asp Ser
 340 345 350
 Gly Thr Phe Phe Thr Asn Asp Ala Phe Trp Ser Val Pro Gly Asp Pro
 355 360 365
 Thr Ala Ala Glu Gly Arg Gln Glu Leu Lys Gln Pro Pro Tyr Tyr Val
 370 375 380
 Val Ala Ala Asp Pro Glu Thr Gly Glu Ser Ser Phe Gln Leu Ile Thr

385	390	395	400
Pro Phe Arg Gly Leu Gln Arg Glu Tyr Leu Ser Ala His Met Ser Ala	405	410	415
Ser Ser Asp Pro Val Thr Tyr Gly Glu Ile Thr Val Arg Val Leu Pro	420	425	430
Thr Asp Ser Val Thr Gln Gly Pro Lys Gln Ala Gln Asp Ala Met Met	435	440	445
Ser Ser Asp Gln Val Ala Gln Asp Gln Thr Leu Trp Arg Gly Ser Asn	450	455	460
Asp Leu His Asn Gly Asn Leu Leu Thr Leu Pro Val Gly Gly Gly Glu	465	470	475
Ile Leu Tyr Val Glu Pro Ile Tyr Ser Gln Arg Lys Asp Gln Ala Ser	485	490	495
Ala Phe Pro Lys Leu Leu Arg Val Leu Val Phe Tyr Lys Gly Gln Val	500	505	510
Gly Tyr Ala Pro Thr Ile Ala Glu Ala Leu Ser Gln Val Gly Ile Asp	515	520	525
Pro Lys Glu Ala Gln Asp Ile Glu Glu Val Asp Gly Thr Ala Thr Thr	530	535	540
Pro Ser Thr Asp Glu Thr Asp Thr Asp Thr Asp Gln Pro Ala Thr Glu	545	550	555
Thr Pro Thr Ala Pro Val Ser Glu Ala Glu Gly Ile Ala Ala Ile Asn	565	570	575
Asp Ala Leu Ser Asn Leu Glu Ala Ala Arg Asp Ser Ser Phe Glu Glu	580	585	590
Tyr Gly Arg Ala Leu Asp Ala Leu Asp Arg Ala Val Asp Ser Tyr Gln	595	600	605
Ser Ala Gln	610		

<210> 437

<211> 867

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(844)

<223> RXS01677

<400> 437

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agttgagggc ttcccagcag ggatgggttaa ggagaattca gtg aac caa cag agt 115
Val Asn Gln Gln Ser

1

5

aaa aag tgg ctc gta ccg aca ctg gtc gtc atc att gca gtg ctc ctc	163
Lys Lys Trp Leu Val Pro Thr Leu Val Val Ile Ile Ala Val Leu Leu	
10 15 20	
atc gca gtt gtt ctg ttg atg tac cga gga aat gcg agt gat acg gcc	211
Ile Ala Val Val Leu Leu Met Tyr Arg Gly Asn Ala Ser Asp Thr Ala	
25 30 35	
gag ggc gtt tca gcc gct gcg act tcg gac tcg gct gct gct tcg act	259
Glu Gly Val Ser Ala Ala Ala Thr Ser Asp Ser Ala Ala Ala Ser Thr	
40 45 50	
gct gct tcg ggt tcc gct tct ggt gct gcg gac tcc gat ctg acc agc	307
Ala Ala Ser Gly Ser Ala Ser Gly Ala Ala Asp Ser Asp Leu Thr Ser	
55 60 65	
gtg gaa gca cgc gac cct tcc gac cct gtt gcg gtg gga gac gtt gat	355
Val Glu Ala Arg Asp Pro Ser Asp Pro Val Ala Val Gly Asp Val Asp	
70 75 80 85	
gca cct gtt ggg tta gtg gtg ttt tcc gac tac caa tgc ccg ttc tgt	403
Ala Pro Val Gly Leu Val Val Phe Ser Asp Tyr Gln Cys Pro Phe Cys	
90 95 100	
gca aag tgg agc gat gaa acc ctg cca cag atg atg aag cat gtg gaa	451
Ala Lys Trp Ser Asp Glu Thr Leu Pro Gln Met Met Lys His Val Glu	
105 110 115	
gat gga aac ctc cgc att gaa tgg cgt gaa gtg aac atc ttt gga gaa	499
Asp Gly Asn Leu Arg Ile Glu Trp Arg Glu Val Asn Ile Phe Gly Glu	
120 125 130	
cca tct gag cgt gga gct cgc gcg gca tac gct gcg ggt ttg cag gac	547
Pro Ser Glu Arg Gly Ala Arg Ala Ala Tyr Ala Ala Gly Leu Gln Asp	
135 140 145	
gca tac ttg gaa tac cac aac gca ctc ttt gcc aac ggt gaa aaa ccc	595
Ala Tyr Leu Glu Tyr His Asn Ala Leu Phe Ala Asn Gly Glu Lys Pro	
150 155 160 165	
agc gaa gac ctg ctc agc gaa gag gga ctt att aag ctt gct ggt gac	643
Ser Glu Asp Leu Leu Ser Glu Glu Gly Leu Ile Lys Leu Ala Gly Asp	
170 175 180	
ctt gga cta gac gaa tcg aaa ttc act gcc gat ttc caa tcc cct gaa	691
Leu Gly Leu Asp Glu Ser Lys Phe Thr Ala Asp Phe Gln Ser Pro Glu	
185 190 195	
act gca gtc gca att gcg caa cat caa cag ctg gga atc gat ctt ggc	739
Thr Ala Val Ala Ile Ala Gln His Gln Gln Leu Gly Ile Asp Leu Gly	
200 205 210	
gcc tac tcc acc cca gct ttc ctc cta ggt ggc cag cca atc atg ggc	787
Ala Tyr Ser Thr Pro Ala Phe Leu Leu Gly Gly Gln Pro Ile Met Gly	
215 220 225	
gct cag cct gct tct gta ttt gaa gcc gcc ttc gag caa gca ctg gca	835
Ala Gln Pro Ala Ser Val Phe Glu Ala Ala Phe Glu Gln Ala Leu Ala	
230 235 240 245	

gcg aaa gaa taaaccgtgg atgtcggcct agt
Ala Lys Glu

867

<210> 438

<211> 248

<212> PRT

<213> Corynebacterium glutamicum

<400> 438

Val	Asn	Gln	Gln	Ser	Lys	Lys	Trp	Leu	Val	Pro	Thr	Leu	Val	Val	Ile
1				5					10					15	
Ile	Ala	Val	Leu	Leu	Ile	Ala	Val	Val	Leu	Leu	Met	Tyr	Arg	Gly	Asn
			20					25						30	
Ala	Ser	Asp	Thr	Ala	Glu	Gly	Val	Ser	Ala	Ala	Ala	Thr	Ser	Asp	Ser
		35					40					45			
Ala	Ala	Ala	Ser	Thr	Ala	Ala	Ser	Gly	Ser	Ala	Ser	Gly	Ala	Ala	Asp
	50					55					60				
Ser	Asp	Leu	Thr	Ser	Val	Glu	Ala	Arg	Asp	Pro	Ser	Asp	Pro	Val	Ala
65					70				75						80
Val	Gly	Asp	Val	Asp	Ala	Pro	Val	Gly	Leu	Val	Val	Phe	Ser	Asp	Tyr
				85					90					95	
Gln	Cys	Pro	Phe	Cys	Ala	Lys	Trp	Ser	Asp	Glu	Thr	Leu	Pro	Gln	Met
			100					105					110		
Met	Lys	His	Val	Glu	Asp	Gly	Asn	Leu	Arg	Ile	Glu	Trp	Arg	Glu	Val
		115					120					125			
Asn	Ile	Phe	Gly	Glu	Pro	Ser	Glu	Arg	Gly	Ala	Arg	Ala	Ala	Tyr	Ala
	130					135					140				
Ala	Gly	Leu	Gln	Asp	Ala	Tyr	Leu	Glu	Tyr	His	Asn	Ala	Leu	Phe	Ala
145					150					155					160
Asn	Gly	Glu	Lys	Pro	Ser	Glu	Asp	Leu	Leu	Ser	Glu	Glu	Gly	Leu	Ile
				165				170						175	
Lys	Leu	Ala	Gly	Asp	Leu	Gly	Leu	Asp	Glu	Ser	Lys	Phe	Thr	Ala	Asp
			180					185					190		
Phe	Gln	Ser	Pro	Glu	Thr	Ala	Val	Ala	Ile	Ala	Gln	His	Gln	Gln	Leu
		195					200					205			
Gly	Ile	Asp	Leu	Gly	Ala	Tyr	Ser	Thr	Pro	Ala	Phe	Leu	Leu	Gly	Gly
	210					215					220				
Gln	Pro	Ile	Met	Gly	Ala	Gln	Pro	Ala	Ser	Val	Phe	Glu	Ala	Ala	Phe
225					230					235					240
Glu	Gln	Ala	Leu	Ala	Ala	Lys	Glu								
					245										

<210> 439

<211> 1095
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1072)
 <223> RXS02932

<400> 439

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agcagcacca tttcagtttt aactttcttg gagttttcta gtg tcc aaa aca gaa 115
                               Val Ser Lys Thr Glu
                               1      5

gaa ggc cgt tca gcg gcc ata att att tac gcg ttt cca act ttc att 163
Glu Gly Arg Ser Ala Ala Ile Ile Ile Tyr Ala Phe Pro Thr Phe Ile
                               10      15      20

ctg ctg ggc gcg atc att gcg ttt atc ttc ccg gaa cca ttc att ccg 211
Leu Leu Gly Ala Ile Ile Ala Phe Ile Phe Pro Glu Pro Phe Ile Pro
                               25      30      35

ctg aca aac tac att aat atc ttc ctc acg atc atc atg ttc acc atg 259
Leu Thr Asn Tyr Ile Asn Ile Phe Leu Thr Ile Ile Met Phe Thr Met
                               40      45      50

ggc ttg acc ttg acg gtg ccc gat ttt cag atg gtg ctt aaa cgt cca 307
Gly Leu Thr Leu Thr Val Pro Asp Phe Gln Met Val Leu Lys Arg Pro
                               55      60      65

ctg cct atc ttg atc ggt gta gta gcg cag ttt gtc atc atg cca ttc 355
Leu Pro Ile Leu Ile Gly Val Val Ala Gln Phe Val Ile Met Pro Phe
                               70      75      80      85

ctg gcg atc gtg gtt gcg aaa atg ttc aac ctc aac cca gca ctc gcc 403
Leu Ala Ile Val Val Ala Lys Met Phe Asn Leu Asn Pro Ala Leu Ala
                               90      95      100

gtt ggc ctt ctc atg ctg gga tcc gtt ccg ggt ggc acc tcc tcc aat 451
Val Gly Leu Leu Met Leu Gly Ser Val Pro Gly Gly Thr Ser Ser Asn
                               105      110      115

gtg att gcg ttt ctc gcc cga gga gat gtc gcg cta tcg gtc acc atg 499
Val Ile Ala Phe Leu Ala Arg Gly Asp Val Ala Leu Ser Val Thr Met
                               120      125      130

acc tct gtg tcc acc att gtt tcc cca atc atg acg cct ttc ctc atg 547
Thr Ser Val Ser Thr Ile Val Ser Pro Ile Met Thr Pro Phe Leu Met
                               135      140      145

ctc atg ctg gca ggt act gaa acc gcc gtc gat ggt gga ggc atg gcg 595
Leu Met Leu Ala Gly Thr Glu Thr Ala Val Asp Gly Gly Gly Met Ala
                               150      155      160      165

tgg act ttg gta caa aca gtg ctg ctg cct gtg atc atc ggc cta gtt 643
Trp Thr Leu Val Gln Thr Val Leu Leu Pro Val Ile Ile Gly Leu Val
                               170      175      180

ctg cgt gtc ttc ttg aac aag tgg atc gac aag att ttg ccg atc ctt 691

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Leu Arg Val Phe Leu Asn Lys Trp Ile Asp Lys Ile Leu Pro Ile Leu
 185 190 195
 cct tat ctc tcc atc ctc ggt atc ggt ggc gtg gtg ttc ggc gca gtc 739
 Pro Tyr Leu Ser Ile Leu Gly Ile Gly Gly Val Val Phe Gly Ala Val
 200 205 210
 gca gcc aac gcg gaa cga ctc gtg tct gtc gga ctc atc gtg ttc gtt 787
 Ala Ala Asn Ala Glu Arg Leu Val Ser Val Gly Leu Ile Val Phe Val
 215 220 225
 gca gtt atc gtg cac aac gta ctt gga tac gtt gtg gga tac ctc acc 835
 Ala Val Ile Val His Asn Val Leu Gly Tyr Val Val Gly Tyr Leu Thr
 230 235 240 245
 ggc cgt gta ttc aaa ttc cca gaa gca gca aac cgc acc atg gcg att 883
 Gly Arg Val Phe Lys Phe Pro Glu Ala Ala Asn Arg Thr Met Ala Ile
 250 255 260
 gaa atc gga acc caa tcc gca ggc ctc gca tcg gga atg gca gga cga 931
 Glu Ile Gly Thr Gln Ser Ala Gly Leu Ala Ser Gly Met Ala Gly Arg
 265 270 275
 ttc ttc acc cca gaa gca gcc ctt cca ggt gct gtc gct gcc ttg gtc 979
 Phe Phe Thr Pro Glu Ala Ala Leu Pro Gly Ala Val Ala Ala Leu Val
 280 285 290
 cac aac atc acc ggc gca gtt tat gtt ggg ctg gta cga aac agg cct 1027
 His Asn Ile Thr Gly Ala Val Tyr Val Gly Leu Val Arg Asn Arg Pro
 295 300 305
 ttg act aag gca tca agg aag aag gaa tcc gtc gcg gtt tcc agc 1072
 Leu Thr Lys Ala Ser Arg Lys Lys Glu Ser Val Ala Val Ser Ser
 310 315 320
 taacttattt gctgcccgtt aga 1095

<210> 440

<211> 324

<212> PRT

<213> Corynebacterium glutamicum

<400> 440

Val Ser Lys Thr Glu Glu Gly Arg Ser Ala Ala Ile Ile Ile Tyr Ala
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 Phe Pro Thr Phe Ile Leu Leu Gly Ala Ile Ile Ala Phe Ile Phe Pro
 20 25 30
 Glu Pro Phe Ile Pro Leu Thr Asn Tyr Ile Asn Ile Phe Leu Thr Ile
 35 40 45
 Ile Met Phe Thr Met Gly Leu Thr Leu Thr Val Pro Asp Phe Gln Met
 50 55 60
 Val Leu Lys Arg Pro Leu Pro Ile Leu Ile Gly Val Val Ala Gln Phe
 65 70 75 80
 Val Ile Met Pro Phe Leu Ala Ile Val Val Ala Lys Met Phe Asn Leu
 85 90 95

Asn Pro Ala Leu Ala Val Gly Leu Leu Met Leu Gly Ser Val Pro Gly
 100 105 110
 Gly Thr Ser Ser Asn Val Ile Ala Phe Leu Ala Arg Gly Asp Val Ala
 115 120 125
 Leu Ser Val Thr Met Thr Ser Val Ser Thr Ile Val Ser Pro Ile Met
 130 135 140
 Thr Pro Phe Leu Met Leu Met Leu Ala Gly Thr Glu Thr Ala Val Asp
 145 150 155 160
 Gly Gly Gly Met Ala Trp Thr Leu Val Gln Thr Val Leu Leu Pro Val
 165 170 175
 Ile Ile Gly Leu Val Leu Arg Val Phe Leu Asn Lys Trp Ile Asp Lys
 180 185 190
 Ile Leu Pro Ile Leu Pro Tyr Leu Ser Ile Leu Gly Ile Gly Gly Val
 195 200 205
 Val Phe Gly Ala Val Ala Ala Asn Ala Glu Arg Leu Val Ser Val Gly
 210 215 220
 Leu Ile Val Phe Val Ala Val Ile Val His Asn Val Leu Gly Tyr Val
 225 230 235 240
 Val Gly Tyr Leu Thr Gly Arg Val Phe Lys Phe Pro Glu Ala Ala Asn
 245 250 255
 Arg Thr Met Ala Ile Glu Ile Gly Thr Gln Ser Ala Gly Leu Ala Ser
 260 265 270
 Gly Met Ala Gly Arg Phe Phe Thr Pro Glu Ala Ala Leu Pro Gly Ala
 275 280 285
 Val Ala Ala Leu Val His Asn Ile Thr Gly Ala Val Tyr Val Gly Leu
 290 295 300
 Val Arg Asn Arg Pro Leu Thr Lys Ala Ser Arg Lys Lys Glu Ser Val
 305 310 315 320
 Ala Val Ser Ser

<210> 441

<211> 844

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(844)

<223> FRXA02402

<400> 441

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agcagacca ttctagtttt aactttcttg gagttttcta gtg tcc aaa aca gaa 115

	Val	Ser	Lys	Thr	Glu	
	1				5	
gaa ggc cgt tca gcg gcc ata att att tac gcg ttt cca act ttc att						163
Glu Gly Arg Ser Ala Ala Ile Ile Ile Tyr Ala Phe Pro Thr Phe Ile						
	10			15	20	
ctg ctg ggc gcg atc att gcg ttt atc ttc ccg gaa cca ttc att ccg						211
Leu Leu Gly Ala Ile Ile Ala Phe Ile Phe Pro Glu Pro Phe Ile Pro						
	25			30	35	
ctg aca aac tac att aat atc ttc ctc acg atc atc atg ttc acc atg						259
Leu Thr Asn Tyr Ile Asn Ile Phe Leu Thr Ile Ile Met Phe Thr Met						
	40			45	50	
ggt ttg acc ttg acg gtg ccc gat ttt cag atg gtg ctt aaa cgt cca						307
Gly Leu Thr Leu Thr Val Pro Asp Phe Gln Met Val Leu Lys Arg Pro						
	55			60	65	
ctg cct atc ttg atc ggt gta gta gcg cag ttt gtc atc atg cca ttc						355
Leu Pro Ile Leu Ile Gly Val Val Ala Gln Phe Val Ile Met Pro Phe						
	70			75	80	85
ctg gcg atc gtg gtt gcg aaa atg ttc aac ctc aac cca gca ctc gcc						403
Leu Ala Ile Val Val Ala Lys Met Phe Asn Leu Asn Pro Ala Leu Ala						
	90			95	100	
gtt ggc ctt ctc atg ctg gga tcc gtt ccg ggt ggc acc tcc tcc aat						451
Val Gly Leu Leu Met Leu Gly Ser Val Pro Gly Gly Thr Ser Ser Asn						
	105			110	115	
gtg att gcg ttt ctc gcc cga gga gat gtc gcg cta tgc gtc acc atg						499
Val Ile Ala Phe Leu Ala Arg Gly Asp Val Ala Leu Ser Val Thr Met						
	120			125	130	
acc tct gtg tcc acc att gtt tcc cca atc atg acg cct ttc ctc atg						547
Thr Ser Val Ser Thr Ile Val Ser Pro Ile Met Thr Pro Phe Leu Met						
	135			140	145	
ctc atg ctg gca ggt act gaa acc gcc gtc gat ggt gga ggc atg gcg						595
Leu Met Leu Ala Gly Thr Glu Thr Ala Val Asp Gly Gly Gly Met Ala						
	150			155	160	165
tgg act ttg gta caa aca gtg ctg ctg cct gtg atc atc ggc cta gtt						643
Trp Thr Leu Val Gln Thr Val Leu Leu Pro Val Ile Ile Gly Leu Val						
	170			175	180	
ctg cgt gtc ttc ttg aac aag tgg atc gac aag att ttg ccg atc ctt						691
Leu Arg Val Phe Leu Asn Lys Trp Ile Asp Lys Ile Leu Pro Ile Leu						
	185			190	195	
cct tat ctc tcc atc ctc ggt atc ggt ggc gtg gtg ttc ggc gca gtc						739
Pro Tyr Leu Ser Ile Leu Gly Ile Gly Gly Val Val Phe Gly Ala Val						
	200			205	210	
gca gcc aac gcg gaa cga ctc gtg tct gtc gga ctc atc gtg ttc gtt						787
Ala Ala Asn Ala Glu Arg Leu Val Ser Val Gly Leu Ile Val Phe Val						
	215			220	225	
gca gtt atc gtg cac aac gta ctt gga tac gtt gtg gga tac ctc acc						835
Ala Val Ile Val His Asn Val Leu Gly Tyr Val Val Gly Tyr Leu Thr						

230

235

240

245

ggc cgt gta
Gly Arg Val

844

<210> 442

<211> 248

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 442

Val Ser Lys Thr Glu Glu Gly Arg Ser Ala Ala Ile Ile Ile Tyr Ala
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Phe Pro Thr Phe Ile Leu Leu Gly Ala Ile Ile Ala Phe Ile Phe Pro
20 25 30

Glu Pro Phe Ile Pro Leu Thr Asn Tyr Ile Asn Ile Phe Leu Thr Ile
35 40 45

Ile Met Phe Thr Met Gly Leu Thr Leu Thr Val Pro Asp Phe Gln Met
50 55 60

Val Leu Lys Arg Pro Leu Pro Ile Leu Ile Gly Val Val Ala Gln Phe
65 70 75 80

Val Ile Met Pro Phe Leu Ala Ile Val Val Ala Lys Met Phe Asn Leu
85 90 95

Asn Pro Ala Leu Ala Val Gly Leu Leu Met Leu Gly Ser Val Pro Gly
100 105 110

Gly Thr Ser Ser Asn Val Ile Ala Phe Leu Ala Arg Gly Asp Val Ala
115 120 125

Leu Ser Val Thr Met Thr Ser Val Ser Thr Ile Val Ser Pro Ile Met
130 135 140

Thr Pro Phe Leu Met Leu Met Leu Ala Gly Thr Glu Thr Ala Val Asp
145 150 155 160

Gly Gly Gly Met Ala Trp Thr Leu Val Gln Thr Val Leu Leu Pro Val
165 170 175

Ile Ile Gly Leu Val Leu Arg Val Phe Leu Asn Lys Trp Ile Asp Lys
180 185 190

Ile Leu Pro Ile Leu Pro Tyr Leu Ser Ile Leu Gly Ile Gly Gly Val
195 200 205

Val Phe Gly Ala Val Ala Ala Asn Ala Glu Arg Leu Val Ser Val Gly
210 215 220

Leu Ile Val Phe Val Ala Val Ile Val His Asn Val Leu Gly Tyr Val
225 230 235 240

Val Gly Tyr Leu Thr Gly Arg Val
245

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<220>
<221> CDS
<222> (101)..(1366)
<223> RXS00654
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<400> 443																
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tgctgtgaag	tgccaäcctgt	ttggaaaggc	gaacacgata	gtg	ctc	gat	att	ttg	115							
				Val	Leu	Asp	Ile	Leu								
				1				5								
att	tac	cgc	gtg	tct	gga	gtg	atg	aag	ctg	tgg	cac	ctg	ctt	ctt	cac	163
Ile	Tyr	Pro	Val	Ser	Gly	Val	Met	Lys	Leu	Trp	His	Leu	Leu	Leu	His	
				10					15					20		
aac	gtt	gcg	ggt	ttg	gac	gat	tca	ctg	gcg	tgg	ttc	ttt	tcc	ctt	ttc	211
Asn	Val	Ala	Gly	Leu	Asp	Asp	Ser	Leu	Ala	Trp	Phe	Phe	Ser	Leu	Phe	
			25					30					35			
ggc	ctt	gtc	atc	acg	atc	cgt	gca	att	atc	gcg	cct	ttc	acc	tgg	cag	259
Gly	Leu	Val	Ile	Thr	Ile	Arg	Ala	Ile	Ile	Ala	Pro	Phe	Thr	Trp	Gln	
		40					45					50				
atg	tat	aag	tcg	ggc	cgc	act	gcc	gca	cat	att	cgt	cct	cac	cgc	gct	307
Met	Tyr	Lys	Ser	Gly	Arg	Thr	Ala	Ala	His	Ile	Arg	Pro	His	Arg	Ala	
	55					60					65					
gcg	ctc	cgc	gaa	gaa	tac	aag	gga	aag	tac	gat	gaa	gcg	tcc	att	cgc	355
Ala	Leu	Arg	Glu	Glu	Tyr	Lys	Gly	Lys	Tyr	Asp	Glu	Ala	Ser	Ile	Arg	
70					75				80					85		
gag	ttg	cag	aag	cgc	cag	aat	gat	ttg	aat	aag	gaa	tac	ggc	att	aac	403
Glu	Leu	Gln	Lys	Arg	Gln	Asn	Asp	Leu	Asn	Lys	Glu	Tyr	Gly	Ile	Asn	
				90					95					100		
cgc	ctg	gca	ggt	tgt	gtg	cct	ggg	ctg	atc	cag	ata	cgc	att	gtc	ctt	451
Pro	Leu	Ala	Gly	Cys	Val	Pro	Gly	Leu	Ile	Gln	Ile	Pro	Ile	Val	Leu	
			105					110					115			
ggt	ctt	tac	tgg	gca	ctt	ctc	cgc	atg	gct	cgc	cct	gaa	ggt	ggt	ttg	499
Gly	Leu	Tyr	Trp	Ala	Leu	Leu	Arg	Met	Ala	Arg	Pro	Glu	Gly	Gly	Leu	
		120					125					130				
gaa	aat	ccc	gtc	ttc	cag	tcg	atc	ggc	ttc	cta	act	cct	gag	gaa	gtg	547
Glu	Asn	Pro	Val	Phe	Gln	Ser	Ile	Gly	Phe	Leu	Thr	Pro	Glu	Glu	Val	
	135					140					145					
gaa	tct	ttc	ctc	gct	ggt	cgc	gtg	agc	aat	gtg	cct	ctg	ccc	gct	tat	595
Glu	Ser	Phe	Leu	Ala	Gly	Arg	Val	Ser	Asn	Val	Pro	Leu	Pro	Ala	Tyr	
150					155				160						165	
gtt	tcg	atg	ccc	act	gag	cag	cta	aaa	tat	ttg	agc	acc	acg	cag	gcg	643
Val	Ser	Met	Pro	Thr	Glu	Gln	Leu	Lys	Tyr	Leu	Ser	Thr	Thr	Gln	Ala	
				170					175					180		

gaa gtt ctt agt ttc gtt ttg cca ctg ttc atc aca gcc gca atc ctc	691
Glu Val Leu Ser Phe Val Leu Pro Leu Phe Ile Thr Ala Ala Ile Leu	
185 190 195	
acc gca atc aac atg gcg atg tcc atg tac cgc agc ttc caa acc aac	739
Thr Ala Ile Asn Met Ala Met Ser Met Tyr Arg Ser Phe Gln Thr Asn	
200 205 210	
gat tac gca tcc gga ttc tct aac ggc atg ctg aag ttc atg atc gtg	787
Asp Tyr Ala Ser Gly Phe Ser Asn Gly Met Leu Lys Phe Met Ile Val	
215 220 225	
atg tcg atc ctc gcg ccg atc ttc cca ctg tcc ctt ggc ctc aca gga	835
Met Ser Ile Leu Ala Pro Ile Phe Pro Leu Ser Leu Gly Leu Thr Gly	
230 235 240 245	
cca ttc ccc aca gca atc gca ctc tat tgg gtc agc aac aac ctg tgg	883
Pro Phe Pro Thr Ala Ile Ala Leu Tyr Trp Val Ser Asn Asn Leu Trp	
250 255 260	
acg ctc ctc caa aca atc atc atg atg gtc att ttg gaa cgc aaa tac	931
Thr Leu Leu Gln Thr Ile Ile Met Met Val Ile Leu Glu Arg Lys Tyr	
265 270 275	
cca ctt acc gac gat ttc aaa gtg cac cac cta gag cag cgc gac atc	979
Pro Leu Thr Asp Asp Phe Lys Val His His Leu Glu Gln Arg Asp Ile	
280 285 290	
tac cgc gca aaa caa aaa gaa aag cgc atc ttc ctg tgg aca cga cgc	1027
Tyr Arg Ala Lys Gln Lys Glu Lys Arg Ile Phe Leu Trp Thr Arg Arg	
295 300 305	
aaa aac cgc gcc ctg atg att ctc acc cca tgg aac gcc tca acg ctt	1075
Lys Asn Arg Ala Leu Met Ile Leu Thr Pro Trp Asn Ala Ser Thr Leu	
310 315 320 325	
cac gca aca aac gtg gaa ctc acc aaa acc cgt act gcc gaa atc aac	1123
His Ala Thr Asn Val Glu Leu Thr Lys Thr Arg Thr Ala Glu Ile Asn	
330 335 340	
gaa gca aaa cag gcc cgc aaa gaa atc gcg aac aag agg cgc gaa acg	1171
Glu Ala Lys Gln Ala Arg Lys Glu Ile Ala Asn Lys Arg Arg Glu Thr	
345 350 355	
caa cgt gaa atg aac cgc gcc gcc atg cag cgc tta aag cag cgt cgc	1219
Gln Arg Glu Met Asn Arg Ala Ala Met Gln Arg Leu Lys Gln Arg Arg	
360 365 370	
gct gag gtt aaa gct aaa aag aag ggg ctt atc gac gcc tcc ccc aac	1267
Ala Glu Val Lys Ala Lys Lys Lys Gly Leu Ile Asp Ala Ser Pro Asn	
375 380 385	
gaa gat acc cct tcg gaa aat gaa gaa act aaa ttg agt agt ccg cag	1315
Glu Asp Thr Pro Ser Glu Asn Glu Glu Thr Lys Leu Ser Ser Pro Gln	
390 395 400 405	
gtg gag ccg aca aca act gcc gag cca aat cgc gag ccg tct caa gag	1363
Val Glu Pro Thr Thr Thr Ala Glu Pro Asn Arg Glu Pro Ser Gln Glu	
410 415 420	

gac tgatgttgatgac gaccaatcga gat
Asp

1389

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<211> 422

<212> PRT

<213> Corynebacterium glutamicum

<400> 444

Val Leu Asp Ile Leu Ile Tyr Pro Val Ser Gly Val Met Lys Leu Trp
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His Leu Leu Leu His Asn Val Ala Gly Leu Asp Asp Ser Leu Ala Trp
20 25 30

Phe Phe Ser Leu Phe Gly Leu Val Ile Thr Ile Arg Ala Ile Ile Ala
35 40 45

Pro Phe Thr Trp Gln Met Tyr Lys Ser Gly Arg Thr Ala Ala His Ile
50 55 60

Arg Pro His Arg Ala Ala Leu Arg Glu Glu Tyr Lys Gly Lys Tyr Asp
65 70 75 80

Glu Ala Ser Ile Arg Glu Leu Gln Lys Arg Gln Asn Asp Leu Asn Lys
85 90 95

Glu Tyr Gly Ile Asn Pro Leu Ala Gly Cys Val Pro Gly Leu Ile Gln
100 105 110

Ile Pro Ile Val Leu Gly Leu Tyr Trp Ala Leu Leu Arg Met Ala Arg
115 120 125

Pro Glu Gly Gly Leu Glu Asn Pro Val Phe Gln Ser Ile Gly Phe Leu
130 135 140

Thr Pro Glu Glu Val Glu Ser Phe Leu Ala Gly Arg Val Ser Asn Val
145 150 155 160

Pro Leu Pro Ala Tyr Val Ser Met Pro Thr Glu Gln Leu Lys Tyr Leu
165 170 175

Ser Thr Thr Gln Ala Glu Val Leu Ser Phe Val Leu Pro Leu Phe Ile
180 185 190

Thr Ala Ala Ile Leu Thr Ala Ile Asn Met Ala Met Ser Met Tyr Arg
195 200 205

Ser Phe Gln Thr Asn Asp Tyr Ala Ser Gly Phe Ser Asn Gly Met Leu
210 215 220

Lys Phe Met Ile Val Met Ser Ile Leu Ala Pro Ile Phe Pro Leu Ser
225 230 235 240

Leu Gly Leu Thr Gly Pro Phe Pro Thr Ala Ile Ala Leu Tyr Trp Val
245 250 255

Ser Asn Asn Leu Trp Thr Leu Leu Gln Thr Ile Ile Met Met Val Ile
260 265 270

Leu Glu Arg Lys Tyr Pro Leu Thr Asp Asp Phe Lys Val His His Leu
 275 280 285
 Glu Gln Arg Asp Ile Tyr Arg Ala Lys Gln Lys Glu Lys Arg Ile Phe
 290 295 300
 Leu Trp Thr Arg Arg Lys Asn Arg Ala Leu Met Ile Leu Thr Pro Trp
 305 310 315 320
 Asn Ala Ser Thr Leu His Ala Thr Asn Val Glu Leu Thr Lys Thr Arg
 325 330 335
 Thr Ala Glu Ile Asn Glu Ala Lys Gln Ala Arg Lys Glu Ile Ala Asn
 340 345 350
 Lys Arg Arg Glu Thr Gln Arg Glu Met Asn Arg Ala Ala Met Gln Arg
 355 360 365
 Leu Lys Gln Arg Arg Ala Glu Val Lys Ala Lys Lys Lys Gly Leu Ile
 370 375 380
 Asp Ala Ser Pro Asn Glu Asp Thr Pro Ser Glu Asn Glu Glu Thr Lys
 385 390 395 400
 Leu Ser Ser Pro Gln Val Glu Pro Thr Thr Thr Ala Glu Pro Asn Arg
 405 410 415
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<223> Description of Artificial Sequence: primer

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18

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

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gtaaaacgac ggccagt

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